Table 1: Representative sample of very highly-abundant named genes in human and baboon CD34+ cells, by functional category.

UniGene Cluster ID	Genbank Accession #	Description	Gene name
I. Growth F	actors/Cytokines		
Hs.56023	AA262988	Brain-derived neurotrophic factor	BDNF
Hs.180577	AA496452	Granulin	GRN
Hs.251664	N54596	Insulin-like growth factor 2	1GF2
Hs.82045	AA968896	Midkine	MDK
Hs.118787	AA633901	Transforming growth factor, beta-induced	TGFBI
II. Cell Surf	ace/Receptors		
Hs.85258	AA443649	CD8 antigen, alpha polypeptide	CD8A
Hs.75626	AA136359	CD58 antigen	CD58
Hs.75564	AA456183	CD151 antigen	CD151
Hs.2175	AA443000	Colony stimulating factor 3 precursor receptor	CSF3R
Hs.110849	AA098896	Estrogen-related receptor alpha	ESRRA
Hs.89650	R68805	Integral transmembrane protein 1	ITM1
Hs.1724	AA903183	Interleukin 2 receptor, alpha	IL2RA
Hs.172689	W44701	Interleukin 3 receptor, alpha	IL3RA
Hs.47860	N63949	Neurotrophic tyrosine kinase, receptor, type 2	NTRK2
Hs.82028	AA487034	Transforming growth factor, beta receptor II	TGFBR2
III. Intracel	lular signalling mo	lecules	
Hs.166154	AA463972	jagged 2	JAG2
Hs.86859	H53703	Growth factor receptor-bound protein 7	GRB7
Hs.78793	AA447574	Protein kinase C, zeta	PRKCZ
Hs.62402	AA890663	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)	PAK1
Hs.75074	AA455056	Mitogen-activated protein kinase-activated protein kinase 2	MAPKAPK2
Hs.73799	AA490256	Guanine nucleotide binding protein, alpha inhibiting activity	GNAI3
Hs.75217	AA293050	Mitogen-activated protein kinase kinase 4	MAP2K4
Hs.138860	AA443506	Rho GTPase activating protein 1	ARHGAP1
V. Cell cyc	le proteins		
Hs.82906	AA464698	Cell division cycle 20, S.cerevisiae homolog	CDC20
Hs.153752	AA448659	Cell division cycle 25B	CDC25B
Hs.172405	T81764	Cell division cycle 27	CDC27
Hs.77550	AA459292	CDC28 protein kinase 1	CKS1
V. Apoptos	sis/Anti-apoptosis f	actors	
Hs.82890	AA455281	Defender against cell death 1	DAD1
Hs.227817	AA459263	BCL2-related protein A1	BCL2A1
VI. Cytosk	eleton/Cell matrix/.	Adhesion	
Hs.183805	AA464755	Ankyrin 1, erythrocytic	ANK1
Hs.171271	AA442092	Catenin, beta 1	CTNNB1
Hs.75617	AA430540	Collagen, type IV, alpha 2	COL4A2
Hs.71346	AA400329	Neurofilament 3 (150kD medium)	NEF3
Hs.78146	R22412	Platelet/endothelial cell adhesion molecule	PECAM1
		Tubulin, alpha 1	TUBA I

VII. Metabol			
Hs.278399	AA844818	Amylase, alpha 2A; pancreatic	AMY2A
Hs.155097	H23187	Carbonic anhydrase II	CA2
Hs.81097	AA862813	Cytochrome c oxidase subunit VIII	COX8
Hs.172690	AA456900	Diacylglycerol kinase alpha	DGKA
Hs.944	AA401111	Glucose phosphate isomerase	GPI
Hs.2795	AA489611	Lactate dehydrogenase A	LDHA
VIII. Transcr	iption factors/Ac	tivators/Inhibitors	
Hs.158195	AA250730	Heat shock transcription factor 2	HSF2
Hs.22554	AA252627	Homeo box B5	HOXB5
Hs.153837	N29376	Myeloid cell nuclear differentiation antigen	MNDA
Hs.79334	AA633811	Nuclear factor, interleukin 3 regulated	NFIL3
Hs.74002	AA495962	Nuclear receptor coactivator 1	NCOA1
Hs.192861	N71628	Spi-B transcription factor	SPI-B
Hs.3005	AA284693	Transcription factor AP-4	TFAP4

Genes highlighted in bold are known to be expressed in hematopoietic tissues

GenBank accession # specifies a cDNA from a specific IMAGE clone spotted on the GeneFilter membrane

Table 2: Selection of very highly-abundant ESTs and partially characterized cDNAs in human and baboon CD34+ Cells.

Cluster ID	accession #		Name
Hs.155545	AA423944	37 kDa leucine-rich repeat (LRR) protein	P37NB
Hs.42322	AA682795	A kinase (PRKA) anchor protein 2	AKAP2
Hs.155586	N90281	B7 protein	B7
Hs.118724	AA406285	DR1-associated protein 1 (negative cofactor 2 alpha)	DRAPI
Hs.183738	AA486435	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-deFARP)	-deFARP1
Hs.9914	AA701860	follistatin	FST
Hs.147189	R01638	HYA22 protein	HYA22
Hs.23119	AA455272	ITBA1 gene	ITBA1
Hs.20149	AA425755	leukemia associated gene 1	LEUI
Hs.118796	AA872001	Annexin A6	ANX6
Hs.102948	AA127096	enigma (LIM domain protein)	ENIGMA
Hs.41007	AA147980	HSPC158 protein	HSPC158
Hs.89650	R68805	integral membrane protein 1	ITMI
Hs.69855	AA504682	NRAS-related gene	D1S155E
Hs.172589	AA485992	nuclear phosphoprotein similar to S. cerevisiae PWP1	PWP1
Hs.2815	N63968	POU domain, class 6, transcription factor 1	POUGF1
Hs.59545	AA195036	ring finger protein 15	RNF15
Hs.172052	AA732873	serine/threonine kinase 18	STK18
Hs.444	H87351	serine/threonine kinase 19	STK19
Hs.98874	AA436479	similar to proline-rich protein 48	LOC54518
Hs.151689	AA043458	zinc finger protein 137 (clone pHZ-30)	ZNF137
Hs.169832	AA120779	zinc finger protein 42 (myeloid-specific retinoic acid- responsive)	ZNF42
Hs.104746	AA406206	ESTs, Highly similar to NBL4 PROTEIN [M.musculus]	
Hs.58643	AA490900	ESTs, Highly similar to JAK3B [H.sapiens]	
Hs.42733	W85875	ESTs, Weakly similar to BC-2 protein [H.sapiens]	
Hs.90020	AA626316	ESTs, Weakly similar to KINESIN LIGHT CHAIN [H.sapiens]	
Hs.118739	AA521439	ESTs, Weakly similar to phosphoinositide 3-kinase [H.sapiens]	
Hs.84640	W93317	ESTs, Weakly similar to proline-rich protein MP3 [M.musculus]	
Hs.24956	AA454654	ESTs, Weakly similar to SH3 domain-binding protein SNP70 [H.sapiens]	
Hs.36779	H53499	ESTs, Weakly similar to Zu-finger-like protein [H.sapiens]	

GenBank accession # specifies a cDNA from a specific IMAGE clone spotted on the GeneFilter membtane

Table 3: Comparison of expression level of apparent species-specific genes by semi-quantitative RT-PCR.

Specificity (by GFs)	Unigene Cluster ID	Primer Pair	Hu/Bab Intensity Ratio (by GFs)	Hu/Bab Intensity Ratio (by RT-PCR)	Gene Name
Human	Hs.1817	R05886	16.3	3.6	MPO
Human	Hs.13818	R85439	6.9	1.5	ESTs
Human	Hs.47956	N55359	4.9	*	ESTs
Human	Hs.43708	N25920	3.7	-1.9	EST
Human	Hs.215595	AA487912	3.2	5.4	GNB1
Baboon	Hs.118409	AA676327	-21.5	1.8	ESTs
Baboon	Hs.107308	R82595	-19.3	1.2	cDNA
Baboon	Hs.114593	N74363	-9.2	*	ESTs

Primer pairs were named after the GenBank Accession number specifying a cDNA from a specific IMAGE clone spotted on GeneFilter membrane. GF, GeneFilters, MPO, myeloperoxidase; (ONB). Guanine melcolide binding protein (G protein), beta polypoptide 1; cDNA, Homo sapiers uncharacterized gene. "indicates no expression in either species. Negative intensity ratio indicates in bethoor than in baboon than in human.

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gene NCOA1 PRKCZ	ANXAB	PDE6H DKFZP566B1346 DKFZP564M182
title EST nuclear receptor coactivator 1 protein kinase C, zeta	Homo sapiens cDNA FLL20640 fis, clone KAT02911 Homo sapiens cDNA FLL30829 fis, clone RT2PF4001138 EST5 EST5 Annexit A6 Homo sapiens mRNA; cDNA DNCZp434R330; partial cds EST5 EST5 Homo sapiens mRNA for publisher nucleolar RNA for publisher nucleolar RNA for publisher nucleolar RNA Pelicase EST5 EST5 EST5 EST5 EST5 EST5 EST5 EST5	phosphodiesterase 6H, cGMP- specific, cone, gamma EST DKFZP568B1346 protein DKFZP564M182 protein
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71833.55 71640.2	71370.23 71360.65 71076.75	71054.48	70690.08 70578.84	69935.09 69853.44	69459.77	69321.67	67377.91		66864.98	65805.4	65401.33	64983.23	64756.71	63960.6	63349.86 63169.59 62758.88
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Hs.12243 Hs.120606	Hs.105033 Hs.153943 Hs.47168	Hs.154443	Hs.121871 Hs.173736	Hs.109047 Hs.111515	Hs.101840	Hs.110667	Hs.6985 Hs.125958		Hs.119502	Hs.5025	Hs.116169	Hs.5372	Hs.121972	Hs.11441	Hs.183211 Hs.44984 Hs.121509
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rycoler AA 60700.79 S88350 AA151697 Hs. 48907 Hs. 103816 114.11.11 BULTYGERASE EC 60640.29 588352 AA424952 Hs. 11473 Hs. 36787 Inding protein 2 GHDZ 60486.73	358887 W94630 Hs.109503 ESTS 62288.61 781003 AA44601Hs.104966 ESTS 6528.61 749048 AA4600TB Hs.104966 ESTS 61953.39 749048 AA400D78 Hs.3000C ESTS 61494.63 745117 AA428379 Hs.25072 Hs.73072 Hs.73072 61738.88 745117 AA428379 Hs.25075 Hs.73072 Hs.73072 Hs.73072 61738.88 286528 N47316 Hs.53996 Hs.53996 Hs.57778 GOTOO.79 60700.79 AA4151697 Hs.53996 Hs.53996 Hs.73996 Hs.74074 GOTOO.79 60700.79 AA4245 Hs.14473 Hs.63996 Hs.53996 Hs.74074 GOTOO.79 60700.79 AA4245 Hs.14473 Hs.103816 1.14.11 Hs.0466 Hs.0466 6040.29 AA4245 Hs.1473 Hs.48507 Hs.103816 1.14.11 Hs.48507 Hs.48507 Hs.48507 Hs.48507 Hs.48507 Hs.48507 Hs.48507 Hs.48507 Hs.48507 Hs.48507 <td>358887 W94630 Hs. 109503 ESTS 62258.61 781003 AA446601 Hs. 104966 ESTS ESTS 62258.61 781003 AA4060778 Hs. 104966 ESTS 6573.39 67853.39 1376827 AA4060778 Hs. 104966 ESTS 6174.63 6174.63 1376827 AA612973 Hs. 73072 Hs. 73072 subunit 88 (rata 2) CCT6B 61838.88 745117 AA262579 Hs. 53976 Hs. 53996 ESTS subunit 88 (rata 2) ECT4L2 60700.79 280528 N47316 Hs. 53996 ESTS SEC14 (S. cerovisiae)-like 2 ECT4L2 60700.79 280528 N47316 Hs. 53996 ESTS Horno sapiens cDNA Horno sapiens cDNA Horno sapiens cDNA AA4174 Hs. 14727 Hs. 10377 Hs. 10377 Hs. 10477 Hs. 10474 Hs. 104014 Hs. 104014<td>358887 W94450 Hs.109503 Hs.109506 Hs.109506 ESTS 62258.61 781003 AA4060778 Hs.109606 Hs.104966 ESTS 61953.39 61953.39 743048 AA4060778 Hs.104060 Hs.104966 ESTS 6178 61953.39 743048 AA4060778 Hs.20406 Hs.20406 ESTS subunit 88 (zeta 2) 61744.63 745117 AA262773 Hs.73072 Hs.73072 SEC14 (S. cerevisiae)-like 2 ECT412 60780.28 745117 AA262579 Hs.23996 Hs.53996 ESTS SEC14 (S. cerevisiae)-like 2 ECT412 60700.79 788350 AA151687 Hs.48907 Hs.10377 Ris, clone NTZHPROBET/AINE.2- CXCGLULAAATE 60700.79 588350 AA42607 Hs.48907 Hs.103816 Hs.10377 Ris, clone NTZHPROBET/AINE.2- CXCGLULAAATE 60440.29 588350 AA4216887 Hs.48504 Hs.103816 Hs.10377 Ris, clone Hr.4111.1 Hs.357.87 Pinding protein C CHDZ 60440.29 588350 AA421688 Hs.48504 Hs.104806 ESTs CXT18 60440.29 <</td></td>	358887 W94630 Hs. 109503 ESTS 62258.61 781003 AA446601 Hs. 104966 ESTS ESTS 62258.61 781003 AA4060778 Hs. 104966 ESTS 6573.39 67853.39 1376827 AA4060778 Hs. 104966 ESTS 6174.63 6174.63 1376827 AA612973 Hs. 73072 Hs. 73072 subunit 88 (rata 2) CCT6B 61838.88 745117 AA262579 Hs. 53976 Hs. 53996 ESTS subunit 88 (rata 2) ECT4L2 60700.79 280528 N47316 Hs. 53996 ESTS SEC14 (S. cerovisiae)-like 2 ECT4L2 60700.79 280528 N47316 Hs. 53996 ESTS Horno sapiens cDNA Horno sapiens cDNA Horno sapiens cDNA AA4174 Hs. 14727 Hs. 10377 Hs. 10377 Hs. 10477 Hs. 10474 Hs. 104014 Hs. 104014 <td>358887 W94450 Hs.109503 Hs.109506 Hs.109506 ESTS 62258.61 781003 AA4060778 Hs.109606 Hs.104966 ESTS 61953.39 61953.39 743048 AA4060778 Hs.104060 Hs.104966 ESTS 6178 61953.39 743048 AA4060778 Hs.20406 Hs.20406 ESTS subunit 88 (zeta 2) 61744.63 745117 AA262773 Hs.73072 Hs.73072 SEC14 (S. cerevisiae)-like 2 ECT412 60780.28 745117 AA262579 Hs.23996 Hs.53996 ESTS SEC14 (S. cerevisiae)-like 2 ECT412 60700.79 788350 AA151687 Hs.48907 Hs.10377 Ris, clone NTZHPROBET/AINE.2- CXCGLULAAATE 60700.79 588350 AA42607 Hs.48907 Hs.103816 Hs.10377 Ris, clone NTZHPROBET/AINE.2- CXCGLULAAATE 60440.29 588350 AA4216887 Hs.48504 Hs.103816 Hs.10377 Ris, clone Hr.4111.1 Hs.357.87 Pinding protein C CHDZ 60440.29 588350 AA421688 Hs.48504 Hs.104806 ESTs CXT18 60440.29 <</td>	358887 W94450 Hs.109503 Hs.109506 Hs.109506 ESTS 62258.61 781003 AA4060778 Hs.109606 Hs.104966 ESTS 61953.39 61953.39 743048 AA4060778 Hs.104060 Hs.104966 ESTS 6178 61953.39 743048 AA4060778 Hs.20406 Hs.20406 ESTS subunit 88 (zeta 2) 61744.63 745117 AA262773 Hs.73072 Hs.73072 SEC14 (S. cerevisiae)-like 2 ECT412 60780.28 745117 AA262579 Hs.23996 Hs.53996 ESTS SEC14 (S. cerevisiae)-like 2 ECT412 60700.79 788350 AA151687 Hs.48907 Hs.10377 Ris, clone NTZHPROBET/AINE.2- CXCGLULAAATE 60700.79 588350 AA42607 Hs.48907 Hs.103816 Hs.10377 Ris, clone NTZHPROBET/AINE.2- CXCGLULAAATE 60440.29 588350 AA4216887 Hs.48504 Hs.103816 Hs.10377 Ris, clone Hr.4111.1 Hs.357.87 Pinding protein C CHDZ 60440.29 588350 AA421688 Hs.48504 Hs.104806 ESTs CXT18 60440.29 <

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	2.49217322		2.19801556	2.00606636	1.67978776	2.33560939		2.30882332	2.90754544	1.89253828			2.02284366		2.23003079	2.7603639		2.2417136			1.88480545	1.9616827			2.04252344	2.36299551		2.15655587		00107	2./2148398
	59055.87	58428.99	58321.98	58310.04	57835.84	57761.01		57592.12	57558.7	57539.92			57439.02		57399.61	57054.9		56783.39		56729.76	55943.41	55907.8			55/34.96	55667.98		55489.25	55413.64	0000	55220.08
	GPX3					DKFZP434H132									EPB49	FGA		MLD			SCLY				Ī			AANAT			LGALSZ
glutathione peroxidase 3	(plasma)	ESTs	ESTs	ESTs	EST	DKFZP434H132 protein	Homo sapiens mRNA for	KIAA1126 protein, partial cds	ESTs	ESTs	ESTs, Highly similar to N-	terminal acetyltransferase	[H.sapiens]	erythrocyte membrane protein	band 4.9 (dematin)	fibrinogen, A alpha polypeptide FGA	memorane ratty acid (lipid)	desaturase	Homo sapiens mRNA; cDNA DKFZp434H2215 (from clone	DKFZp434H2215)	putative selenocysteine lyase	ESTs	tryptophan hydroxylase	(tryptophan 5-	monooxygenase) Novel human gene manning to	chomosome 22	arylalkylamine N-	acetyltransferase	ESTs	lectin, galactoside-binding,	soluble, 2 (galectin 2)
	Hs.172153	Hs.186566	Hs.100256	Hs.223323	Hs.117159	Hs.17936		Hs.44087	Hs.12286	Hs.16959			Hs.109253		Hs.274122	Hs.90765		Hs.185973		Hs.120369	Hs.44049	Hs.210506			Hs.144563	Hs.38628		Hs.152972	Hs.58323		Hs.113987
	AA664180 Hs.119708	AA777050 Hs.122519	AA486864 Hs.100256	N56948 Hs.114446	AA679279 Hs.117159	AA459421 Hs.111968		N29778 Hs.44087	R43026 Hs.12286	AA463249 Hs.16959			AA421291 Hs.109253		N55461 Hs.75936	AA865707 Hs.90765		AA039929 Hs.112320		AA719238 Hs.120369	W70222 Hs.108156	AA283926 Hs.51501			AA702193 Hs.114292	N23135 Hs.38628		AA757429 Hs.57688	AA701234 Hs.58323		AA872397 Hs.113987
	855523	378265	841022	280084	432074	810983		259627	31979	797057			731073		245979	1469138		485738		1292501	343967	700671			384134	266851		395440	434868	!	1472743
	GF202	GF204	GF202	GF203	GF203	GF202		GF202	GF202	GF202			GF203		GF203	GF203		GF202		GF204	GF203	GF203			GF203	GF203		GF203	GF204		GF203

2.3032412	2.1388748 2.69931776	2.28509341	1.65482044 2.19879638	2.26507735 1.94255209	2.5487216	30700070	2.09858225		2.25931089	2.4541108	2.56562065	1.74524144 2.53715117 2.41980306	2.39449932
55065.05 54932.88	54656.55 54645.92	54644.09 54627.96 54649.56	54348.50 54487.47 54448.52	54433.58 54190.89	53920.27	53801.7	53412.36	52996.26	52937.97	52844.92	52774.88 52714.73	52663.28 52314.89 52063.66	51991.95
KIAA1086	C220RF4	VELI1			APBB2	CCT7	200	KIMO7	CDC20	ESRRA	BA12		MSH5
ESTs KIAA1086 protein chromosome 22 open reading	frame 4 ESTs Variabrate I IN7 homolog 1	Tax interaction protein 33 ESTs	ESTS ESTS ESTS	EST ESTs	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	chaperonin containing TCP1, subunit 7 (eta)	ESTS	KIAA 1034 protein LIM domain only 7 cell division cycle 20.	S.cerevisiae homolog estroden-related receptor	alpha brain-specific andiogenesis	inhibitor 2 ESTs	ESTS ESTS ESTS	mutS (E. coli) homolog 5 Homo sapiens cDNA FLJ10505 fis, clone NT2RP2000503
Hs.47234 Hs.65750	Hs.20017 Hs.112692	Hs.178215 Hs.273704	HS.29808 HS.248705	Hs.105043 Hs.15768	Hs.15740	Hs.108809	Hs.28471	Hs.5978	Hs.82906	Hs.110849	Hs.200586 Hs.131629	Hs.269397 Hs.36280 Hs.14832	Hs.112193 Hs.152335
N51335 Hs.47234 AA778611 Hs.65750	AA25552 Hs.66999 AA609334 Hs.112692	AA757170 Hs.73211 AA779817 Hs.122116	AA682779 HS.117229 AA782314 HS.29808 AA609861 HS.112772	AA460254 Hs.105043 N26621 Hs.15768	AA866113 Hs.24957	AA883865 Hs.125516	AA416547 Hs.28471	AA777749 Hs.114273	AA464698 Hs.92249	AA098896 Hs.110849	AA777034 Hs.4869 AA608857 Hs.112604	R08311 Hs.113189 AA131267 Hs.36280 AA447726 Hs.14832	AA872677 Hs.126196 AA045075 Hs.62751
283142 1048965	682479 743416	1309620	857574 1031027	796519 269185	1470333	1467972	730953	1642145 448556	810217	489553	378243 1048588	127267 503555 813813	1475697
GF202 GF204	GF203 GF202	GF203 GF204	GF203 GF203 GF202	GF202 GF203	GF203	GF204	GF202	GF204	GF202	GF203	GF204 GF202	GF203 GF202 GF203	GF204 GF202

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GF202 GF203	130288 825240	R21226 Hs.91419 AA504144 Hs.22315	419 315	Hs.139033 Hs.22315		PEG3	51807.04 51786.29	2.20028307 1.92272105
GF203	1469425	AA866160 Hs.43627	627	Hs.43627	SRY (sex-determining region Y)-box 22 ESTs	SOX22	51710.98	2.34775115
GF204	1475734		964	Hs.184297	KIAA0808 gene product	KIAA0808	51243.14	
GF203	1376828	AA812964 Hs.118640	8640	Hs.118640	Drosophila dsh) phosphoinositide-3-kinase,	DVL2	51165.32	1.87703748
GF203 GF203	811779 824728	AA463460 Hs.92095 AA488979 Hs.25313	095 313	Hs.6241 Hs.25313		PIK3R1 MCRS1	51136.7 51135.3	2.26870041 2.4545054
GF201	878449	AA670382 Hs.82503	203	Hs.82503	unknown protein heparan sulfate 2-0-		51118.27	
GF203	713324	AA283046 Hs.57914	914	Hs.169939	sulfotransferase 1	HS2ST1 KIAA0258	50934.93	2.00419412
GF204	436456	AA699644 Hs.113096	3096	Hs.113096	ESTs		50466.38	
GF203 GF200	868517 144915 1460636	AA775033 Hs.3769 R78516 Hs.8148 AA868722 Hs 125237	69 48 5237	Hs.3769 Hs.8148 Hs 125237	ESTs selenoprotein T ESTs	LOC51714	50264.33 49963.89 49936.86	2.12105/38 1.16416094
GF203	449428	AA777883 Hs.121935	1935	Hs.121935	EST Surfactant, pulmonary-		49919.02	1.72213087
GF204 GF202 GF204	1584551 1032072 745531	AA972350 Hs.76305 AA609887 Hs.112776 AA626249 Hs.116139	305 2776 6139	Hs.76305 Hs.112776 Hs.116139	associated protein B ESTs ESTs	SFTPB	49903.21 49895.17 49800.64	2.14706033
0000	700706	AA200007 Us 118550	9550	He 118550	ESTs, Weakly similar to GSG1		49660.96	1.86784377
GF203 GF203	1160618 365227	AA877618 Hs.24781 AA024898 Hs.103368	781 3368	Hs.24781 Hs.103368	fatty acid amide hydrolase ESTs	FAAH	49421.12 49399.04	2.33243199
GF203 GF203	823588 151248	AA497050 Hs.30204 H02328 Hs.116253	204 6253	Hs.81170 Hs.229612	pim-1 oncogene EST	PIM1	49230.71 49202.68	2.10781198 2.49038533
GF203	725746	AA399410 Hs.1618	8	Hs.142258	signal transducer and activator of transcription 3 (acute-phase response factor)	STAT3	49187.62	2.22897417

Atty Docket No. 217	2.32511853	2.69659394	2.29648333	2.15750093	2.19455828	2.41848449		2.16108795	2.13211816		2.60493849		2.282344		1.92255713	1.86430316	2.01517534	1.99468928	2.49709169	2,42565944		1.15906256	2.74751646	1.84438941	2.26326843
∢	49180.57	49090.05	48894.53	48874.3	48859.47	48758.05		48706.06	48653.38		48433.96		48422.37	48385.94	48318.84	48272.15	48206.44	48143.98	48111.94	48070.7		47879.75	47833.3	47813.49	47723.38
		AMY2A	EIF4B								EIF4EBP3					HOXB5		ADM				CSF2RA	ADCY7	KIAA0792	
APPENDIX A	ESTs	amylase, alpha 2A; pancreatic eukaryotic translation initiation	factor 4B Homo sapiens cDNA FLJ11238 fis, clone	PLACE1008532 Homo sapiens mRNA; cDNA DKFZp434A119 (from clone	DKFZp434A119)	ESTs Homo saniens mRNA from	chromosome 5q21-22,	clone:357Ex	ESTs	eukaryotic translation initiation	factor 4E binding protein 3	ESTs, Weakly similar to BC-2	protein [H.sapiens]	EST	ESTs	homeo box B5	ESTs	adrenomedullin	ESTs	EST	colony stimulating factor 2 receptor, alpha, low-affinity	(granulocyte-macrophage)	adenylate cyclase 7	KIAA0792 gene product	mRNA sequence
	Hs.112242	Hs.278399	Hs.93379	Hs.103702	Hs.274292	Hs.104778		Hs.26968	Hs.61246		Hs.106711		Hs.42733	Hs.103679	Hs.88528	Hs.22554	Hs.250746	Hs.394	Hs.26791	Hs.47403		Hs.182378	Hs.172199	Hs.119387	Hs.48802
	1056172 AA620995 Hs.112242	AA844818 Hs.75733	AA206865 Hs.104146	AA172039 Hs.103702	N51625 Hs.129894	AA412498 Hs.104778		AA481425 Hs.26968	AA025061 Hs.61246		AA496801 Hs.81658		W85875 Hs.42733	AA101840 Hs.103679	AA279015 Hs.88528	AA252627 Hs.85818	AA069519 Hs.114856	AA521008 Hs.62206	N48673 Hs.26791	N52043 Hs.47403		N92646 Hs.140	AA488428 Hs.18171	AA434402 Hs.119387	AA418387 Hs.48802
k et al.	1056172	1412238	648056	594946	281625	730145		752873	365062		897649		416069	489572	703864	685182	382649	826300	279340	282489		289337	843206	770875	767283
Westbrook et al.	GF202	GF203	GF203	GF202	GF203	GF202		GF202	GF202		GF202		GF202	GF204	GF203	GF203	GF203	GF203	GF202	GF202		GF200	GF202	GF203	GF203

1.87485592	1.833746	2.04921103	2.02144343 2.65166492	2.45693656 2.0185339	2.0712382 2.03105361 2.3013018 2.44735019 1.83400958	1.9367046 2.57380463 1.72505413	2.59852802 2.24609259
47473.18 47354.54 47177.92	47061.89	46979.71	46702.58 46677.43 46504.02	46489.22 46487.3	46271.13 46074.37 45948.39 45946.32 45862.83	45630.61 45554.18 45449.57 45438.7	45438.7 45345.86 45314.48
BAZ1B		NCAM2		DKFZP56601646	UQCRC1 DKFZP586N0819 NRF1 KIAA0781	PEX14	FUS KIAA0808 KIAA0585
bromodomain adjacent to zinc finger domain, 1B ESTs ESTs	Homo sapiens cDNA FLJ20391 fis, clone KAIA4640 neural cell adhesion molecule	2 ESTs, Weakly similar to IIII ALU SUBFAMILY J	WARNING EN INY !!!! [H.sapiens] EST EST FOR Sapiens cDNA	FLYZOZS3 IIS, CIONE COLF6895 DKFZP56601646 protein	underfund-sylounome creductase core protein I DKFZP586N0819 protein nuclear respiratory factor 1 ESTs KIAA0781 protein	peroxisomal biogenesis factor 14 ESTs ESTs ESTS	rusion, derived from (12; 19) malignant liposarcoma KIAA0808 gene product phosphatidylserine receptor
Hs.194688 Hs.98968 Hs.127286	Hs.11747	Hs.177691	Hs.12845 Hs.94100 Hs.116186	Hs.235712 Hs.24427	Hs.119251 Hs.47144 Hs.180069 Hs.23107 Hs.42676	Hs.19851 Hs.12035 Hs.119845 Hs.221513	Hs.99969 Hs.184297 Hs.72660
AA485132 Hs.21289 N68942 Hs.98968 AA865960 Hs.127286	AA456827 Hs.11747	AA709271 Hs.113596	W47017 Hs.12845 N58488 Hs.94100 AA626942 Hs.116186	AA488901 Hs.6425 N49079 Hs.24427	AA293215 Hs.115382 AA479362 Hs.47144 AA454935 Hs.99566 H09759 Hs.107443 AA701465 Hs.113760	AA505122 Hs.19851 AA459392 Hs.105042 AA704752 Hs.119845 AA019226 Hs.40086	AA779569 Hs.122103 N66992 Hs.102764 AA459945 Hs.72660
815683 297908 1470220	815549	1343468	324620 248258 1048775	824897 27 9 752	714414 753957 814760 46565 435075	825798 810943 451169 362973	1032645 287261 796408
GF203 GF204 GF204	GF203	GF203	GF203 GF202 GF204	GF203 GF203	GF203 GF203 GF203 GF202 GF202	GF203 GF202 GF203 GF204	GF204 GF202 GF202

2.12582276	2.30304559	2.87195252 2.57839588	1.69389112 2.03026045 2.55642136 2.74445937	1.14539219	2.35375591 2.83086118 2.28810363 2.50027249
45166.07	45114.36	44856.61 44771.15 44701.05	44613.95 44528.2 44417.81 44406.33 44362.1	44353.38 44305.15 44220.66	44181.34 44177.91 44032.71 43974.33
NDUFB10	FANCG	KIAA0376	DKFZP586C1619	рот	SCN8A
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22KD, PDSW)	ESTs, Highly similar to dolichly: P-Glic:Man9GicNAc2-PP- doichly glucosytransforase [H sapiens] Fanconi anemia, complementation group G	ESTs, Weakly similar to KIAA0877 protein [H.sapiens] ESTs KIAA0376 protein Homo sapiens cDNA	COL08503 ESTs ESTs DKFZP586C1619 protein EST	Homo sapiens (clone s22/71) mRNA fragment D-dopachrome tautomerase ESTs Homo sapiens mRNA; cDNA	DKFZp588H0623) DKFZp688H0623) sodium channel, voltage gated, type VIII, alpha potyseptide ESTs ESTs
Hs.198274	Hs.80042 Hs.8047	Hs.260816 Hs.53656 Hs.4791	Hs.34045 Hs.237492 Hs.35135 Hs.108169 Hs.102892	Hs.159471 Hs.180015 Hs.171870	Hs.59548 Hs.124189 Hs.177706 Hs.192394
AA620565 Hs.3398	N63143 Hs.80042 AA430675 Hs.8047	N40211 Hs.45063 A459873 Hs.53656 AA773104 Hs.121752	AA465342 Hs.34045 N50662 Hs.114421 N74531 Hs.131857 AA495810 Hs.108169 N90609 Hs.102892	22	W94419 Hs.59548 W96187 Hs.124189 AA251146 Hs.57660 AA628192 Hs.116210 AA455130 Hs.99394
951216	285238	276441 897981 857093	814072 280787 291772 768396 306302	741852 725503 416483	357985 361668 684216 1055834 809863
GF202	GF202 GF201	GF202 GF202 GF204	GF203 GF203 GF204 GF203 GF203	GF201 GF200 GF203	GF202 GF203 GF203 GF204 GF202

ESTs, Moderately similar to

1.76777554	2.09944139	1.88206677	2.44121975		1.88459241		2.04041614	2.05321769	2.15281743	2.63100906	1.16167386 2.25777483 2.56296949	2.77023876 2.50430708 2.14271259 2.04537159
43749.51	43172.7 43074.47 43000.41	42958.08	42956.96	42914.46	42727.14 42694.75		42620.09	42565.8 42481.96	42367.77	42356.46 42235.72	42223.47 42200.6 42147.7	42112.2 42077.38 42064.63 42033.01 41973.3
		DOK2						EPB41L2	GRN		CARP NY-REN-57	PIK3CD
neuronal thread protein AD7c- NTP [H.sapiens] Homo sapiens cDNA FI.10659 fis. clone	NT2RP2006071 ESTs ESTs	docking protein 2, 56kD ESTs, Moderately similar to	sorting nexin 3 [H.sapiens] Homo sapiens clone 24703 beta-tubulin mRNA, complete	cds ESTs, Weakly similar to	unknown [M.musculus] ESTs	Human LZ-9 transcript or unrearranged immunoglobulin	V(H)5 pseudogene erythrocyte membrane protein	band 4.1-like 2 ESTs	granulin	ESTs EST	cardiac ankyrin repeat protein CARP F-box protein Fbx9 NY-RE ESTs	phosphoinostiide-3-kinase, catalytiic, delta polypeptide ESTs ESTs ESTs
Hs.9851	Hs.107882 Hs.71428 Hs.86828	Hs.71215	Hs.5076	Hs.179661	Hs.61790 Hs.42997		Hs.81221	Hs.7857 Hs.62314	Hs.180577	Hs.163703 Hs.112895	Hs.74019 Hs.11050 Hs.217413	Hs.162808 Hs.104779 Hs.86663 Hs.103118 Hs.55962
AA459265 Hs.9851	R77239 Hs.107882 AA609392 Hs.71428 AA905925 Hs.86828	AA133189 Hs.71215	N34358 Hs.131852	AA427899 Hs.27727	AA035137 Hs.61790 AA863470 Hs.42997		AA505045 Hs.81221	AA449738 Hs.7857 N50419 Hs.62314	AA496452 Hs.75451	W96205 Hs.103268 AA620746 Hs.112895	AA488072 Hs.105679 AA609770 Hs.112764 AA405532 Hs.82262	AA281784 Hs.14207 AA412499 Hs.104779 AA215414 Hs.86663 W58209 Hs.103118 AA026927 Hs.55962
814482	144808 743481 1505405	490767	271021	773479	471835 1469379		825648	785967	755762	358567 1049282	840683 1031951 772408	712401 730147 683481 341095 469415
GF203	GF201 GF202 GF204	GF202	GF203	GF201	GF203 GF204		GF203	GF202 GF203	GF203	GF201 GF202	GF200 GF202 GF202	GF203 GF202 GF203 GF203 GF204

2.47921376	2.43935425 2.53883016	1.85353965 1.74536201 2.00460017	2.50383307 2.60107953 2.08031206 2.16096281	2.74025662 1.13579938 2.20381301 1.97848878	2.52258949
41861.45 41831.81 41714.48	41710.75 41599.24 41598.96	41529.63 41369.93 41240.91	41221.38 41194.35 41187.62 41127.79 41039.54	40953.56 40925.43 40900.18 40774.24 40440.86	40334.47
CH3L1 ZNF262	LAP18 NEF3		KIAA0601 HIBCH BARI 2R	KIF5B	NLVCF
ESTs chitinase 3-like 1 (cartilage glycoprotein-39) zinc finger protein 262	eukemia-associated ohosphoprotein p18 (stathmin) LAP18 ESTs ESTs medium) 3 (150kD medium) NEF3 Homo saplens mRNA; cDNA NETA-Ada-EN3 ffrom clone	NKT2434F053) SSTS SSTS SSTS SSTS SSTS SSTS SSTS SS	DKFZp586F0219) KIRA0601 protein ESTS Shydroxyisobutyryl-Coenzyme A hydrolase A hydrolase of RAS Ma, member of RAS	Angelin damping more 20 miles in family member 5B = ST = S	objects rocalization signal syndrome SSTs, Weakly similar to salivary proline-rich protein R.norvegicus]
Hs.6526 E cl Hs.75184 g Hs.150390 zi	Hs.81915 p Hs.98163 E Hs.71346 m	Hs,46848 D Hs,119991 E Hs,6522 E Hs,62798 E	Hs.28785 D Hs.174174 K Hs.59558 B Hs.236642 A Hs.236642 A	,	Hs.19500 s E E Hs.97176
H24317 Hs.6526 AA434115 Hs.75184 AA001835 Hs.103278	AA873060 Hs. 81915 AA416889 Hs. 98163 AA400329 Hs. 71346	AA135886 Hs.46848 AA707117 Hs.119991 AA677984 Hs.6522 AA046829 Hs.62798	AA598949 Hs.28785 AA193381 Hs.104090 W94620 Hs.59558 AA055335 Hs.63174	A4122049 Hs.110199 A4122049 Hs.110199 AA046690 Hs.43704 AA421718 Hs.104842 AA609483 Hs.112715 AA975680 Hs.8016	AA775857 Hs.19500 AA447724 Hs.97176
51951 H2 770212 A/ 427980 A/	1476065 AV 729962 AV 743229 AA	502674 AA 452045 AA 430763 AA 376771 AA	898054 AA 665830 AA 358872 W 377205 AA		878525 A/
GF202 GF200 GF201	GF203 GF202 GF201	GF201 GF203 GF203 GF202	GF202 GF203 GF202 GF202	GF202 GF203 GF203 GF204 GF204	GF204 GF203

GCN5 (general control of

	1.15930194	1.77441049	1.98598002	2.05303095	2.38721968		1.42556412					2.32707886	2.2901204		1.21367487	1.08354365										1.14321696	1.94420686	
	40242.06	40220.19	40158.78	40091.26	40073.66		40040.24			39969.38	39951.38	39935.71	39882.63		39851.87	39848.58	39803.94	39774.89			39769.86	39690.13	39572.99			39569.42	39563.55	
	GCN5L1	HLA-DQB1	KIAA1248				SNCG									SCAMP2					PPFIA2					MEF2B		
amino-acid synthesis, yeast,	homolog)-like 1 maior histocompatibility	complex, class II, DQ beta 1	KIAA1248 protein	ESTs	ESTs	synuclein, gamma (breast	cancer-specific protein 1)	Homo sapiens cDNA	LJ 107 20 11S, CIOHE	NT2RP3001236	ESTs	ESTs	ESTs	Human clone 23867 mRNA	sequence secretory carrier membrane	protein 2	ESTs	ESTs	protein tyrosine phosphatase,	eceptor type, I polypeptide PTPRF), interacting protein	liprin), alpha 2	EST	ESTs	MADS box transcription	enhancer tactor 2, polypeptide B (mvocyte enhancer factor	28)	ESTs	
	Hs.94672	Hs.73931	0		Hs.112529		Hs.63236			Hs.167135	Hs.116141	Hs.173688	Hs.7473		Hs.19555	Hs.238030	Hs.127790	Hs.97130			Hs.30881	Hs.116296	Hs.97418			Hs.78881	Hs.58314	
	Hs.94672	Hs.16041	_	4A425694 Hs.61484	AA256174 Hs.112529		AA443638 Hs.63236			AA779718 Hs.116793	AA626256 Hs.116141	4A609430 Hs.56732	AA669536 Hs.7473		AA486332 Hs.19555	Hs.10761	AA862814 Hs.127790	AA884317 Hs.97130			N51002 Hs.47170	AA629040 Hs.116296	AA610028 Hs.97418			AA282642 Hs.78881	3 Hs.58314	
	H94857	N35397	AA6776	AA4256	AA2561		AA4436			AA7797	AA6262	AA6094	AA6695		AA4863	R32802	AA8628	AA8843			N51002	AA6290	AA6100			AA2826	W73523	
	230218	272097	897252	773185	681910		771303			1034472	745544	743531	853985		840658	135527	1469211	1466883			281243	744005	1032044			704760	344505	
	GF200	GF203	GF203	GF202	GF203		GF203			GF204	GF204	GF202	GF203		GF200	GF200	GF204	GF204			GF201	GF204	GF204			GF200	GF202	

2.11825556 1.96747453 2.89316499	1.74907499	2.20316741 2.21733026 2.40430728 1.98230493	2.06301253	1.1862723	1.1862723 2.37000706 2.52451922 1.88009744	2.26031443 1.96527636 2.88137426
39463.62 39377.96 39371.86	39346.71 39276.13 39252.2	39244.25 39180.78 39112.79 38983.86	38790.02	38754.3	38754.3 38637.43 38618.29 38475.16	38407.76 38344.91 38260.04 38233.7
SPINK2	WHSC1	GPR30 RNF15	PPM1G	SLC25A16	SLC25A16	DKFZP586D1519
Homo sapiens cDNA FLJ10394 fis, clone NT2RM4000197 ESTs serine protease Inhibitor, Kazal type, 2 (acrosin-trypsin inhibitor)	Wolf-Hirschhorn syndrome candidate 1 ESTs ESTs	G protein-coupled receptor 30 ring finger protein 15 ESTs ESTs protein phosphatase 1G	(formerly 2C), magnesium- dependent, gamma isoform solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen) member	16 solute carrier family 25 (mitochondrial carrier, Graves disease autoantigen) member	16 ESTs ESTs ESTs	DKFZP586D1519 protein EST ESTs ESTs
Hs.22975 Hs.58394 Hs.98243	Hs.127073 Hs.127073 Hs.191396	Hs.113207 Hs.59545 Hs.112761 Hs.98007	Hs.17883	Hs.180408	Hs.180408 Hs.104830 Hs.15898 Hs.16064	Hs.7946 Hs.121921 Hs.112347 Hs.11270
AA609348 Hs.22975 AA644335 Hs.58394 AA625888 Hs.98243	W69960 Hs.19416 AA865912 Hs.127073 AA682785 Hs.114708	AA810225 Hs.113207 AA195036 Hs.59545 AA609760 Hs.112761 AA406083 Hs.98007	AA465723 Hs.17883	AA411554 Hs.119564	AA411554 Hs.18203 AA421282 Hs.104830 AA417373 Hs.15898 N62729 Hs.16064	0110
743426 845604 744940	343919 1470111 450424	1367900 665373 1031942 743058	814989	754490	754490 731047 730942 289016	744395 449384 321693 359539
GF202 GF203 GF203	GF203 GF204 GF204	GF203 GF202 GF202 GF202	GF203	GF200	GF200 GF202 GF202 GF203	GF202 GF203 GF202 GF201

1.96210058	2.5616315 1.545054 2.37215486	1.93323747 2.33882863 2.40356771	2.23247929	2.0793113	2.79047492 1.64737533 2.45481868
38229.45	38106.51 38106.51 38029.77	38008.88 37948.34 37900.92 37819.28 37797.28	37656.11 37633.05 37626.97 37488.24	37396.84 37375.82	37366.04 37319.13 37273.39
NDUFV1	PMS1 KLK11	HSPC158 YR-29	CYP3A7 RPS6	EIF4B	GRLF1
NADH dehydrogenase (ubiquinone) flavoprotein 1 (51kD) Homo sapiens mRNA for KIAA1347 protein, partial cds ESTs, Weakly similar to	P25H9.7 (C.elegans) postmeiotic segregation increased (S. cerevisiae) 1 Kallikrein 11 ESTs Human DNA topoisomerase III	mRNA, complete cds ESTs HSPC/158 protein hypothetical protein ESTs	ESTs, Weakly similar to ORF YGRO39M (S.cerevisiae) cyrochrome P460, subramily IIIA, polypeptide 7 ESTS ribosomal protein S6 elekaryotic translation initiation	factor 4B ESTs ESTs, Weakly similar to SH3 domain-binding protein SNP70	[H.sapiens] glucocorticoid receptor DNA binding factor 1 ESTs
Hs.7744 Hs.106778	Hs.42785 Hs.111749 Hs.57771 Hs.55304	Hs.91175 Hs.48790 Hs.41007 Hs.8170 Hs.6321	Hs.13144 Hs.172323 Hs.125843 Hs.241507	Hs.93379 Hs.117117	Hs.24956 Hs.102548 Hs.5331
	N71709 Hs.42785 AA504838 Hs.111749 AA477283 Hs.57771 W04649 Hs.55304	N21546 Hs.91175 N63452 Hs.48790 AA147980 Hs.41007 AA172048 Hs.8170 R40191 Hs.6321	AA461486 Hs.47012 R91078 Hs.118475 W69997 Hs.125843 H90912 Hs.106489	AA056484 Hs.103493 AA700967 Hs.117117	AA454654 Hs.24956 AA489679 Hs.102548 AA176483 Hs.5331
770043	290642 825726 740780 320379	266094 277999 590398 594724 27396	796663 194949 344158 240989	489109 447256	824354 611239
GF203 GF201	GF204 GF203 GF203 GF202	GF201 GF202 GF204 GF202 GF202	GF202 GF200 GF204 GF204	GF202 GF204	GF202 GF203 GF202

Homo sapiens DNA sequence from P1 p373c6 on chromosome 6p21.31-21.33.

	1.75801099	2,84596211	1.98838598 2.17110623 1.91795106	1.84631253	2.21645116		1.98414454	2.69241138
37238.66	37218.42	37163.1 37018.3	36927.36 36887.16 36798.02 36713.65	36695.12	36680 97	36634.54	36615.81	36563.73
	, FCGR3A	_		TSSC4	0 0	YDD19	MIR16	TRIP12
Contains zinc finger proteins, pseudogenes, ESTs and STS	Fc fragment of IgG, low affinity Illa, receptor for (CD16) ESTs, Moderately similar to zinc finger protein 2NE49	ESTS EST SINGLED TO THE STREET STREET STREET STREET STREET SINGLE	(H.sapiens) ESTs EST	tumor suppressing subtransferable candidate 4	Human DNA sequence from clone 633020 on chromosome 20q11.23-12 Contains 5' end of a gene similar to Bos taurus P14 protein, ESTs, CA repeat(IQ20S859), STSs and GSSs.	YDD19 protein membrane interacting protein	of RGS16 thyroid hormone receptor	interactor 12
Hs.44720	Hs.176663	Hs.248447 Hs.43866	Hs.187908 Hs.104705 Hs.112949	Hs.165743	Пе 478578	Hs.25615	Hs.107014	Hs.138617
N67634 Hs.44720	AA703460 Hs.120972	AA701913 Hs.114077 AA452572 Hs.43866	N25598 Hs.38805 AA401488 Hs.104705 AA621192 Hs.112949	AA679286 Hs.26816	A AA 87 A 82 Ho 28060	AA127923 Hs.47681	AA191356 Hs.28753	AA700390 Hs.83218
290735	450155 /	435547 <i>H</i> 788507 <i>H</i>	267778 1 743290 <i>H</i> 744367 <i>H</i>		841633		626861	460515 /
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2.32742978 2.08667489	1.98727821 1.20836204	2.09175294	1.7056456 1.86702447 2.12807509	2.60288393	1.90974514	2.22952042 1.66245417 2.05979791	1.7006223	2.03703163 2.29166197 2.10669519
36523.25 36488.87	36272.11 36242.59 36130.87	36070.9 35961.04	35900.42 35868.63 35833.22	35807.62 35801.38 35801.38	3564.29	35522.42	35447.31 35418.41	35365.12 35340.59 35300.09 35287.54 35218.28
	ABT1 RNF5					LOC51275		PSK-1 DKFZP564C186 CUL4A
ESTs, Highly similar to CGI-44 protein [H.sapiens] ESTs TATA-binding protein-binding	protein ring finger protein 5 ESTs Homo sapiens mRNA for	KIAA1427 protein, partial cds ESTs ESTs, Moderately similar to	sorting nexin 3 [H.sapiens] EST ESTs	ESTS ESTS ESTS	ESTs ESTs apoptosis-related protein	PNAS-1 ESTs ESTS Human DNA from chromosome 19-specific cosmid R30923, genomic	sequence ESTs	type I transmembrane receptor (seizure-related protein) ESTs ESTs DKFZP564C186 protein
Hs.8185 Hs.55563	Hs.109428 Hs.216354 Hs.236044	Hs.12365 Hs.89310	Hs.5076 Hs.112678 Hs.43914	HS.11/202 HS.116076 HS.169943 Hs.33905	Hs.26339 Hs.46524	Hs.52166 Hs.58609 Hs.30135	Hs.77876 Hs.30487	Hs.6314 Hs.21379 Hs.54539 Hs.134200 Hs.183874
W15319 Hs.55337 W37833 Hs.55563	AA480876 Hs.109428 AA402960 Hs.34606 N49763 Hs.107189	R38678 Hs.12365 AA284181 Hs.89310	AA629796 Hs.5076 AA609282 Hs.112678 N27303 Hs.43914	AA683346 Hs.117202 AA625774 Hs.116076 AA478962 Hs.19530	N59808 Hs.26339 N48707 Hs.46524	AA521316 Hs.52166 AA678388 Hs.58609 N53520 Hs.30135	AA644097 Hs.77876 N67991 Hs.30487	AA458645 Hs.119674 R20650 Hs.106056 N89814 Hs.54539 AA026278 Hs.90222 H95248 Hs.114307
322643 \\ 322033 \\	814562 / 741815 / 282356	23443 F	–	744896 / 753993 / 754990		827197 431955 284175	845375 / 290505	813408 7 26203 305485 1 366353 7 234325
GF202 GF202	GF203 GF200 GF201	GF204 GF202	GF203 GF202 GF202	GF204 GF203 GF203	GF203 GF203 GF202	GF203 GF203 GF203	GF204 GF203	GF202 GF202 GF202 GF201 GF201

Westbrook et al.	k et al.					Atty	Atty Docket No. 217
				APPENDIXA			
				ceroid-lipofuscinosis, neuronal			
GF204	292071	N73307 Hs.42182	Hs.30213	S	CLN5	35192.66	
GF204	460877	AA704169 Hs.117172	Hs.117172	ESTs		35179.86	
GF202	490723	AA101811 Hs.69506	Hs.69506	ESTs		35130.29	2.24800981
				creatine kinase, mitochondrial			
GF200	363086	AA019482 Hs.75690	Hs.153998	1 (ubiquitous)	CKMT1	35087.11	1.11959533
GF201	730677	AA411771 Hs.7034	Hs.169836	KIAA0671 gene product	KIAA0671	35079.88	
GF202	276413	N40195 Hs.45056	Hs.45056	EST		35070.36	2.65703366
				chromosome 4 open reading			
GF203	395436	AA757427 Hs.44053	Hs.270956	frame 1	C40RF1	35064.18	2.16152749
GF201	504982	AA151210 Hs.42397	Hs.42397	ESTs		35047.95	
GF202	73960	T55189 Hs.9801	Hs.9801	ESTs		35016.36	2.14976163
GF203	449508	AA777930 Hs.121995	Hs.121995	EST		34907.02	1.91916656
				interleukin 3 receptor, alpha			
GF200	320903	W44701 Hs.1726	Hs.172689	(low affinity)	IL3RA	34875.04	1.15852989
GF203	1375309	AA815407 Hs.89631	Hs.89631	ryanodine receptor 1 (skeletal)	RYR1	34845.76	1.69949389
				immunoglobulin superfamily,			
GF204	1593658	AI002566 Hs.130857	Hs.81234	member 3	IGSF3	34649.67	
GF202	730838	AA417012 Hs.98176	Hs.28921	ESTs		34640.64	2.47476584
				putative G protein-coupled			
GF203	685516	AA291259 Hs.97101	Hs.97101	receptor	GPCR150	34620.95	1.66193988
GF203	686594	AA255900 Hs.88110	Hs.184523	KIAA0965 protein	KIAA0965	34572.52	1.60415258
GF202	587595	AA132964 Hs.110915	Hs.110915	ESTs		34514.49	1.58861364
				I GFB1-induced anti-apoptotic			
GF200	781222	AA446222 Hs.75822	Hs.75822	factor 1	TIAF1	34423.93	1.09896675
				Ras-GTPase-activating protein			
GF202	564756	AA136500 Hs.112013	Hs.220689	SH3-domain-binding protein	G3BP	34316.02	1.94465313
GF202	286661	N67891 Hs.90250	Hs.90250	ESTs		34249.86	2.05943586
GF203	281922	N48169 Hs.46829	Hs.46829	ESTs		34193.78	1.67123309
				ESTs, Highly similar to LENS			
				FIBER MEMBRANE			
				INTRINSIC PROTEIN			
GF202	1055217	1055217 AA621457 Hs.112989	Hs.162754	[H.sapiens]		34183.82	2.65879902

	2.50617555 1.60390642 2.37900533 2.29415986	1.87353986	2.93280693	2.18851675 2.67446383 2.90914182	1.87136427 1.57197589	1.20063498	2.8599853		1.62865795	2.21664073 2.66136749	1.90948225	2.1555786	1.64264642
34167.82	34149.95 34100.47 33908.76 33905.01 33838.91	33758.2	33736.76 33524.41	33457.3 33449.59	33314.27 33222.61	33221.78	33209.39	33155.62	33031.39 33020.38	32979.48 32970.95	32910.91 32874.05	32864.36	32764.94
HSU53209		RAB5B	NHP2L1 DKFZP566C243	RAB18			LSM4		C6ORF1			KIAA1098	USP18
transformer-2 alpha (htra-2 alpha) ESTs, Weakly similar to hynothatical profein	ryponious process ESTs EST EST EST ESTS	RAB5B, member RAS oncogene family	non-histone chromosome protein 2 (S. cerevisiae)-like 1 DKFZP566C243 protein	ESTs RAB18 small GTPase	ESTS ESTS	ESTs U6 snRNA-associated Sm-like	protein ESTs, Moderately similar to	Lasp-1 protein [H.sapiens] chromosome 6 open reading	frame 1 ESTs	ESTs ESTs	ESTs FSTs	KIAA1098 protein	ubiquitin specific protease 18
Hs.119523	Hs.1338 Hs.119834 Hs.103426 Hs.60740 Hs.112642	Hs.77690	Hs.182255 Hs.107747	Hs.117163 Hs.21094	Hs.58049 Hs.182384	Hs.24553	Hs.76719	Hs.4832	Hs.62620 Hs.18618	Hs.191580 Hs.104967	Hs.112881 Hs 271762	Hs.137732	Hs.38260
N47341 Hs.82491	AA007591 Hs.110227 AA704602 Hs.119834 AA035770 Hs.103426 AA019062 Hs.60740 AA778680 Hs.112642	R06712 Hs.77690	AA608583 Hs.2112 AA465530 Hs.107747	e –	N48078 Hs.46814 W69743 Hs.58049 AA626022 Hs.27302	R32754 Hs.24553	AA454096 Hs.76719	AA458882 Hs.4832	AA491208 Hs.62620 AA879119 Hs.18618	AA412185 Hs.97706 AA446019 Hs.104967	AA620707 Hs.112881	AA129896 Hs.42323	AA626356 Hs.38260
280581	429390 450776 359901 362985 1049042	126455	950709 814945		281756 344194 745030		788253	810809	824052 1499830	1- 1-	_		
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2.61224875	2.11510015 -1.3068592	2.03036733	2.89175557	2.00689249	2.60420543	000001	2.6848993		2.81574781	2.39704612
32716.89	32706.83 32595.19	32561.61	32506.07	32453.93 2 32441.75				32313.72	32291.4	32227.53
ELA3	WDR1	TACC3				PDK3	COLSAZ	YDD19	FANCA	
elastase 3, pancreatic (protease E) ESTs, Weakly similar to Weak similarity with Haemophilus influenzae protein HI0701	io		NT2RP2003108 ESTs Homo sapiens cDNA FLJ10422 fis. clone	NT2RP1000243 ESTs	EST ovruvate dehydrogenase		collagen, type v, alpina z ESTs	YDD19 protein =anconi anemia,	complementation group A F	Human DNA sequence from clone RH246F112.on clone RH246F112.on chromosome 1(32.1-41. Contains up to two novel agenes, and 713 (suppression of turnorigenicity 13 (cubon carcinoma) (Hs)7 Chineracting protein) (HiP) pseudogene, a ribonuclease H type 2.
ela: Hs.181289 (pro	Hs.156971 [C.4 Hs.85100 WE	Hs.104019 con Hor	Hs.5105 NT: Hs.8135 ES' Hor	Hs.267905 NT.		4	Hs.91567 ES	Hs.25615 YD Far	Hs.86297 con	Hun chn Con Gon gen car car car hb.170313 pse
1412502 AA845167 Hs.119091	N30256 Hs.125831 AA293182 Hs.85100	AA279990 Hs.104019	AA195648 Hs.5105 AA150505 Hs.8135	AA482031 Hs.20223 AA868042 Hs.25427	H97496 Hs.42385	V63567 Hs.54148	4A458837 HS.11576 4A460977 HS.91567	4A459697 Hs.21085	R32897 Hs.121707	AA608531 Hs.111812
1412502 AA	257452 N3 714196 AA	705064 AA	665144 AA 491770 AA	746072 AA		_	796129 AA	795598 AA	135609 R3	950594 AA
GF203	GF203 GF203	GF203	GF203 GF204	GF203 GF204	GF202	GF201	GF203 GF202	GF201	GF203	GF202

2.32865101	2.23398828 1.96712746 2.06935755 1.13582831	2.04262785 1.75791119 1.87671912	2.17724617 1.14708177 1.78024771 1.0937424	2.57206389 1.89805594 2.023029 2.34579119 2.29444037
2.3	2 2 3. 9. 9 1. 9.	2.0- 1.75 1.87	2.1. 7.1. 7.1.	2, 12, 12, 13, 13, 13, 13, 14, 15, 15, 15, 15, 15, 15, 15, 15, 15, 15
32193.74 32020.41	31961.19 31947.94 31907.9 31907.49 31837.88	31822.61 31733.18 31641.55 31548.48	31505.8 31451.66 31430.7 31429.46 31389.47 31265.74	31131.1 31122.67 31075.01 31066.42 31017.22 30957.92
	PTGS1 CKS1	UNC13 PPIE	NDUFB8 DKFZP434J1813 NRP2 ACTG1 CSF3R	KIAA1068
ESTs EST	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) PTGS1 ES1s CDC28 protein kinase 1 CKS1 ES1s ES1s	Homo sapiens clone 23904 mRNA sequence ESTs UNC13 (C. elegans)-like peptidylprolyl isomerase E (cyclophilin E) NADH dehydrogenase (ubliquinone) 1 beta	subcomplex, 8 (19kD, ASHI) MCFZp4341813 protein neuropilin 2 EST's actin, gamma 1 colony, stimulating factor 3	Horno sapiens mRNA, cDNA DNA DNA DNA DNA DNA DNA DNA DNA DNA
Hs.44577 Hs.130341	Hs.88474 Hs.23193 Hs.112874 Hs.77550 Hs.249989	Hs.250175 Hs.250824 Hs.155001 Hs.33251	Hs. 198273 Hs. 1098 Hs. 1778 Hs. 191915 Hs. 14376 Hs. 2175	Hs.26860 Hs.208985 Hs.4770 Hs.6831 Hs.230622 Hs.88417
N47902 Hs.44577 Al003621 Hs.130341	AA454668 Hs.88474 R21423 Hs.117418 AA620632 Hs.112874 AA459292 Hs.77550 AA181207 Hs.49414	AA700773 Hs.106273 R19408 Hs.14787 AA416685 Hs.11232 AA994801 Hs.33251	AA677499 Hs.109840 AA456833 Hs.6550 R37519 Hs.28823 AA682419 Hs.17252 AA676961 Hs.14376 AA443000 Hs.2175	AA608718 Hs.26860 AA455483 Hs.98060 AA521297 Hs.4770 AA255954 Hs.6831 W33192 Hs.55504 AA490088 Hs.88417
	4	435738 AA 130031 R1 731257 AA 1631682 AA		
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2.5758185 1.98446798		1.98403626			1.88718516	1.50800186	1.03782398	1.8843042	2.01565943	2.05756071			1.65879875					2.0299541	1.87148197	
30937.23 30909.21	30789.37	30709.31	30675.91	30670.39	30581.09	30478.12	30435.2	30421.95	30407.18	30344		30308.9	30300.24		30246.19	2001017	30184.69	30168.65	30167.26	
	APEX	M6PR	POLR2G				PFN1		ING1			SLC34A2			HLA-A	800	FADSDA		E2F1	
Homo sapiens mRNA for KIAA1343 protein, partial cds ESTs APEX nuclease (multifunctional DNA repair	enzyme) mannose-6-phosphate	receptor (cation dependent) polymerase (RNA) II (DNA	directed) polypeptide G Homo sapiens cDNA FLJ11200 fis, clone	PLACE1007725	FLJ20420 fis, clone KAT02462	Homo sapiens clone 24582 mRNA sequence		ESTs inhibitor of growth family,	member 1	ESTs	solute carrier family 34 (sodium phosphate), member	2	ESTS	major histocompatibility	complex, class I, A		delta-6 fatty acid desaturase	ESTS	E2F transcription factor 1	
Hs.94042 Hs.178379	Hs.73722	Hs.75709	Hs.14839	Hs.107381	Hs.6693	Hs.15535	Hs.75721	Hs.14713	Hs.46700	Hs.57079		Hs.105039	Hs.86693	13.1002.13	Hs.181244	070707	Us 19/6/1	Hs 112681	Hs.96055	
N63150 Hs.48723 AA481164 Hs.86522	AA478273 Hs.73722	AA465223 Hs.75709	AA477428 Hs.14839	AA974222 Hs.108797	AA133166 Hs.6693	N27165 Hs.15535	_	AA287325 Hs.14713	N47309 Hs.114409			AA459296 Hs.105039	AA505051 Hs.86693	AAG09991 IIS.11207.5	AA644657 Hs.119732	110000	AA6/034/ HS.1096/4	AA609292 Hs 112681	AA424950 Hs.96055	
285260 815189	740907	814211	740672	1585904	490753	257379	826173	701120	280508	261745		810911	825654	2661501	853906	9	878406	1031545	768260	
GF202 GF203	GF201	GF203	GF201	GF204	GF203	GF203	GF200	GF203	GF203	GF202		GF201	GF203	GFZUZ	GF201	i	01201	GF204	GF202	

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K et al				APPENDIX A		, find	`
280633	N50432	Hs.102648	Hs.102648	ESTs		30151.62	
364362	AA022541 Hs.61146	4s.61146	Hs.165205	ESTs		30125.64	
810040	AA455272 Hs.23119 W19228 Hs 107750	Hs.23119 Hs 107750	Hs.23119 Hs.100748	ITBA1 gene ESTs	ITBA1	30111.28	
				ESTs, Weakly similar to !!!! ALU CLASS C WARNING			
588561	AA147044 Hs.103861	4s.103861	Hs.103861	ENTRY !!!! [H.sapiens] Homo sapiens partial mRNA		30068.39	
				for G5b protein (G5b gene located in the class III region			
				of the major histocompatibility			
141675	H69566	Hs.73527	Hs.73527	complex)		30046.16	
201040	A A 9004 770 LTs 754 46	10.754.46	U. 157145	tetracycline transporter-like	TETRAN	30001 21	
1040100	_	18.73140 4s 199069	Hs 150655	FSTs		29954.19	
1055410		4s.116121	Hs.116121	EST		29904.46	
				protein tyrosine phosphatase			
375827	AA039851 Hs.43666	4s.43666	Hs.43666	type IVA, member 3	PTP4A3	29883.57	
				Homo sapieris cione 24006		1000	
773446	AA426049 Hs.17481	4s.17481	Hs.17481	mRNA sequence		29797.57	
376735	AA046311 Hs.62929	4s.62929	Hs.62929	ESTs		29752.73	
				solute carrier family 6			
				(neurotransmitter transporter,			
282501	N49856	Hs.82535	Hs.82535	betaine/GABA), member 12 olutamyl-prolyl-tRNA	SLC6A12	29729.03	
949914	AA599158 Hs.55921	4s.55921	Hs.55921	synthetase	EPRS	29727.05	
				major histocompatibility			
809298	AA458472 Hs.115756	4s.115756	Hs.73931	complex, class II, DQ beta 1	HLA-DQB1	29708.92	
884455	AA629712 Hs.116741	4s.116741	Hs.31731	antioxidant enzyme B166	AOEB166	29701.95	
913065	AAAEEE30 He 84169	Te 8/169	He 8/162	chromosome opzii.i gene	HIMAGGGB	29697.43	
3	10000			UDP-N-acetyl-alpha-D-			
				galactosamine:polypeptide N-			
				acetylgalactosaminyltransferas			
280544		Hs.117464	Hs.80120	e 1 (GalNAc-T1)	GALNT1	29634.04	
154610	R54969	Hs.111429	Hs.26209	ESTs		29564.06	

2.35376478 1.41075293

1.73372703

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1.9555911 2.17568319

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APPENDIX A Homo sapiens mRNA; cDNA

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	1.1650284		2.4347407							1.9043295	2.35144444	1.91538708		2.17750052		1.11080611		1.71404054	1.73026712
29090.4	29058.08		29044.65		28935.21		28900.96	28853.46		28818.98	28816.76	28806.78		28771.31		28767.64		28703.46	28646.96 28641
	ST16		BBOX		MALT1					COX6C		SHOX2		EEF1A1				QPRT	TPMT GCS1
DKFZp434D115 (from clone DKFZp434D115)	suppression of tumorigenicity 16 (melanoma differentiation)	butyrobetaine (gamma), 2- oxoglutarate dioxygenase		mucosa associated lymphoid tissue lymphoma translocation		ESTs, Weakly similar to microtubule-vesicle linker	CLIP-170 [H.sapiens]	ESTs	cytochrome c oxidase subunit	Vic	EST	short stature homeobox 2	eukaryotic translation	elongation factor 1 alpha 1	ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	[H.sapiens] quinolinate	phosphoribosyltransferase (nicotinate-nucleotide	pyropriospriorylase (carboxylating))	thiopurine S-methyltransferase TPMT glucosidase I
Hs.252723	Hs.66576		Hs.9667		Hs.180566		Hs.98640	Hs.105735		Hs.74649	Hs.229675	Hs.55967		Hs.181165		Hs.7107		Hs.8935	Hs.202669 Hs.83919
AA707531 Hs.23711	AA281635 Hs.66576		AA455988 Hs.9667		AA827405 Hs.22170		AA453618 Hs.98640	AA504626 Hs.105735		3 Hs.82758	AA429804 Hs.98630	4A425419 Hs.55967		4 Hs.4263		4 Hs.7107		3 Hs.8935	N74617 Hs.118689 AA291490 Hs.83919
	AA2816		AA4558				AA4536	AA5046		N66158	AA4298	AA4254		N34764		H68464		H99843	N74617 AA291490
1292053	712049		812074		1422794		795437	825608		278531	780938	773322		271398		139199		263894	296429 724893
GF204	GF200		GF202		GF204		GF201	GF204		GF203	GF202	GF203		GF203		GF200		GF203	GF203 GF201

1.7905103 2.16779064 1.21672101		2.18692791 2.15931858 1.31700973	2.21380281	1.97535804	1.85150475 2.33320516 2.53802874 2.42266525	2.03074922	2.31176562
28604.53 28582.48 28536.5 28521.95		28384.87 28358.21 28353.83	28342.98 28328.38 28293.85	28292.55 28231.58 28230.12	28218.21 28185.27 28175.69 28174.05	28140.62	28100.4
COMP KIAA0365		MTCP1		STK19	DKFZP566K1924	YDD19	
carrilage oligomeric matrix protein (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) E.STS KIAA0365 gene product ESTS	E-50.15 Human DNA sequence from clone 742C19 on chromosome 224(12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide VB and (parts of the four novel genes; two with homology to Phorbolin genes and one a novel chromobox profein gene.	Conta EST mature T-cell proliferation 1	ESTs ESTs EST	serine/threonine kinase 19 ESTs ESTs	DKFZP566K1924 protein ESTs ESTs	YDD19 protein	Homo sapiens cuiva FLJ20643 fis, clone KAT02633
Hs.1584 Hs.16614 Hs.190452 Hs.134314	1 7 7 8 1 7 1 7 1 7 1 7 1 7 1 7 1 7 1 7	Hs.7442 Hs.93956 Hs.3548	Hs.110835 Hs.93135 Hs.26038	Hs.444 Hs.43334 Hs.41654	Hs.26358 Hs.30627 Hs.112237	Hs.25615	Hs.5245
AA625900 Hs.7728 AA446188 Hs.16614 AA485539 Hs.64123 W74123 Hs.58352	AA490 I 3 PS: I 307 /	AA455261 Hs.7442 N48325 Hs.93956 AA029842 Hs.3548	AA121938 Hs.110835 AA702809 Hs.117287 R53442 Hs.26038	H87351 Hs.444 AA233646 Hs.43334 W15542 Hs.41654		N33243 Hs.43537	AA417825 Hs.5245
744945 781145 811029 346281		814815 279690 470175	490075 448048 40036	252412 666180 320201	263341 281190 415816	270561	752744
GF203 GF200 GF201 GF201	4 ZO	GF203 GF202 GF200	GF202 GF204 GF204	GF204 GF203 GF201	GF203 GF203 GF203	GF203	GF203

Aily Dooner 140. 217	2.16102468 1.67755626	2.03173971	2.16165923				1.16999999		1.04734974			1.22921745	2.31413139	2.54333024		2.18784472		2.69959205		1.24462992	2.47280999	1.85550025				
and the second	28079.58 28076.11	28067.58	28019.04	27970.89	27929.52		27896.07		27835.99			27766.67	27758.33	27689.01	27670.16	27638.2		27604.75		27558.44	27528.87	27495.48			27495.36	
	MPHOSPH9								MNDA						CAST					P5	BCHE					
APPENDIX A	M-phase phosphoprotein 9 ESTs	ESTs	ESTs	ESTs	EST	ESTs, Weakly similar to	KIAA0681 protein [H.sapiens]	myeloid cell nuclear	differentiation antigen	ESTs, Weakly similar to	proline-rich protein MP3	[M.musculus]	ESTs	ESTs	calpastatin	EST	Homo sapiens clone 23851	mRNA sequence	protein disulfide isomerase-	related protein	butyrylcholinesterase	ESTs	ESTs, Moderately similar to !!!!	ALU SUBFAMILY SC WABNING ENTRY !!!	[H.sapiens]	
	Hs.226989 Hs.69293	Hs.54713	Hs.85564	Hs.47701	Hs.113154		Hs.251757		Hs.153837			Hs.84640	Hs.44648	Hs.72150	Hs.247043	Hs.49230		Hs.10065		Hs.182429	Hs.1327	Hs.48527			Hs.5473	
	N23137 Hs.86178 AA101833 Hs.69293	191481 Hs.54713	4A187955 Hs.85564	AA676945 Hs.117017	AA700445 Hs.113154		Hs.93097		Hs.3197			Hs.84640	Hs.44648	4A156997 Hs.72150	AA416952 Hs.78220	Hs.49230		AA489073 Hs.10065		R01669 Hs.85200	AA885311 Hs.1327	Hs.48527			AA458471 Hs.5473	
	N23137 AA101833	N91481	AA187955	AA676945	AA700445		R76499		N29376			W93317	N34895	AA156997	AA416952	N66593		AA489073		R01669	AA88531	N62376			AA45847	:
∢etal.	266855 489549	306077	626037	460179	460614		143756		260200			357120	276712	502383	730002	278846		824802		123627	1461664	290561			809596	
Westbrook et al.	GF203 GF202	GF202	GF202	GF204	GF204		GF200		GF200			GF200	GF202	GF202	GF201	GF202		GF203		GF200	GF203	GF202	!		GF201	3

2.83567018 2.18012988 27270.95 27261.55 27205.75 27205.63 27200.96 27179.69 27149.96 27469.98 27444.03 27416.68 27251.17 27310.03 27293.7 27240.21 27289.7 **DNMT3B** CLDN10 ADAR NRAS HBG2 HTR6 stranded-DNA-binding protein SSDP PM5 DKFZp434D0412 (from clone adenosine deaminase, RNA-Homo sapiens mRNA; cDNA Human DNA sequence from KIAA06460 protein, an EST, neuroblastoma RAS viral (vchromosome 6p21.1-21.33 similar to ribosomal protein estis)), part of the gene for sequence-specific singlenethyltransferase 3 beta .35a, ZNF76 (zinc finger protein 76 (expressed in Contains a pseudogene as) oncogene homolog nemoglobin, gamma G STSs, GSSs and CpG serotonin) receptor 6 slone RP3-329A5 on Homo sapiens cDNA 5-hydroxytryptamine FLJ10713 fis, clone ONA (cytosine-5-)-DKFZp434D0412) NT2RP3000980 oM5 protein claudin 10 slands.n specific STS ESTS EST 4s.227823 4s.251673 Hs.235975 4s.177708 4s.266914 Hs.260523 4s.103174 4s.272812 4s.98632 4s.15476 1s.98771 4s.26126 Hs.22180 Hs.7957 Hs.9536 Hs.127419 Hs.103174 AA251192 Hs.104351 4A777002 Hs.121889 AA436473 Hs.15476 AA480851 Hs.26126 Hs.22797 AA429807 Hs.98632 4A629923 Hs.75663 Hs.96323 AA443704 Hs.98771 AA464195 Hs.7295 AA495991 Hs.9536 AA775212 Hs.8837 AA600189 Hs.7957 N72724 R41981 194627 N39452 753062 884673 345132 810761 256284 780944 276915 810389 784013 368815 768508 950367 377801 684595 31955 GF203 GF200 GF203 GF202 GF202 GF202 GF200 GF204 GF203 GF202 GF203 GF201 GF203 GF201 3F204

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1.57518985 2.05427016 1.46743467	2.79751216 2.56778881 2.30714691 2.38036108 2.051354 1.25398301 2.28644038	1.74687808 1.16550601 1.04190831	1,12554193 1,99688097 2,92452046 1,84858329 2,85616561 2,05046688
27124.17 27119.13 27058.26 27037.77	27026.94 27025.79 27022.72 27022.72 27008.06 26915.78 26905.66 26905.66 26901.24	26837.55 26834.6 26829.15 26828.17	26727.49 26695.36 26671.76 26654.97 26604.7 26613.2 26513.2
P4HA2 HSMU1B	EHP28 KIAA0569 FARA HSPF1	RPS4Y LDLC	GPI DKFZP58611023
procollagen-proline, 2- oxogularate 4-dioxygenase grown 4-dioxygenase grown 5-grown 4-dioxygenase polypeptide II adaptor-related protein complex 1, mu 2 subunit EST 8 EST 8 EST 8	arroopsance including including and properation of the part region of the part shock 40kD protein 1 EST ests	ribosomal protein S4, Y-linked RPS4Y ESTS brefeldin A-sensitive, peripheral Golgi protein LDLC ESTs	glucose phosphate isomerase GPI DKSTS DKSTS DKSTS Horno sapiens mRNA for Horno sapiens mRNA for KIAA1263 protein, partial cds ESTS ESTS ESTS
Hs.3622 Hs.18894 Hs.117112 Hs.16187	Hs.75841 Hs.59752 Hs.168303 Hs.47543 Hs.4871 Hs.250505 Hs.82646 Hs.15611 Hs.24476	Hs.187873 Hs.82399 Hs.98288	Hs.944 Hs.96423 Hs.111515 Hs.32452 Hs.104349 Hs.172140 Hs.172140 Hs.83243
W49522 Hs.3822 AA773478 Hs.18894 AA705092 Hs.117112 R87531 Hs.16187	AA62951 Hs.75841 W95948 Hs.59752 AA62564 Hs.98834 AA70508 Hs.487543 AA70508 Hs.1890 AA417558 Hs.28646 AA437758 Hs.28646 AA437758 Hs.28646 AA27764 Hs.15611 AA165400 Hs.24476	T69468 Hs.90653 AA757457 Hs.122024 AA504526 Hs.82399 AA418273 Hs.98288	AAA01111 Hs.944 AA629531 Hs.96422 AA5995531 Hs.83851 AA72944 Hs.82452 AA251347 Hs.104349 AA4036568 Hs.4891 AA025746 Hs.106597 W31540 Hs.89243
324785 V 845345 A 435161 A	450307 A 361798 V 745364 A 282838 N 461516 A 810787 A 703732 A	83011 T 395463 A 825296 A 767642 A	741474 A 745090 A 897807 A 565014 A 684561 A 753092 A 366315 A
GF204 GF203 GF203 GF203	GF201 GF203 GF202 GF202 GF202 GF203 GF203 GF203	GF203 GF204 GF200 GF203	GF200 GF204 GF203 GF203 GF203 GF203 GF203

2.3568856	1.18828063 1.15664321 1.99146804	1.88908888 1.79866124 2.34542853	2.30355554 2.04498516 1.95294098	1.92946207				2.16466792 1.32432322	2.16060015 2.21027878	2.44842155 2.44255612	2.12268082
26447.8	26445.34 26436.48 26436.33	26379.87 26350.54 26329.07	26278.57 26277 26276.44	26270.34		26209.22	26197.24 26107.04	26081.3 26064.09 26034.42	26017.92 25986.42	25975.15 25949.98	25921.53 25911.76 25909.46
HSPCA	PSPHL CDC27	KIAA0964		UST		KCNA5	SPIB	TASR	ID4	BPGM	STK18
heat shock 90kD protein 1, alpha phosphoserine phosphatase-	like cell division cycle 27 EST	KIAA0964 protein ESTs EST	ESTs EST EST	uronyl 2-sulfotransferase erythroblast macrophage	protein potassium voltage-gated channel, shaker-related	subfamily, member 5 Spi-B transcription factor (Spi-	1/PU.1 related) ESTs TLS-associated serine-	arginine protein ESTs ESTs	inhibitor of DNA binding 4, dominant negative helix-loop- helix protein ESTs	EST	serine/threonine kinase 18 ESTs ESTs
Hs.180532	Hs.76845 Hs.172405 Hs.103093	Hs.177425 Hs.115572 Hs.100839	Hs.16063 Hs.21939 Hs.104292	Hs.134015	8.20013	Hs.150208	Hs.192861 Hs.120868	Hs.3530 Hs.271399 Hs.62654	Hs.34853 Hs.48556	Hs.198365 Hs.252014	Hs.172052 Hs.33033 Hs.47068
AA159669 Hs.11601	W05628 Hs.76845 T81764 Hs.73151 W52353 Hs.103093	<u>ω</u>	≥ 22 -	AA703125 Hs.114170	AA078026 DS.20615		N71628 Hs.2981 AA776771 Hs.120868	N51307 Hs.44045 AA478556 Hs.72164 AA235330 Hs.62654	AA454080 Hs.107892 N62516 Hs.48556	AA678065 Hs.79537 AA131240 Hs.103819	AA732873 Hs.26888 AA455078 Hs.33033 N52874 Hs.47068
593223	299679 109708 325520	773649 130364 28243	683695 726830 684265	434825	242032	1556044	295093 1276652	283088 753110 687393	788234 288800	430614	1343971 812277 283615
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ARHGAP1	MEN1 DKFZP586I1023		ммзрн				MDK DKFZP586M1523	
Rho GTPase activating protein 1	multiple endocrine neoplasia MENI ESTs ESTs DKFZP58611023 protein DKFZ	ESTs, Weakly similar to PROBABLE ATP- DEPENDENT RNA HELCASE HRH1 [H.saplens] ESTs	methylmalonate-semialdehyde dehydrogenase ESTs Homo sapiens mRNA; cDNA DKFZp434N1221 (from clone	DKFZp434N1221) ESTs, Weakly similar to	62D9.p [D.melanogaster] ESTs	ESTS ESTS midking (nounth	infantic (rednie growii) promoting factor 2) DKFZP586M1523 protein ESTs, Moderately similar to copper transport protein HAH1	[H.sapiens] ESTs EST
Hs.138860	Hs.24297 Hs.5309 Hs.143684 Hs.111515	Hs.29403 Hs.193132 Hs.163070	Hs.170008 Hs.102349	Hs.183454	Hs.80021 Hs.172510	Hs.235/09 Hs.99540 Hs.104836	Hs.82045 Hs.22981	Hs.121986 Hs.150395 Hs.132755 Hs.7739
AA443506 Hs.83262	AA261796 Hs.24297 AA916780 Hs.5309 AA398281 Hs.97597 AA044664 Hs.37438	H99845 Hs.117988 W96463 Hs.47134 AA718954 Hs.120839	N62179 Hs.921 H96668 Hs.102349	AA505082 Hs.8932	N57731 Hs.80021 AA136618 Hs.50833	AA465168 Hs.3/262 AA461450 Hs.99540 AA470073 Hs.104836	AA968896 Hs.82045 AA465218 Hs.22981	AA121142 Hs.121986 T56982 Hs.118546 W44923 Hs.55779 AA456595 Hs.7739
771196	685371 1556259 726721 488421	263883 358671 1292487	289818 251876	825669	246686	815051 796614 730377	1574594 814222	548995 68340 322838 809397
GF200	GF200 GF204 GF203 GF201	GF203 GF201 GF204	GF200 GF202	GF203	GF200 GF204	GF203 GF203 GF202	GF204 GF204	GF203 GF204 GF202 GF201

1.89054859 2.19014904	1.64348346 2.21622649	2.88427372	000010001	1.3310866	1.97387514		2.17701975 1.67218155	1.69283085	2.23376477
25263.07 25253.45 25195.13	25182.3 25156.48	25154.09	20149.03	25149.63	25146.36	25101.3	25099.75	24977.99	24976.47 24909.29
BM-009		MTHFD1	2	IGF2			HSPC192	HDCMA18P	
Homo sapiens cDNA FL20807 fis, clone ADSE01784 hypothetical protein ESTs (Weakly similar to Weak similarity with the Ysv6 protein	[C.elegans] ESTs methyleneterahydrofolate dehydrogenase (NADP+ dependent), methenytterahydrofolate cyclorydrolase, formyterahydrofolate	synthetase insulin-like growth factor 2	(somatomedin A) insulin-like growth factor 2	(somatomedin A) ESTs, Highly similar to CGI-	113 protein [H.sapiens]	Homo sapiens mHNA for inositol 14,5-trisphosphate 3- kinase isoenzyme, partial cds ESTs, Weakfy similar to cytochrome P450db1	[H.sapiens] hypothetical protein	ES1 HDCMA18P protein Homo sapiens mRNA; cDNA DKFZp434B231 (from clone	DKFZp434B231) ESTs
Hs.169384 Hs.92918 Hs.119178	Hs.11252 Hs.16331	Hs.172665	HS.251664	Hs.251664	Hs.19077	Hs.21453	Hs.16846 Hs.6762	Hs.28350	Hs.267445 Hs.216756
W69184 Hs.23973 AA173423 Hs.92918 AA427782 Hs.10093	AA181868 Hs.14484 AA099706 Hs.16331			N54596 Hs.75963	AA504139 Hs.19077	N46828 Hs.21453	AA449325 Hs.16846 AA701379 Hs.6762	AA682888 RS.117240 N64387 HS.28350	AA452406 Hs.20925 N93454 Hs.54950
343699 595213 771133	510845				825229	279146		290240	307302
GF203 GF202 GF201	GF202 GF202	GF202	GF200	GF200	GF203	GF201	GF202 GF203	GF203	GF203 GF204

1.55172328	1.00793071	2.58390144	2.5011726	1.25764178	2.12182505	1.18676983	1.68353751	1.8789448 2.19861801	2.10332084 2.31616716 2.49836139
24901	24876.6 24842.5 24834.45	24810.34	24801.71	24793.98	24779.04	24750.87 24716.79	24638.71	24632.91 24610.4 24598 24596.22	24591.39 24563.57 24543.57 24541.62
	SLC7A5 CA5A	MIPEP	TRAP240	RNASE4	SNX2	SLC2A1 CNN2	UBE2E1	KIAA1066 ITM1	KIAA0652 DKFZP547E1010
ESTs	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 carbonic anhydrase VA, mitochondrial ESTs	mitochondrial intermediate peptidase thyroid hormone receptor-	subunit ribonuclease, RNase A family,	4 ESTs, Weakly similar to CGI- 89 protein [H.sapiens]	sorting nexin 2 solute carrier family 2 (facilitated glucose	transporter), member 1 calponin 2 ubiquitin-conjugating enzyme E2E 1 (homologous to yeast	UBC4/5) ESTs KIAA1066 protein; JSAP1 homolog (mouse). JIP3	homolog (mouse) integral membrane protein 1 EST ESTs	EST ESTs KIAA0652 gene product DKFZP547E1010 protein
Hs.269597	Hs.184601 Hs.177446 Hs.71989	Hs.68583	Hs.11861	Hs.169617 Hs.38270	Hs.11183	Hs.169902 Hs.169718	Hs.7766 Hs.83196	Hs.88500 Hs.89650 Hs.121893 Hs.264079	Hs.208398 Hs.112732 Hs.79672 Hs.227391
AA707306 Hs.120971	AA419177 Hs.63052 AA699469 Hs.137 B67602 Hs.71989	AA843592 Hs.68583	AA457462 Hs.59878	T60223 Hs.10716 AA432270 Hs.9508	AA045230 Hs.118669	AA775509 Hs.23579 AA284568 Hs.89111	AA044025 Hs.7766 AA644183 Hs.83196	AA489245 Hs.5682 R68805 Hs.89650 AA777084 Hs.121893 N22776 Hs.42405	က ထ ထ
451470	755578 433553 141171	1390584	838262	81417	487704	378365 713886	486607 845454	825083 141972 377874 266643	395459 782307 32076 1455257
GF203	GF201 GF201 GF201	GF203	GF202	GF200 GF201	GF203	GF204 GF200	GF203 GF204	GF203 GF202 GF204 GF201	GF203 GF202 GF202 GF204

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1.04627424 1.18657746 2.2796884	1.86795552 2.16830809	2.790107 2.26989026	2.32466283 2.06504927 1.31207704	1.85270282	1.89664514 1.64826874	2.13932746 2.46890914 1.7735543
24537.26 24520.38 24477.02	24444.48 24425.76 24394.11	24360.46 24344.07 24311.57	24291.14 24272.87 24269.22 24210.67	24206.85	24194.86 24183.3	24149.46 24133.14 24132.6
GSTM4 RAI3	BCKDHA IFI35		CPA2 METTL1	AMD1		ARHA XRCC3
ESTs glutathione S-transferase M4 retinoic acid induced 3 branched chain keto acid advitogenase E1, alpha polykrogenase E1, alpha		KIAA0428 [H.saplens] Homo sapiens mRNA; cDNA DKFZp434K152 (from clone DKFZp434K152) CESTs carboxypeptidase A2	-	Homo sapiens cDNA FLJ20514 fls, clone KAT09756 S-adenosylmethionine decarboxylase 1	ESTS, Moderately similar to TGF-BETA RECEPTOR TYPE III PRECURSOR [H.sapiens] ESTs ras homolog gene family,	member A X-ray repair complementing defective repair in Chinese hamster cells 3 ESTs
Hs.93231 Hs.5233 Hs.194691	Hs.78950 Hs.180793 Hs.50842	Hs.41891 Hs.46798 Hs.262172	Hs.89717 Hs.112705 Hs.42957 Hs.261372	Hs.44423 Hs.262476	Hs.12927 Hs.179964	Hs.77273 Hs.99742 Hs.85432
W15465 Hs.93231 AA290737 Hs.105976 AA172400 Hs.62720	7 4 7	H93450 Hs.41891 N47989 Hs.46798 W42459 Hs.119535	AA844831 Hs.89717 AA609422 Hs.112705 AA422058 Hs.42957 AA150487 Hs.73847	AA444046 Hs.44423 R82299 Hs.75744	N26658 Hs.12927 AA678098 Hs.116373	AA426324 Hs.27486 AA459013 Hs.99742 AA180882 Hs.85432
322723 713922 595037	460837 413066 1422723	230202 281565 323077	1412245 743536 755239 491727	756575	269269 430723	769019 814287 612024
GF200 GF200 GF202	GF204 GF203 GF203	GF200 GF202 GF202	GF203 GF202 GF200 GF201	GF203	GF203 GF203	GF203 GF203 GF202

Atty Docket No. 2172	2.21352169	1.20957672	1.20957672	1.90830113	2.10743358			1.22184535		1.74812169		2.21346954	1.08469779	0000000	1.11/639/9	2.00030140	1.79103868	1.93584203	2.13043371	2.2000000
Atty	24127.05 24076.39	24015.16	24015.16	24008.18	23986.2		23984.41	23924.85		23911.7		23803.74	23750.89	Fores	23/31./9	50.12162	23/06.1/	23686.33	23556 13	23538.67
07897	CHN2	SLC25A16	SLC25A16		SOX22			C14ORF2		GNG2			SLN		בסמ		LOC51264		KNICI 1	Nigh
TD2020'86226860 APENDIXA	chimerin (chimaerin) 2 ESTs solute carrier family 25 (mitochondrial carrier; Graves	16 solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen) member	16 FSTs	EST	SHY (sex-determining region Y)-box 22	FLJ20208 fis, clone	COLF1623 chromosome 14 open reading	frame 2	guanine nucleotide-binding protein G(I)/G(O) gamma-2	subunit	Homo sapiens mHNA; cUNA DKFZp434C107 (from clone	DKFZp434C107)	sarcolipin	deleted in oral cancer (mouse,	homolog) 1	ESIS	hypothetical protein	ESIS	ESIS Kinonin liko 1	ESTs
	Hs.15202 Hs.112699	Hs.180408	Hs.180408 Hs 16936	Hs.103789	Hs.43627		Hs.131776	Hs.109052		Hs.23767		Hs.101651	Hs.15219	:	Hs.3436	HS.99139	Hs.7736	Hs.32232	HS.29604	Hs.42196
	AA521339 Hs.78866 AA609368 Hs.112699	AA411554 Hs.119564	AA411554 Hs.18203	AA127851 Hs.103789	AA425701 Hs.13050		AA669057 Hs.131776	T90621 Hs.109052		AA115300 Hs.103720		H06273 Hs.101651	AA196465 Hs.15219		R78607 Hs.3436	_	W88752 Hs.7736	AA191510 Hs.32232	AA121366 HS.29604	AA251826 Hs.42196
ik et al.	826142 743452	754490	754490	501700	773203		854425	110772		501431		44292	628295		144932	813633	417801	626619	490055	684835
Westbrook et al.	GF203 GF202	GF200	GF200	GF202	GF202		GF204	GF200		GF202		GF202	GF200		GF200	GF203	GF203	GF202	GF202	GF204

1.17383412	2.11469208	2.07464876 1.17666307 2.68951525	1.18018831	2.02272118	2.45422548 2.12851527 2.31171363	2.28327554
23534.84 23515.89 23507.05 23498.42 23491.44	23427.81	23388.92 23384.09 23366.37	23342.31	23242.84 23238.72	23230.27 23166.31 23156.38	23130.45 23042.16
DAF RABSEP BCL2A1	KMO ARL1	VIL2 THBS1	GFAP SYCP1		KIAA0439	
decay accelerating factor for complement (CDSS, Corner blood group system) rabaptin-5 ESTs ESTs BCL2-related protein A1	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) ADP-ribosylation factor-like 1 Homo sapiens mRNA; cDNA DKFZp588B1922 (from clone	DKFZp586B1922) villin 2 (ezrin) thrombospondin 1	glial fibrillary acidic protein synaptonemal complex protein 1	ESTs, Weakly similar to KIAA0822 protein [H.sapiens] ESTs KIAA0439 protein; homolog of yeast ubiquitin-protein ligase	Rsp5 ESTs EST	ESTs, Weakly similar to GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP [H.sapiens] ESTs
Hs.1369 Hs.250535 Hs.108829 Hs.116304 Hs.227817	Hs.107318 Hs.242894	Hs.184779 Hs.155191 Hs.87409	Hs.1447 Hs.112743	Hs.270618 Hs.43725	Hs.12017 Hs.43233 Hs.104862	Hs.180320 Hs.98587
R09561 Hs.1369 AA479888 Hs.109729 H98134 Hs.108829 AA629110 Hs.116304 AA459263 Hs.38768	AA152183 Hs.107318 N51280 Hs.77102	AA485688 Hs.29937 AA411440 Hs.75683 AA088749 Hs.107421	AA669414 Hs.1447 AA609655 Hs.112743	N80032 Hs.54372 N26031 Hs.43725	AA458578 Hs.127640 N64145 Hs.43233 AA425295 Hs.104862	AA600214 Hs.107567 AA460313 Hs.98587
128126 772890 261102 1035762 814478	504461 283034	811121 755145 511820	382693	299918 268877	837953 285760 773279	949988 795755
GF200 GF201 GF201 GF204 GF200	GF201 GF203	GF202 GF200 GF202	GF200 GF201	GF204 GF203	GF202 GF202 GF202	GF202 GF201

1.9913894 2.51495919	1.80252787	1.20224549 1.129053 2.25053376 2.07799164	2.48856178 2.77321356 2.03870652	1.9874666 2.40930586 2.63772575	1.59580848 2.07078884 1.4478952 1.23119007 2.23116686 2.0564728
23040.46 23008.87	22996.29 22968.9	22961.35 22955.55 22952.71 22932.03	22881.64 22880.82 22864.01	22842.85 22831.11 22758.58	22752 22738.39 22719.72 22702.08 22652.1 22610.32
KIAA1025		FCER1G RPS23	CHST1 ZMPSTE24	NRXN3 TRIO	PRSS21 KIAA0696
ESTS, Weakly similar to IIII ALU CLASS B WARNING ENTRY IIII [H.sapiens] KIAA1025 protein ESTs, Weakly similar to phosphoinositide 3-kinase	[H.sapiens] ESTs Fc fragment of IgE, high	animity i, receptor for, garinna polypeptide ribosomal protein S23 ESTs ESTs	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1 zinc metalloproteinase, STE24 (yeast, homolog)	Homo sapiens mRNA for KIAA1204 protein, partial cds neurskin III triple functional domain (PTPAF interacting)	PLAD II 12 II 18, done PLACE 1006139 ESTS Professe, serine, 21 (testisin) ESTS F-box protein Fbwtb; beta- transducin repeat-containing protein 2 ESTS
Hs.109333 Hs.4084	Hs.118739 Hs.59774	Hs.743 Hs.3463 Hs.48008 Hs.96464	Hs.104576 Hs.25846 Hs.111128	Hs. 98438 Hs. 22269 Hs. 171957	Hs.273230 Hs.177698 Hs.72026 Hs.44649 Hs.21229 Hs.109851
W85900 Hs.109333 AA496000 Hs.91734	AA521439 Hs.29098 W96022 Hs.59774	H79353 Hs.743 AA490300 Hs.8653 N56947 Hs.48008 AA417250 Hs.96464	ω 4:	H96630 H8.42212 AA425435 H8.98438 AA450336 H8.22269 AA191348 H8.96178	AA401457 Hs.5249 AA521387 Hs.887661 AA620757 Hs.72026 N34896 Hs.44649 H97827 Hs.21229 AA045641 Hs.109881
416113	826194 358544	235155 824426 280082 731183	53039 361922 626842	251565 773329 785542 626822	742049 827003 1049287 276714 251698 489407
GF202 GF203	GF203 GF202	GF200 GF200 GF202 GF202	GF202 GF203 GF202	GF202 GF203 GF203 GF202	GF203 GF203 GF203 GF203 GF202 GF202

1.1666658	2.3266694	1,57403927	1.08951939	2.20450713 2.07196359		1.33620821	1.69213244	1.67232983	1.19573663 2.12076061 2.61099458 1.75555477	-1.0006549 2.19352716 1.87281597
22516.76 22503.42	22481.87 22461.72	22410.37 22410.37	22400.11	22400.03 22393.94	22366.21	22345.43	22328.43 22326.52 22319.81	22306.45	22306.12 22292.46 22290.25 22274.17	22270.55 22257.13 22254.91
GNL1	L2RA	CHN2 KIAA0909		FARP1	EEF1A1		FAT2 PIM1	DUSP11		CSTF2
	r, alpha		ARHGEF) nain protein		ے	[H.sapiens]		_		
guanine nucleotide binding protein-like 1 ESTs Homo sapiens cDNA FLJ20282 fis, clone	HEP03828 interleukin 2 receptor, alpha	chimerin (chimaerin) 2 KIAA0909 protein ESTs, Weakly similar to C06A6.3 gene product	[C.elegans] FERM, RhoGEF (ARHGEF) and pleckstrin domain protein	(chondrocyte-derived) ESTs eukarvotic translation	elongation factor 1 alpha 1 ESTs. Weakly similar to Zn-	finger-like protein [H.sapiens] FAT tumor suppressor	(Drosophila) homolog 2 pim-1 oncogene EST	dual specificity prospirates 11 (RNA/RNP complex 1- interacting) Homo sapiens clone 23596	mRNA sequence ESTs ESTs EST	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kD EST ESTs
Hs.83147 Hs.163813	Hs.72782 Hs.1724	Hs.15202 Hs.107362	Hs.24025	Hs.183738 Hs.103046	Hs.181165	Hs.36779	Hs.158159 Hs.81170 Hs.116930	Hs.14611	Hs.3850 Hs.161851 Hs.86379 Hs.121978	Hs.693 Hs.141707 Hs.54808
Hs.83147 Hs.23807	AA169226 Hs.72782 AA903183 Hs.1724	W93108 Hs.59417 AA458480 Hs.89124	Hs.24025	AA486435 Hs.106786 W42928 Hs.103046	AA775453 Hs.18623	Hs.36779	H10939 Hs.92060 N72855 Hs.43561 AA664024 Hs.116930	Hs.14611	R94775 Hs.3850 AA431736 Hs.98748 AA454543 Hs.86379 AA777817 Hs.121978	Hs.693 Hs.103047 Hs.54808
N30302 R25153	AA169226 Hs.7278; AA903183 Hs.1724	W93108 AA458480	R26337	AA486435 W42928	AA775453	H53499	H10939 N72855 AA664024	AA463480 Hs.14611	R94775 AA431736 AA454543 AA777817	AA291995 Hs.693 W42996 Hs.1030 N92571 Hs.5480
257523 131877	609910 1517171	415046 809595	133084	842918 323396	878173	202692	47234 2 9 1490 855413	811813	198509 782270 838048 449316	714426 323251 304786
GF201 GF200	GF202 GF204	GF203 GF201	GF200	GF202 GF202	GF204	GF200	GF201 GF203 GF204	GF202	GF200 GF202 GF202 GF203	GF200 GF202 GF202

Atty Docket No. 21 / 26/92	2.65650269	2.24932221 1.74777026	1.26740767			2.06091639	1.9741595	1.77690594	2.63831034	1.87280389		1.89584736	1.01566052	1.24020479		2.28419802			2.03322686		2.0532938	1.58579411				1.80020086
Atty	22239.15 22196.51 22168.7	22148.41 22099.48	22052		22041.16	22010.79	21961.79	21959.67	21951.18	21940.45	21924.1	21922.32	21921.91	21901.26	21828.18	21815.32			21778.39	21773.57	21763.21	21751.64	21738.39	21732.35	21695.8	21689.18
			or PIG7	_	NME5	TXNL2			B7			RPL13	ANK1	RBL2							PCNT			SKB1	TRB®	
APPENDIX A	ESTS ESTS ESTS Home conjunc mDNA for	KIAA1205 protein, partial cds ESTs	LPS-induced TNF-alpha factor PIG7	non-metastatic cells 5, protein expressed in (nucleoside-	diphosphate kinase)	thioredoxin-like	ESTs	ESTs	B7 protein	ESTs	ESTs	ribosomal protein L13	ankyrin 1, erythrocytic	retinoblastoma-like 2 (p130)	ESTs	EST	Homo sapiens mRNA; cDNA	DKFZp586F1822 (from clone	DKFZp586F1822)	ESTs	pericentrin	ESTs	ESTs	skb1 (S. pombe) homolog	T cell receptor beta locus	ESTs
	Hs.112797 Hs.146278 Hs.93966	Hs.104417 Hs.22701	Hs.76507		Hs.72050	Hs.42644	Hs.243118	Hs.72838	Hs.155586	Hs.87779	Hs.188361	Hs.180842	Hs.183805	Hs.79362	Hs.21364	Hs.112503			Hs.82719	Hs.105201	Hs.15896	Hs.120863	Hs.28482	Hs.12912	Hs.2003	Hs.182123
	AA609983 Hs.112797 AA454840 Hs.12304 N49068 Hs.93966	AA278757 Hs.104417 AA521416 Hs.22701	AA625666 Hs.76507		AA453579 Hs.72050	H99205 Hs.114329	AA279172 Hs.88577	AA169230 Hs.72838	N90281 Hs.94610	AA250962 Hs.87779	AA045847 Hs.62908	AA459104 Hs.119436	AA464755 Hs.1242	W52803 Hs.108620	N62279 Hs.21364	AA599042 Hs.112503			AA620597 Hs.55547	N64753 Hs.34797	N45326 Hs.15896	AA706664 Hs.120863	AA862496 Hs.28482	AA496357 Hs.12912	N91921 Hs.75727	N66138 Hs.57911
k et al.	1031976 809969 279728	703577 826103	745347		795208	261840	704076	609682	302632	684508	488769	814316	810625	321247	290277	950378			951325	284531	283341	1240062	1456983	755302	306841	278502
Westbrook et al.	GF202 GF201 GF201	GF203 GF203	GF200		GF201	GF203	GF203	GF202	GF202	GF203	GF201	GF203	GF200	GF200	GF204	GF202			GF202	GF201	GF203	GF203	GF204	GF201	GF201	GF203

COP9 (constitutive

	2.53251422	1.51081392	1.19708864			1.98526816										1.90584952	1.80305272				1.62714535	2.40380092				2.30888422			1.23993455		
	2.532	1.510	1.197			1.985										1.905	1.803				1.627	2.403				2.308			1.239		
	21658.52	21629.22	21608.27		21590.89	21566.64			21544	21541.35	21536.84	21532.67				21531.74	21523.18	21487.73		21445.72	21440.52	21437.2			21357.22	21356.79	21345.69		21305.07		21242.23
	COPS3		RBM5			ART-4			ATP6DV								KIAA0590			ADTD	UNRIP				APPBP2						GRB2
photomorphogenic, Arabidopsis, homologi subunit	3	ESTs	RNA binding motif protein 5	DKFZp43411216 (from clone	DKFZp434I1216)	ART-4 protein	Vacuolar proton-ATPase,	subunit D; V-ATPase, subunit	Q	ESTs	EST	ESTs	Homo sapiens HMT-1 mRNA	for beta-1,4	mannosyltransferase,	complete cds	KIAA0590 gene product	ESTs	adaptor-related protein	complex 3, delta 1 subunit	unr-interacting protein	ESTs	amyloid beta precursor protein	(cytoplasmic tail)-binding	protein 2	ESTs	EST	Homo sapiens cDNA	COLF0307	growth factor receptor-bound	protein 2
	Hs.6076	Hs.237517	Hs.201675		Hs.13768	Hs.3566			Hs.106876	Hs.122677	Hs.116314	Hs.165464				Hs.44592	Hs.111862	Hs.192002		Hs.75056	Hs.3727	Hs.28454			Hs.84084	Hs.54699	Hs.121862		Hs.272972		Uo 6300
	Hs.6076	Hs.7941	Hs.74594		4A521470 Hs.13768	Hs.3566			AA702541 Hs.106876	AA009628 Hs.103297	AA629254 Hs.116314	AA826324 Hs.110832				Hs.121056	4A481751 Hs.111862	4A780191 Hs.122123		AA630776 Hs.75056	Hs.3727	Hs.28454			AA431206 Hs.81539	N91347 Hs.54699	AA776705 Hs.121862		Hs.79601		Un 400000
	AA455640 Hs.6076	N62403	W73892		AA521470	AA489080 Hs.3566			AA702541	AA009628	AA629254	AA826324				R95684	AA481751	AA780191		AA630776	AA481155 Hs.3727	AA399260 Hs.28454			AA431206	N91347	AA776705		R69153		TA7040
	813983	288681	345559		826219	824799			384078	365543	744029	1420830				199337	810773	1034740		856434	815190	726471			782161	305937	1292836		142134		10000
	GF203	GF203	GF200		GF204	GF203			GF201	GF201	GF204	GF204				GF203	GF202	GF204		GF201	GF203	GF203			GF201	GF202	GF204		GF200		V COL

GF203 279516 GF202 726684	N48820 Hs.122974 AA398233 Hs.111894		ESTs KIAA0108 gene product	KIAA0108	21223	1.62418018
705265 826193 782710	AA280677 Hs.1162 AA521448 Hs.103845 AA447603 Hs.99123	Hs.250904 5 Hs.103845 Hs.99123	zinc finger protein 258 ESTs EST	ZNF258	21201.92 21173.5 21152.43	1.10258694 2.33846547 2.2792814
GF200 135713	R32428 Hs.106194	t Hs.79946	cytochronie Fagor, subianny XIX (aromatization of androgens) three prime repair	CVP19	21150.26	1.26383652
GF203 704410 GF201 280286	AA279658 Hs.23595 N49224 Hs.46911	Hs.23595 Hs.159448	exonuclease 1 H.sapiens mRNA for SURF-2 DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 19	TREX1	21144.16 21134.78	1.81991201
GF200 139872 GF202 286253 GF203 43709 GF202 309983 GF200 194600 GF204 811914	R64251 HS.28500 N66296 HS.49170 H05734 HS.30559 N95440 HS.102941 R84242 HS.33436 AA454986 HS.54973	Hs.226396 Hs.49170 Hs.30559 I Hs.102941 Hs.268337 Hs.54973	(Dbp5, yeast, homolog) ESTs ESTs ESTs ESTs	DDX19	21105.75 21101.99 21095.67 21035.54 21026.21 21025.72	1.29301512 2.18743605 1.72851925 1.96038256 1.47844928
GF201 1030769 GF200 705265	AA608988 Hs.2051 AA280676 Hs.118973	Hs.2051 3 Hs.250904	testis specific protein, Y-linked TSPY zinc finger protein 258 ZNP2: Homo sapiens mRNA; cDNA DKTZp566B213 (from clone	TSPY ZNF258	21018.37 20981.46	1.25685163
324694 489644 306540 415145	W47327 HS.8878 AA099390 Hs.23657 N91821 Hs.118253 W95082 Hs.1376	Hs.194051 Hs.177532 Hs.25298 Hs.1376	DKFZp568B213) ESTs ESTs ESTs Hydroxysteroid (11-beta) hydroxysteroid (11-beta) Homen sapiens mRNA; cDNA PKFZp58B6 171 (from done	HSD11B2	20977.75 20975.72 20960.93 20954.75	1.33146371

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APPENDIX A

1.27982697		1.86692501	1.12090300	2.26723964	1.15984733 2.549751		2.62933217 1.96352918	1.97820249
20892.8 20887.64 20885.31 20878.78 20860	20853.95	20814.15	20809.03	20805.04	20777.65 20776.72 20763.5	20756.25	20752.25 20751.51	20743.64
	MCSP	ī	TALDO1	KIAA0981	UQCRFS1			
Homo sapiens cDNA PLA119936 fis., clone OVAFC1000958, weakly similar to HYPOTHETICAL PROTEIN MJ0933 ESTS ESTS ESTS	mitochondrial capsule Nelenoprotein ESTs, Highly similar to PEROXISOME ASSEMBLY	FACTOR-2 [H.sapiens] endothelin converting enzyme		KIAA0981 protein ubiquinol-cytochrome c reductase, Rieske iron-sulfur	polypeptide 1 ESTs ESTS ESTS, Moderately similar to !!!! MALU SUBFAMILY J	[H.sapiens] ESTs, Weakly similar to	ootential CDS [H.sapiens] ESTS Homo sapiens cDNA FLJ10739 fis, clone RT2PR9001472, weakfy similar to NONHISTONE CHROMOSOMAL PROTEIN	
Homo FLJ10 OVAR similar Hs.7337 PROT Hs.99566 ESTs Hs.117142 ESTS Hs.712070 ESTS Hs.97641 EST	mit Hs.111850 selv ES			Hs.158135 KIA ubi red	Hs.3712 pol Hs.106795 ES Hs.169444 ES AL/		Hs.64754 pot Hs.23871 ES Ho.23871 FO Ho NT NT Sim	Hs.69594 6A
AA775246 Hs.7337 AA460156 Hs.99556 AA63174 Hs.117142 AA719131 Hs.120870	AA609976 Hs.111850	AA460646 Hs.115570	AA279429 HS.88611 AA955007 Hs.77290	AA488976 Hs.25931	AA448184 Hs.3712 344714 Hs.106795 AA004528 Hs.60027	AA862339 Hs.127051	M95061 Hs.64754 AA426022 Hs.23871	AA489207 Hs.69594
878588 A 795885 A 1031006 A 1292534 A 726889 A	1031185 A			824720 A	782800 A 33814 B 428632 A	~	415211 V 773443 A	825036 A
GF204 GF202 GF204 GF204 GF203	GF201	GF202	GF204	GF203	GF200 GF202 GF201	GF204	GF202 GF202	GF203

1.0900129	1.20563655	1.14255194 1.14255194 1.84845782	2.26907528	2.63305536 1.87469495	1.17352235 2.24130792 1.40526071
20694.53 20626.99 20590.82 20573.27	20563.12 20546.23	20504.06 20504.06 20491.3	20425.94 20423.1 20385.23	20384.43 20378.52 20376.61 20350.63 20317.81	20284.24 20278.36 20202.85
P84 UNC5C DXS52E	UVRAG GMPS	GRP58 GRP58	HSPA4 APOB PI8	НВР	LRP1 HSU79274
nuclear matrix protein p84 ESTs unc5 (C.elegans homolog) C DNA segment on Arhomosome X (unique) 522 expressed sequence	associated gene guanine-monophosphate synthetase	glucose regulated protein, 58kD glucose regulated protein, 58kD	ESS 18 heat shock 70kD protein 4 apolipoprotein B (including Ag(x) antigen) protease inhibitor 8 (ovalburnin type) ESTs, Moderately similar to !!!! ALU SUBFAMILY SP	MARNING ENTRY !!!! H-saplens ESTs ESTS	protein 1 (alpha-2- macroglobulin receptor) protein predicted by clone 23733 ESTs
Hs.1540 nu Hs.94842 Eg Hs.44553 un Hs.83363 ex	Hs.13137 as gu Hs.5398 sy	gli Hs.183760 58 gli Hs.183760 58 Hs.78085 ES		W Hs.120200 Hs.063022 E: Hs.98131 Hs.99126 Hs.75257 Hs.46630 Follows	pr Hs.89137 m pr Hs.150555 23 Hs.5161 E8
AA039512 Hs.95221 N94234 Hs.49093 N34287 Hs.44553 AA463924 Hs.83363	AA490771 Hs.13137 N59764 Hs.5398	0 Hs.110029 0 Hs.84298 6 Hs.78085	9	R60795 Hs.120200 AA70274 Hs.14030 AA412441 Hs.89131 AA448271 Hs.99126 AA629558 Hs.75257 NG3099 Hs.46630	AA464566 Hs.89137 AA451900 Hs.72257 N50786 Hs.5161
376462 AA0395 283785 N94234 277074 N34287 810264 AA46395	823901 AA4907 248531 N59764	135083 R33030 135083 R33030 131791 R24506		42044 R60795 383938 AA702714 782840 AA412847 782840 AA428271 884718 AA629558	810551 AA46456 786690 AA4519C 283888 N50786
GF201 GF200 GF204 GF201	GF200 GF200	GF200 GF200 GF203	GF203 GF204 GF204 GF201	GF202 GF203 GF204 GF201 GF201 GF201	GF200 GF203 GF203

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	1.15509199		.95943321	2.18500181 2.0291231			2.03397703		1.1865622						1.18779692				.91242644	.08695282	.61299319		2.19877128		1.21788299	2.18576845			1.98646586	
	20184.32 1.15 20184.32 1.15	20182.51		20155.37 2.18 20137.67 2.02	20114.35	20100.46	20094.49 2.05				1.78				20079.41 1.18				_	_	-	6.3	20054.32 2.19							
	2018	2018	2017	2015	2011	2010	2009		20082.5		20081.78				2007				2007	20069.41	20069.2	20066.3	2002		20037.5	20034.57		2002	20019.89	
	EPHA1 EPHA1	UQCR			UNG2		HSU79253		GNAI3		NUDTS				COPS5		_		KCNN4		LYPLA2		RAD51L3		DGKA					
APPENDIX A	EphA1 EphA1	ubiquinol-cytochrome c reductase (6.4KD) subunit	ESTs	ESTs	uracil-DNA glycosylase 2	ESTs	ESTs hypothetical protein	guanine rucieotide binding protein (G protein), alpha	inhibiting activity polypeptide 3 GNAI3	nudix (nucleoside diphosphate	linked moiety X)-type motif 5	COP9 (constitutive	photomorphogenic,	Arabidopsis, nomologi suburin	۵	potassium intermediate/small	conductance calcium-activated	diamen, sapianing is, inclined	4	ESTs	lysophospholipase II	ESTs	RAD51 (S. cerevisiae)-like 3	diacylglycerol kinase, alpha	(80kD)	ESTs	Homo sapiens mRNA for	KIAA1294 protein, partial cds	ESIS	
	Hs.89839 Hs.89839	Hs.8372	Hs.119338	Hs.30131 Hs.187564	Hs.3041	Hs.125381	Hs.119594 Hs.56155		Hs.73799		Hs.11817				HS.198/6/			0000	HS.10082	Hs.260725	Hs.76057	Hs.10225	Hs.125244		Hs.172690	Hs.28002		Hs.183639	Hs.13/68/	
	RG.35 Hs.89839	AA629862 Hs.8372	72	Hs.30131 Hs.114735	AA425900 Hs.3041	4A878129 Hs.125381	AA707063 Hs.119594 V53000 Hs.91865		AA490256 Hs.73799		AA490236 Hs.11817				AA460599 Hs./5889			00007	4A443903 HS.10082	193906 Hs.41817	AA521038 Hs.6672	~	Hs.125244			Hs.28002		AA432248 Hs.6738	AA4481/2 HS.99155	
	3 N90246 5 N90246	_	ω.	H05037 T97921		_	-												•	_	_		N29765		_	N23283				
	305606	w		121580	_		321163		823775		824421			·	/9584/					.,	ω		259579			267738			1821/3	
	GF200 GF200	GF201	GF203	GF202	GF201	GF204	GF203 GF201		GF200		GF204			L	GF 200			000	GF203	GF200	GF203	GF204	GF203		GF200	GF203	1	GF201	GF202	

		1.29210842	2.10992816	1 00079574	100 1300:	2.41988671		2.36842431	2.38221861	2.44231329	1.2148437	2.4012661		1.52971157		2.15751754		2.46140006		1.30166779		1.0863672		2.38280902	
•	19992.13	19987.89 19963.6	19963.33	10010 00	19909.24	19899.36		19883.86	19880.46	19869.59	19865.27	19831.4		19824.06		19817.64	19809.39	19776.2		19772.49		19743.92		19733.47	19703.24
	KRT6B	PLCG1		CICAB) 						P115					PPM1B				ADAM15		MYL6		EIF4G3	
APPENDIX A	keratin 6B phospholipase C. gamma 1	(formerly subtype 148) ESTs	ESTs	eukaryotic translation initiation	ESTs	EST	ESTs, Moderately similar to	alpha tubulin [H.sapiens] Homo sapiens mRNA for	KIAA1270 protein, partial cds	ESTs	vesicle docking protein p115	ESTs	Homo sapiens mRNA; cDNA DKFZp434O1230 (from clone	DKFZp434O1230); partial cds	protein phosphatase 1B (formerly 2C), magnesium-	dependent, beta isoform	ESTs	ESTs	a disintegrin and metalloproteinase domain 15	(metargidin)	myosin, light polypeptide 6, alkali, smooth muscle and non-	muscle	eukaryotic translation initiation	factor 4 gamma, 3	ESTs
	Hs.111758	Hs.268177 Hs.112095	Hs.20995	U2 00020	Hs.105153	Hs.46831		Hs.112015	Hs.197668	Hs.125316	Hs.7763	Hs.106356		Hs.7517		Hs.5687	Hs.130710	Hs.21119		Hs.92208		Hs.77385		Hs.25732	Hs.32135
	AA026418 Hs.91539	R76365 Hs.29551 AA626018 Hs.112095	R50759 Hs.20995	A A 950000 Ho 55956	AA481066 Hs.105153	N48181 Hs.46831		AA425384 Hs.112015	R88672 Hs.34175	N95230 Hs.55124	AA504342 Hs.7763	R44770 Hs.106356		AA775840 Hs.7517		H99661 Hs.5687	AA904797 Hs.130710	R42667 Hs.21119		AA292676 Hs.92208		AA488346 Hs.77385		7	N78909 Hs.32135
	366481	143748 745018	38618	700007	814694	281970		773304	166510	307362	825451	32991		878505		262916	1504101	32082		713782		842989		838744	300038
	GF201	GF200 GF204	GF202	00000	GF204	GF202		GF202	GF203	GF202	GF200	GF202		GF203		GF203	GF204	GF202		GF200		GF200		GF202	GF201

phosphorylase, glycogen; liver

	2.16355389	1.01804963		2.02303486	1.77471796	1.57261802			1.79134015	2.69825852				1.95078932	1.41422547	1.23597373	2.39600711		1.92312577		1.99197999	2.2289636	2.44062133	1.62718918		1 70301218		1.1791273	2.14948298	
	19687.78	19684.58	19669.9	19669.36	19649.64	19577.16	19574.93	19569.12	19558.82	19556.94		19544.59	19532.7	19513.69	19481.96	19459.43	19457.11	19445.45	19436.11		19434.44	19429.47	19417.05	19378.82	40004	19350 16		19301.4	19284.05	19259.55
	PYGL	TMSB10		RAI		YDD19	PCBP2	ENIGMA		LOC51254		CYP4A11	CNN3			LDHA	KIAA1332				RBPMS				90	2		PPE		
(Hers disease, glycogen	storage disease type VI)	thymosin, beta 10	ESTs	ReIA-associated inhibitor	EST	YDD19 protein	poly(rC)-binding protein 2	enigma (LIM domain protein)	ESTs	hypothetical protein	cytochrome P450, subfamily	IVA, polypeptide 11	calponin 3, acidic	ESTs	ESTs	lactate dehydrogenase A	KIAA1332 protein	EST	ESTs	RNA-binding protein gene with	multiple splicing	EST	ESTs	ESTs	protein phosphatase 1,	ESTS	peptidylprolyl isomerase E	(cyclophilin E) ESTs, Weakly similar to	RFXANK [H.sapiens]	ESTs
	Hs.771	Hs.76293	Hs.123106	Hs.8468	Hs.114394	Hs.25615	Hs.63525	Hs.102948	Hs.66418	Hs.8083		Hs.1645	Hs.194662	Hs.9469	Hs.98751	Hs.2795	Hs.62767	Hs.125686	Hs.169982		Hs.80248	Hs.101686	Hs.59982	Hs.104091	78061	Hs.112724		Hs.33251	Hs.220676 Hs 238809	Hs.4768
	H91680 Hs.108685	AA486085 Hs.76293	Ξ				H90894 Hs.82727	AA127096 Hs.102948	AA701006 Hs.66418	AA598872 Hs.8083		W84868 Hs.1645	AA043228 Hs.5318	AA521373 Hs.9469	AA431740 Hs.98751	AA489611 Hs.2795	AA447083 Hs.57080	AA884826 Hs.125686	N35038 Hs.44687			H10059 Hs.101686	AA456078 Hs.59982	AA193603 Hs.104091	N66900			W17246 Hs.118220	R63682 Hs.124959 H04274 Hs.29790	55
	241705	840788	1434969	246704	279826	148650	240966	502682	397262	897979		415817	486787	826994	782257	897567	784306	1468148	271497		1031029	46629	813501	666059	070650	1031728		302310	138841	487882
	GF202	GF200	GF204	GF203	GF203	GF203	GF201	GF201	GF203	GF202		GF201	GF201	GF203	GF202	GF200	GF202	GF204	GF202		GF202	GF202	GF203	GF203	10000	GF202		GF200	GF202	GF204

2.27238547 2.66094045 2.12462544	2.43998993	2.24190822 2.14669426 1.05926235	1.12580084	1.72794684
19259.38 19245.02 19241.75 19232.81	19175.37	19159.07 19111.78 19107.79 19075.25	19025.46 19025.46 19008.22 19004.74	18998.35 18995.34 18944.58 18928.55
PPIB	SPS TAT-SF1	SNT1 MLD GPZ	ADTG JAG2	
peptidyprolyl isomerase B (syclophilin B) ESTs ESTs ESTS ESTS ESTS ESTS ESTS SMEENOPHOSPHATE	SYN I HE I ASE: ; Human selenium donor protein colactor required for Tat activation of HIV-1 sacription syntrophin, alpha (dystrophin-associated reviein A 1 50kD).	associated priver A 1, 3950, acidic component) ESTs ESTs membrane fatty acid (lipid) desaturase carboxypaptidase Z ESTs, Moderately similar to HYPOTHETICAL PROTEIN	KIAA0273 [H.sapiens] adaptov-realted protein complex 1, gamma 1 subuni Homo sapiens mRNAt; cDNA DKFZp434K0115, (from clone DKFZp434K0115); partial cost jagged 2 Homo sapiens cDNA	FLJ10847 fis, clone NT2RP4001379 ESTs EST
Hs. 699 Hs. 111458 Hs. 69169 Hs. 238205 Hs. 97584	Hs.124027 Hs.171595	Hs.31121 Hs.70614 Hs.28921 Hs.185973 Hs.78068	Hs.22567 Hs.5344 Hs.32360 Hs.166154	Hs.48403 Hs.126090 Hs.125478 Hs.34359
AA481464 Hs.699 AA443939 Hs.111458 AA101144 Hs.125081 AA287347 Hs.105088 AA398193 Hs.97584	W80692 Hs.108647 AA857131 Hs.71134	AA69926 Hs.31121 AA132524 Hs.70614 AA172370 Hs.28921 W49667 Hs.34535 AA427724 Hs.78068	AA63475 Hs.22657 W07300 Hs.26275 AA046704 Hs.32360 AA463972 Hs.109802	W85883 Hs.48403 AA867983 Hs.126090 AA883612 Hs.125478 AA453437 Hs.34359
756600 757158 548465 701115 726602	347213	435330 587430 594988 324891 770462	743902 300474 487381 810664	416096 1461100 1460391 788217
GF201 GF202 GF203 GF204 GF203	GF201 GF203	GF201 GF202 GF202 GF201 GF200	GF200 GF200 GF204 GF201	GF204 GF204 GF204 GF203

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2.20381934	1.1310284		1 71010504	1.9825248					2.57804712				1.63403975			1.86561541				2.31391132	1.99550039			1.33940044	2.9052478	2.47438519		
18926.68 18923.53	18889.82	18865.61	18855.67	18846.42		18831.06	18817.38	18751.67	18746.9	18733.47	18733.22		18727.46			18727.04		18717.54		18709.72	18703.9	18689.74	18679.43	18662.67	18654.57	18648.23		18639.64
SUPT5H	MERTK			EPHA8								į	cox8			KIAA0439		IKBKB		ALPI	RPL35	LMNB1			COMT			PSMC4
suppressor of Ty (S.cerevisiae) 5 homolog EST	c-mer proto-oncogene tyrosine kinase	ESTs	ESTs	EphA8	Homo sapiens cDNA FLJ10309 fis, clone	NT2RM2000287	ESTs	ESTs	ESTs	ESTs	ESTs	cytochrome c oxidase subunit	III/	KIAA0439 protein; homolog of	yeast ubiquitin-protein ligase	Rsp5	inhibitor of kappa light polypeptide gene enhancer in	B-cells, kinase beta	alkaline phosphatase,	intestinal	ribosomal protein L35	lamin B1	ESTs	EST	catechol-O-methyltransferase COMT	ESTs	proteasome (prosome, macropain) 26S subunit,	ATPase, 4
Hs.70186 Hs.99151	Hs.78941	Hs.97408	Hs.13234	Hs.145731		Hs.26700	Hs.138467	Hs.117020	Hs.44410	Hs.22629	Hs.194589		Hs.81097			Hs.12017		Hs.226573		Hs.37009	Hs.182825	Hs.89497	Hs.97837	Hs.23596	Hs.240013	Hs.45109		Hs.211594
AA706107 Hs.119951 AA448012 Hs.99151	AA436591 Hs.78941	AA437090 Hs.97408	AA60862 Hs.13234	N90703 Hs.54645		AA455267 Hs.26700	N70088 Hs.107665	AA676987 Hs.117020	00	R44769 Hs.22629	H19234 Hs.100825		AA862813 Hs.81097			AA463445 Hs.12017		N94412 Hs.20593		AA190871 Hs.37009	AA625634 Hs.105660	AA983462 Hs.89497	AA454756 Hs.97837	R23924 Hs.23596	AA425664 Hs.78534	AA598780 Hs.45109		AA464568 Hs.3842
506270 782757	753069	757340	1569876	306375		810026	297949	454065	768039	32989	50904		1469230			811766		309563		626967	877835	1591599	809789	131104	773367	898074		810558
GF204 GF202	GF200	GF204	GF204	GF202		GF201	GF201	GF204	GF203	GF201	GF201		GF203			GF203		GF204		GF203	GF202	GF204	GF201	GF200	GF203	GF202		GF201

2.05379298 1.56308764 1.76743971	1.12998711	1.30770213	1.42087072	2.08052691	2.09262536	2.07388287
18631.02 18628.73 18619.98 18610.87		18596.06 18594.04 18584.32	18561.11 18551.72 18544.21 18520.82 18508.73		18422.08 18422.08 18403.68	18397.87 18394.16 18382.96
HP10328		TGFBI SEC22A	NFIL3 CKS2 MMP23A HBG2	GRB7 HSA9761	MID1	PRIM2A KIAA0435
putative type II membrane protein EST ESTS Homo sapiens mRNA for Homo sapiens (TR2/D15 gane) ESTS, Weakly smillar to TRANACRIPATION ACTION	SOX-5 [H.sapiens] ESTs transforming growth factor,	beta-induced, 68kD sec22 homolog ESTs nuclear factor, interleukin 3	regulated CDC28 protein kinase 2 EST metrix metalloproteinase 23A nemoglobin, gamma G growth factor receptor-bound	orotein 7 ESTs outative dimethyladenosine ransferase ESTs	cardinoria associated ESTs midline 1 (Opitz/BBB syndrome)	ESTs, Weakly similar to B0041.5 [C.elegans] primase, polypeptide 2A (58kD) KIAA0435 gene product
Hs.69009 P Hs.120057 E Hs.89014 H Hs.180545 G Hs.18054	- 0, 11	Hs.18787 b Hs.183655 se Hs.98424 E	90	0	Hs.27695 E Hs.29235 E Hs.27695 sy	E Hs.108812 B Pl
H03436 Hs.69009 AA707915 Hs.120057 AA282495 Hs.89014 M48602 Hs.46696	AA428135 Hs.128789 N73115 Hs.47701	AA633901 Hs.118787 W47156 Hs.12166 AA425877 Hs.98424	- 6 8	H53703 Hs.86859 AA485896 Hs.103331 AA021628 Hs.25834 N48292 Hs.46849	W/Z400 ns.20029 AA456140 hs.99235 AA460270 hs.26833	AA465381 Hs.105072 AA434404 Hs.74519 AA505117 Hs.31438
150897 H 392365 A 712957 A 279302 N		868212 A 324745 V 773253 A		_ , ,_,	796359 A 796539 A	814107 A 770880 A 825785 A
GF203 GF203 GF203 GF201	GF204 GF200	GF201 GF200 GF202	GF201 GF201 GF202 GF204 GF201	GF201 GF202 GF203 GF201	GF202 GF203 GF203	GF204 GF201 GF203

					これのいことは、これのことのことには、これのことには、これには、これには、これには、これには、これには、これには、これには、これ			
Westbrook et al.	ok et al.				APPENDIX A		Atty	Atty Docket No. 217
GF203	826991	AA521371 Hs.3592 AA282922 Hs.9550	Hs.3592	Hs.3592 Hs.9550	ESTs ESTs		18381.28 18362.65	2.11596207
i					Homo sapiens cDNA			
					FLJ11191 fis, clone			
					PLACE1007598, weakly			
					similar to ZINC FINGER			
GF204	1638479	AI016074 Hs.21838	Hs.21838	Hs.21838	PROTEIN 184		18351.76	
					Homo sapiens mRNA; cDNA			
					DKFZp762H177 (from clone			
GF200	66919	T67474	Hs.52763	Hs.52763	DKFZp762H177)		18338.14	1.22286224
GF202	304903	N92526	Hs.54802	Hs.54802	ESTs		18332.94	1.89499073
GF202	629968	AA219315	AA219315 Hs.86835	Hs.86835	EST		18314.72	1.86753618
GF200	781050	AA446453	AA446453 Hs.80686	Hs.80686	prefoldin 5	PFDN5	18309.23	1.21650072
GF204	472009	AA036723	AA036723 Hs.26985	Hs.26985	KIAA0457 protein	KIAA0457	18304.33	
GF203	277708	N49574	449574 Hs.21542	Hs.21542	KIAA1035 protein	KIAA1035	18301.47	2.27212058
GF201	771294	AA443624	4A443624 Hs.98570	Hs.98570	ESTs		18296.92	
GF202	259870	N29850	Hs.44098	Hs.44098	ESTs		18285.9	1.65311962
GF200	120823	T95462	Hs.17575	Hs.259981	ESTs		18256.19	1.25752555
GF200	809784	AA454743	AA454743 Hs.79361	Hs.79361	kallikrein 6 (neurosin, zyme)	KLK6	18246.49	1.23118306
GF200	782543	AA448487	4A448487 Hs.94466	Hs.208344	ESTs		18245.63	1.10344408
GF200	292519	N91311	Hs.31731	Hs.31731	antioxidant enzyme B166	AOEB166	18236.48	1.21424429
					ATP synthase, H+			
					transporting, mitochondrial F0			
GF201	825312	AA504465	AA504465 Hs.73851	Hs.73851	complex, subunit F6	ATP5J	18209.64	
					Human DNA sequence from			

18182.68

gene, a PUTATIVE ZNF127 LIKE gene, and the PPARD for

Peroxisome Proliferato

Hs.203846

1034691 AA779888 Hs.122124

GF204

clone 109F14 on chromosome

6p21.2-21.3. Contains the Transcriptional Enhancer

alternatively spliced gene for Ribosomal Protein RPL10A

Factor TEF-5, the 60S

								1.10571312		1.2260462	1.48468505			1.68590953	1.96007579					1.22626575		1.19508776			2.27056694	2.53579135	1.13390446					2.07671582		1.65108708
	18176.04	18170.38		18162.54	18120.16	18115.6		18109.27		18106.71	18104.68			18097.98	18096.78					18094.9	18078.81	18025.18	17994.08		17987.63	17977.56	17951.93			17938.96		17926.97		17926.91
	SSPN					DKFZP564A2416		AIP		P37NB												RPS5			L0C54518									KCHIP3
sarcospan (Kras oncogene-	associated gene)	EST	ESTs, Weakly similar to	putative p150 [H.sapiens]	EST	DKFZP564A2416 protein	aryl hydrocarbon receptor-	interacting protein	37 kDa leucine-rich repeat	(LRR) protein	ESTs	Homo sapiens mRNA; cDNA	DKFZp566M0947 (from clone	DKFZp566M0947)	EST	Homo sapiens cDNA	FLJ10390 fis, clone	NT2RM4000104, moderately	similar to ZINC FINGER	PROTEIN 135	ESTs	ribosomal protein S5	ESTs	similar to proline-rich protein		EST	ESTs	ESTs, Highly similar to	R26660_1, partial CDS	[H.sapiens]	Homo sapiens mRNA; cDNA	DKFZp566C034)	DRE-antagonist modulator;	calsenilin
	Hs.260039	Hs.125528		Hs.32100	Hs.117358	Hs.5297		Hs.75305		Hs.155545	Hs.35493			Hs.108806	Hs.103241					Hs.133475	Hs.219647	Hs.76194	Hs.46808		Hs.98874	Hs.42235	Hs.117330			Hs.180549		Hs.29464		Hs.13228
	AA620859 Hs.119477	AA883973 Hs.125528		Hs.32100	4A699964 Hs.117358	Hs.5297		AA455316 Hs.75305		AA423944 Hs.64227	AA704650 Hs.35493			Hs.108806	Hs.103241					Hs.101750	AA778636 Hs.126760	AA456616 Hs.76194	Hs.46808		AA436479 Hs.98874	Hs.42235	AA699714 Hs.117330			AA279337 Hs.115210		Hs.29464		Hs.13228
	AA620859	AA883973		N59866	AA699964	AA156796 Hs.5297		AA455316		AA423944	AA704650			H88486	W92738					H20045	AA778636	AA456616	N48057		AA436479	H96791	AA699714			AA279337		N50983		H39123
	1049330	1468010		284783	435696	502446		814731		759873	383823			252904	356940					172783	1048998	809578	281681		753076	260259	433287			704237		281191		192441
	GF201	GF204		GF201	GF204	GF204		GF200		GF200	GF203			GF202	GF202					GF200	GF204	GF200	GF201		GF202	GF202	GF203			GF204		GF203		GF203

26/92526																										
Atty Docket No. 21726/92526	2.10152673	1.87831292	1.38397637			1.08385185				1.00247791	1.13147186	1.13147186			2.35834215				1.88105978		1.10306106					1.49227819
Atty	17917.04	17894.66	17880.62		17848.02	17841.54	17822.13	17812 15	17792.35	17754.4	17751.86	17751.86	17742.42		17727.27		17720.28	17706.21	17700.29		17684.33	17663.51	17637.88	17636.37		17618.04
	DKFZP58611023	!	HYAZZ		HSPA5	NUCB1	PLI	i bid	<u> </u>	KIAA0224	EPHA1	EPHA1	KIAA0939		DKFZP434B187		UCHL3				POLR2J		SURF1	TFDP1		
APPENDIX A	DKFZP58611023 protein ESTs, Moderately similar to similar to molybdoterin biosynthesis MOEB proteins	[C.elegans]	HYA22 protein EST	heat shock 70kD protein 5 (glucose-regulated protein,	78KD)	nucleobindin 1	alpha-2-plasmin inhibitor	phosphatidylinositol glycan,	ESTS	KIAA0224 gene product	EphA1	EphA1	KIAA0939 protein	N-acetylglucosamine- phosphate mutase;	DKFZP434B187 protein	ubiquitin carboxyl-terminal esterase L3 (ubiquitin	thiolesterase)	ESTs	ESTs	polymerase (RNA) II (DNA directed) polypeptide J	(13.3kD)	ESTs	surfeit 1	transcription factor Dp-1	FLJ10684 fis, clone	NT2RP3000220
	Hs.111515	Hs.170737	Hs.147189 Hs.259667		Hs.75410	Hs.172609	Hs.159509	He 120003	Hs 114160	Hs.78054	Hs.89839	Hs.89839	Hs.12785		Hs.237323		Hs.77917	Hs.6119	Hs.269104		Hs.80475	Hs.25044	Hs.3196	Hs.79353		Hs.106861
	Hs.43242	Hs.126060	R01638 Hs.31389 AA001879 Hs.59890		AA775255 Hs.10979	Hs.953	Hs.1	AA709510 Hs 190003	AA703046 Hs 114160	AA456352 Hs.78054	RG.35	Hs.89839	Hs.101722		Hs.101365		Hs.77917	AA708618 Hs.6119	Hs.109730		AA460830 Hs.80475	4A137073 Hs.29980	4A699560 Hs.3196	Hs.108714		Hs.106861
	N36927	R32014	R01638 AA001879		AA775255	AA452725 Hs.953	T68859	0.4202640	AA703046	AA456352	N90246	N90246	H15689		H01516		N27190	AA708618	N62132		AA460830	AA137073	AA699560	N73611		N93507
ketal.	273536	134408	123980		878587	788472	82195	450114	436531	809696	305606	305606	49515		149406		257445	506514	287598		796253	491186	433474	296095		307475
Westbrook et al.	GF203	GF203	GF200 GF202		GF204	GF200	GF201	70010	GF204	GF200	GF200	GF200	GF204		GF203		GF201	GF204	GF202		GF200	GF201	GF201	GF201		GF203

Atta Desket Ne 2470	Docker No. 2112	1.18966356	2.41133392	1.12884399		2.54699106		1.15390458	1.71398462	1.59357115	1.92766039
ŧ		17614.7 17613.06	17590.91	17544.99	17542.05	17519.87 17508	17495.6	17471.2 17467.23	17466.14 17462.99	17447.84	17408.54
CORDYY		CKS2 ADORAZA		RIIT	POU6F1			CUTL1		KRT8	
09897798.070201	APPENDIX A	CDC28 protein kinase 2 adenosine Aza reseptor adenosine Aza reseptor Human DNA sequence from clone CTB-1048E9 on chromosome 22 Contains an RPSA (Ribosomal Protein SAA) pseudogene, the gene (or a novel protein smirlar to ASPH (aspartate bearilar to ASPH (aspartate basilar))	the gene for anovel protein, ortholog of mouse tuftel	expressed in many tissues	transcription factor 1 Homo sapiens mRNA; cDNA	DKFZp586N2119) ESTs Homo sapiens mRNA; cDNA	DKFZp4340071 (from clone DKFZp4340071)	cut (Drosophila)-like 1 (CCAAT displacement protein) CUTL1 EST ESTs, Highly similar to NBL4	PROTEIN [M.musculus] EST	ESTS keratin 8 ESTs. Weakly similar to tro	[R.norvegicus]
		Hs.83758 Hs.1613	Hs.6657	Hs.96038	Hs.2815	Hs.204290 Hs.71738	Hs.7089	Hs.147049 Hs.121819	Hs.104746 Hs.125486	ns.2003 Hs.242463	Hs.93560
		AA397813 Hs.83758 N57553 Hs.1613	N68512 Hs.6657	AA027840 Hs.96038	N63968 Hs.2815	AA779727 Hs.59561 AA142923 Hs.71738	AA045308 Hs.95265	AA284408 Hs.648 AA775448 Hs.121819	AA406206 Hs.104746 AA883670 Hs.125486 AA400863 Hs.5663	W32281 Hs.109833	R38919 Hs.106318
io to		725454 A. 279970 N	294089 N	469686 Av	289447 N	1034494 Av 505227 Av	487087 Av		742859 Av 1466628 Av	-	24822 R
Weethrook of a		GF201 GF201	GF203	GF200	GF201	GF204 GF202	GF201	GF200 GF204	GF202 GF204	GF202	GF202

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1.8631601 1.03513885	1.30786937 1.92131509	2.1045103	1.93533094	1.76619509	1.15337649	1.15337649	2 211 01 007	2.02251268 1.45998304 1.28939672 1.7410243
17407.53	17369.97 17357.27	17322.2 17310.72	17260.04	17258.73 17247.19	17219.49	17219.49 17200.18	17198.61	17195.24 17184.58 17179.49
CRSP9 KIAA0018	DGKD		LEU1	RNAHP	GRP58	GRP58 LOC51323	INPP4A	ZH260
cofactor required for Sp1 transcriptional activation, subunit 9 (33KD) KIAA0018 gene product	diacylglyceror nifase, dena (130kD) ESTs Homo canions mBNA for	KIAA1419 protein, partial cds ESTs EST leukemia associated gene 1, candidate tumor suppressor	frequently deleted in B-cell chronic lymphocytic leukemia (B-CLL)	RNA helicase-related protein ESTs	glucose regulated protein, 58kD alucose regulated protein,	58kD hypothetical protein inositol polyphosphate-4-	phosphatase, type I, 107kD ESTs p53-inducible ribonucleotide reductase small subunit 2	nomolog Homo sapiens mRNA; cDNA DKFZp434G1115 (from clone DKFZp434G1115); partial cds ESTs ESTs
Hs.262823 Hs.75616	Hs.115907 Hs.112943	Hs.23467 Hs.109307 Hs.112614	Hs.20149	Hs.8765 Hs.78088	Hs.183760	Hs.183760 Hs.65403	Hs.32944 Hs.116240	Hs.94262 Hs.22983 Hs.11197 Hs.11288
AA042812 Hs.7558 AA482324 Hs.75616	AA280691 Hs.89979 AA621065 Hs.112943	R23148 Hs.23467 AA62087 Hs.109307 AA608907 Hs.112614	AA425755 Hs.20149	AA464704 Hs.8765 AA429859 Hs.78088	R33030 Hs.110029	R33030 Hs.84298 AA490494 Hs.65403	AA634283 Hs.116240 AA634283 Hs.116240	AA495950 Hs.94262 AA424567 Hs.22983 AA488191 Hs.11197 AA421470 Hs.30744 AA609657 Hs.112744
486538 840878	705274 1056260	131012 1055582 1048655	773383	810229 780969	135083	135083 823902	745060	768466 767187 877664 731039 1031803
GF203 GF200	GF200 GF202	GF201 GF204 GF202	GF202	GF201 GF202	GF200	GF200 GF203	GF204 GF204	GF203 GF202 GF202 GF202 GF202

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	1.13686276	1.30893357	1.30672996	1.99670668	1.73239491	2.18773619	1.06651578	1 79018965	2.02087214	2.30765733	2.45504767						1.82150853		1.2880845	1.2880845	2.51573899 2.31824579
17167.87	17158.88 17158.29	17142.01	17133.48	17120.27	17102.07	17065.12	17058.04	17042.33	17027.42	17025.89	17020.94		17019.31		16990.8	16965.51	16952.36		16892.61	16892.61	16874.04 16862.44
PC4	EGFR FOXF2	DRAP1																	IGF2	IGF2	GPC5
activated RNA polymerase II transcription cofactor 4 epidermal growth factor receptor (avian erythroblastic lerikemia viral (v-erb-b).	oncogene homolog) forkhead box F2	(negative cofactor 2 alpha)	mRNA sequence Homo sapiens mRNA; cDNA	DKFZp434E2321); partial cds ESTs	ESTs	ESTs	ESTs	ESTS	ESTS	EST	ESTs	ESTs, Weakly similar to	dJ425C14.2 [H.sapiens]	Homo sapiens mHNA; cDNA DKFZp434P1514 (from clone	DKFZp434P1514); partial cds	EST	ESTs	insulin-like growth factor 2	(somatomedin A) insulin-like growth factor 2	(somatomedin A)	glypican 5 ESTs
Hs.74861	Hs.77432 Hs.44481	Hs.118724	Hs.12460	Hs.29383 Hs.32501	Hs.55513	Hs.29444	Hs.38022	HS.112218	Hs.24276	Hs.50199	Hs.24633		Hs.8254		Hs.105036	Hs.125693	Hs.183114		Hs.251664	Hs.251664	Hs.76828 Hs.169855
Hs.42994	RG.41 Hs.82320	AA421977 Hs.79736	AA677322 Hs.12460	AA156269 Hs.29383	Hs.55513	Hs.29444	Hs.38022	4A489024 HS.112218	Hs.24276	Hs.50199	Hs.120906		AA434390 Hs.8254		AA457117 Hs.105036	AA884929 Hs.125693	Hs.59476		Hs.822	Hs.75963	AA878391 Hs.76828 N39077 Hs.44935
N21407	W48713 N98485	AA421977	AA677322	AA156269 H41203	W32470	W47106	N91307	AA489024	R28191	N72196	R33402		AA434390		AA457117	AA884929	W93585		N54596	N54596	AA878391 N39077
265592	324861 310138	754538	454459	590310	321536	324674	292522	824915	134662	291222	136169		270866		810450	1468268	357264		245330	245330	1416502 276490
GF201	GF200 GF201	GF200	GF203	GF204	GF202	GF203	GF200	GF204	GF203	GF202	GF203		GF201		GF201	GF204	GF202		GF200	GF200	GF203 GF202

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16836.79 16828.17 16822.63 16813.38	16775.27 16774.35 16772.08	16750.59	16725.56 16697.62	16693.4	16693.23	16687.96 16682.18
DKFZP586I1023 NDUFB2	KIAA0957 KIAA0344	ТІММЭ				TGM2
ESTs DKFZP58611023 protein ESTs MADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2 (8kD, AGGG)	Homo sapiens cDNA FLJ20505 fis, clone KAT09459 KIAA0957 protein KIAA0344 gene product translocase of inner mitochondrial membrane 9	(yeast) homolog ESTs, Weakly similar to PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE	PEROXIDASE [H.sapiens] ESTs Horno sapiens cDNA FLJ10450 fis, clone NT2RP1000954, weakly, similar to RING CANAL	PROTEIN Homo sapiens clone 24787	mRNA sequence transolutaminase 2 (C	utamine- erase)
Hs.10494 Hs.231100 Hs.111515 Hs.8352 Hs.198272	Hs.69388 Hs.30991 Hs.184592	Hs.271934	Hs.57772 Hs.57772	Hs.267604	Hs.13429	Hs.8265 Hs.183702
AA134862 Hs.10494 AA164750 Hs.72499 W79425 Hs.58566 R73089 Hs.101505 AA045239 Hs.13724	AA629345 Hs.69388 R59489 Hs.26660 AA865342 Hs.87479	1603424 AA987943 Hs.108527	W46629 Hs.44426 W60286 Hs.57772	N78929 Hs.109757	AA678084 Hs.13429	R97066 Hs.8265 AA115197 Hs.43220
502436 594500 346972 141548	743724 37728 1469934	1603424	324148 342033	300055	430710	199945 491612
GF203 GF202 GF202 GF204 GF204	GF204 GF203 GF203	GF204	GF201 GF201	GF202	GF203	GF200 GF204

	1.64873994		1.8020031	1.42232497	1.0146671	1.67937335	1.21189651	1.64916252 1.82282271 2.64227316
16636.76	16635.69 16612.96	16610.2 16594.05	16563.68 16548.63	16543.78	16542.28 16541.95	16539.51 16465.58	16464.42 16457.34 16451.49	16447.65 16443.2 16431.88 16414.69
TIMP1		ACACA	PDPK1 DKFZP434D2135	DFFA	HNRPF CDH18		SOD2	
tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) Homo sapiens partial mRNA for NICE4 protein, 3' end,	clone 1056f5 ESTs acetyl-Coenzyme A	carboxylase alpha ESTs, Weakly similar to ORF YKR081c [S.cerevisiae] 3-phosphoinositide dependent	protein kinase-1 DKFZP434D2135 protein DNA fragmentation factor, 45	KD, alpha subunit heterogeneous nuclear	ribonucleoprotein F cadherin 18	ESTS ESTS ESTS, Weakly similar to !!!! ALU SUBFAMILY JII WARNING FNTRY !!!	[H.sapiens] superoxide dismutase 2, mitochondrial ESTs ESTs	protease with Idr-binding motif [H.sapiens] ESTs ESTs
Hs.5831	Hs.273229 Hs.83332	Hs.172515 Hs.10600	Hs.154729 Hs.4876	Hs.155344	Hs.808 Hs.57691	Hs.25717 Hs.25717	Hs.117440 Hs.177781 Hs.42714	Hs.60440 Hs.188138 Hs.17782 Hs.48728
3 Hs.6525	AA054954 Hs.84111 W46773 Hs.83332	AA939275 Hs.127215 AA425436 Hs.10600	AA278320 Hs.67722 W80455 Hs.4876	AA487452 Hs.91047	AA490991 Hs.808 AA865745 Hs.57691	N49275 Hs.5484 AA705184 Hs.25717	R06033 Hs. 19583 AA488084 Hs. 73830 H99650 Hs. 42714	4A428183 Hs.60440 N73792 Hs.103187 AA670160 Hs.17782 V63178 Hs.48728
_		6			` _			
	377271 324396	1587933	703808 415489	841357	824591 1469249	280390	124909 840708 262865	773558 344133 845672 289829
GF204	GF201 GF202	GF204 GF204	GF203 GF204	GF200	GF200 GF204	GF203 GF204	GF200 GF201 GF201	GF204 GF200 GF203 GF202

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APPENDIX A

DIBOYY98 DYDEDI

		1.67599082	1.0473604		1.1021908					2.90788387	1.21279975	1.87916163	2.80277318		1.26337747		1.93121832		1.98417076		1.4109165	1.7871629
		16394.74	16386.43		16386.21	16381.21	16364.64		16350.67	16344.26	16332.18	16328.29	16327.82	16325.42	16316.52		16315.42		16295.05	16275.13	16266.16	16260.76 16252.95 16246.3
			COL18A1		CHGA	SH2D2A	DJ1042K10.2		KIAA0765		KIAA0019	KIAA0477			DKFZP547G1110		CAP-C		EIF2B1			WNT-4 ABR
ESTs, Moderately similar to !!!!	ALU SUBFAMILY SO WARNING ENTRY IIII	[H.sapiens]	collagen, type XVIII, alpha 1	chromogranin A (parathyroid	secretory protein 1)	SH2 domain protein 2A	hypothetical protein	putative brain nuclearly-	targeted protein	ESTs	KIAA0019 gene product	KIAA0477 gene product	ESTs	ESTs	SH2-B homolog	chromosome-associated	polypeptide C	eukaryotic translation initiation factor 2B, subunit 1 (alpha,	26kD)	ESTs	ESTs	Human DNA sequence from clone 22446 on chromosome 1/95.1-36.25 Contains part of a gene similar to Mouse Wnt-4 protein, the gene for CDC42 (cell division cycle 42 (GTP-binding protein, 254D)), ESTs, binding system a CpG island WNT-4 ESTs active BCR-related gene ABR
		Hs.131748	Hs.78409		Hs.172216	Hs.103527	Hs.22129		Hs.180895	Hs.129132	Hs.278526	Hs.7765	Hs.43590	Hs.11607	Hs.15744		Hs.50758		Hs.78592	Hs.188577	Hs.48752	Hs.146409 Hs.118121 Hs.118021
		AA701368 Hs.131748			R71531 Hs.107171	AI003610 Hs.103527	AA971563 Hs.128493		AA677513 Hs.62318	AA131315 Hs.129132	AA281137 Hs.5174	AA401341 Hs.7765	AA424940 Hs.43590	AA443570 Hs.11607	W23931 Hs.15744		AA452095 Hs.30663		N30225 Hs.109044	H52503 Hs.114007	AA490469 Hs.48752	AA630164 Hs.77322 R68169 Hs.118121 W24076 Hs.118021
		435510	301061		142851	391949	1583501		897219	567055	711826	742562	768248	771233	309894		786504		256983	202154	823867	854746 138378 309993
		GF203	GF200		GF200	GF204	GF204		GF204	GF203	GF200	GF202	GF203	GF201	GF200		GF202		GF203	GF204	GF203	GF201 GF202 GF200

1.0934181	1.24885194		2.11177029	2.10146188	2.17516628			1.83601867			2.01450802				1.30754335	2.3069482	1.28767643	1.32646563						2.48019001		1.7704838		1.20644375	1.05604587			
16216.79	16213.52 16204.18			₹+	16126.4		16080.3	16074.83			16070.22		16065.91	16051.79	16051.58	16049.96	16039.89	16037.52				!			16017.24	15965.32	15947.16	15922.53	15920.71		15898.16	
РАР	KIAA0711				DKFZP547E1010					FUS	HSPF2		FSTL3		LOC51241		CD151							TYZ		KIAA0640	DKFZP566B183		PFDN4		DBP	
poly(A) polymerase ESTs, Weakly similar to ZINC FINGER PROTEIN 85	[H.sapiens] KIAA0711 gene product	ESTs	ESTs	EST	DKFZP547E1010 protein	Homo sapiens mRNA for	KIAA1393 protein, partial cds	ESTs	fusion, derived from t(12;16)	malignant liposarcoma	heat shock 40kD protein 2	follistatin-like 3 (secreted	glycoprotein)	ESTs	hypothetical protein	ESTs	CD151 antigen	ESTs	Homo sapiens cDNA	FLJ10574 fis, clone	NT2RP2003265, highly similar	to Homo sapiens CGI-53	protein mRNA	lysozyme (renal amyloidosis)	ESTs	SWAP-70 protein	DKFZP566B183 protein	ESTs	prefoldin 4	D site of albumin promoter (albumin D-box) binding	protein	
Hs.49007	Hs.29899 Hs.5333	Hs.21638	Hs.55896	Hs.275089	Hs.227391		Hs.33317	Hs.177537		Hs.99969	Hs.172847		Hs.25348	Hs.44288	Hs.171566	Hs.98204	Hs.75564	Hs.58879					Hs.24994	Hs.234734	Hs.173648	Hs.153026	Hs.12305	Hs.44899	Hs.91161		Hs.155402	
AA100296 Hs.49007	N91582 Hs.29899 AA702544 Hs.5333	H19315 Hs.21638	AA400422 Hs.111912	H63952 Hs.32473	AA406292 Hs.111843		AA992906 Hs.33317	AA776908 Hs.5886		H93393 Hs.13182	W60283 Hs.109954		AA417274 Hs.25348	N31985 Hs.44288	AA775863 Hs.31026	AA416584 Hs.98204	AA456183 Hs.75564	W86648 Hs.58879					AA705343 Hs.24994	AA708440 Hs.104716	AA137078 Hs.44048	H99855 Hs.42748	AA974348 Hs.12305	N48103 Hs.44899	AA253430 Hs.91161		AA630354 Hs.33477	
511066	303043 384088	51226	743297	209194	754539		1624213	858927		241847	342027		731203	259417	878544	730990	809494	416769					462064	506016	491196	263916	1586340	243350	669435		854879	
GF200	GF203 GF201	GF201	GF202	GF202	GF203		GF204	GF203		GF201	GF202		GF204	GF201	GF203	GF202	GF200	GF202					GF204	GF203	GF201	GF203	GF204	GF200	GF200		GF201	

,	7			FORDY CALADROP		×***	Atty Dooloot NIC 2472
Westdrook et al.	K et al.			APPENDIX A		Ally	Docket No. 2172
GF204	884720	AA629559 Hs.114073	Hs.114073	ESTs solute carrier family 16 (monocarboxylic acid		15887.61	
GF200	773344	AA425612 Hs.75317	Hs.75317	transporters), member z (putative transporter)	SLC16A2	15868.8	1.16870678
GF201	744917	AA625806 Hs.11342	Hs.11342	ninjum 1, nerve injury-induced protein-1 Homo sapiens cDNA	NINJ1	15861.74	
				FL/10283 fis, clone HEMBB1001339, weakly similar to DXS8237E			
GF203	490789	AA133204 Hs.7393	Hs.7393	PROTEIN		15825.87	1.87724479
GF201	200018	AA454864 HS.85015	HS.85015	ESTS N-acetvlolucosaminy		13812.88	
GF202	346942	W94289 Hs.124746	Hs.18079	transferase component Gpi1	GP11	15797.51	1.87047766
GF204	700538	စ္တ	Hs.99706	EST		15792.62	
GF204	251664		Hs.42339	ESTs		15787.1	
GF203	703526	AA278721 Hs.103104	Hs.103104	ESTs	VIA A 1000	15775.7	2.02637432
GF201	203554		Hs.176624	ESTs		15760.18	1
0	14	100004	70007	ESTs, Weakly similar to		46751	
GF204	745283	AA62556/ HS.112094	HS. I 12094	mannose phosphate		13/31.40	
GF200	824704	AA482198 Hs.75694	Hs.75694	isomerase	MPI	15744.93	1.2560373
GF202	323611	W44508 Hs.55915	HS.55915	chromosome 21 open reading	_	15/33.83	1.72195/54
GF200	290124	N90335 Hs.100486	Hs.9042	frame 1	, C21orf4	15728.98	1.28620118
GF200	167032	R89715 Hs.2890	Hs.90037	ESTs		15724.42	1.16200756
GF204	745465	AA625966 Hs.60288	Hs.60288 Hs 121970	ESTs		15693.91	1 59167032
3				N-acetylneuraminic acid			
	20000	700001 OL 1021014	Us 974494	phosphate synthase; sialic	v V	15644.48	9 46987119
GF203	745520	AA626240 Hs 116137	Hs 111138	KIAA0712 gene product	KIAA0712	15633.85	10201.7
GF201	376316	AA039640 Hs.75188	Hs.75188	wee1+ (S. pombe) homolog	WEE1	15632.42	

2.09084947	2.10153155 1.16189246	1.50159493	1.38544794	1.19662497	2.1843216	2.24978238 2.11247277 1.87701545	2.13959051	1.37072736	1.68649599 2.00538678
S/ L	7 -	-	-	-	8	7 77 -	8	-	- 2
15630.14	15613.44 15610.67	15604.35	15596.72 15583.63 15548.71	15548.44 15537.2 15520.36	15519.06	15500.87 15476.37 15449.84 15425.74	15424.4	15424.09 15422.12	15414.71 15406.78
	DXS1283E	SLC5A3	RAB2L MLANA	SCG2		TAF1C		HLA-DQB1	, F2R DKFZP58611023
Homo sapiens cDNA FLJ10134 fis, clone HEMBA1003096 ESIs Integrin bets 3 (alternatively spliced, clone beta 3C)	[human, erythroleukemia cell HEL, mRNA Partial, 409 nt] GS2 gene	solute carrier family 5 (inositol transporters), member 3 RAB2, member RAS	oncogene family-like ESTs melan-A	Secretagrammer (smonrogrammer)	ESTs, Weakly similar to a2- chimaerin [H.sapiens] TATA box binding protein (TBP)-associated factor, RNA	polymerase I, C, 110kD EST ESTs ESTs	ESTS, Weakly similar to pou katanin [H.sapiens] maior histocompatibility	complex, class II, DQ beta 1 ESTs	receptor DKFZP58611023 protein
Hs.104800 Hs.112765	Hs.85296 Hs.264	Hs.268016	Hs.170160 Hs.207409 Hs.154069	Hs.75426 Hs.59503 Hs.100754	Hs.177812	Hs.153022 Hs.102731 Hs.36793 Hs.55950	Hs.100861	Hs.73931 Hs.47408	Hs.128087 Hs.111515
AA419622 Hs.104800 AA609774 Hs.112765	AA037229 Hs.85296 AA449678 Hs.264	AA621183 Hs.127415	AA401972 Hs.75840 V29860 Hs.82255 V32199 Hs.81996	427864 Hs.75426 4A628462 Hs.59503 4A644587 Hs.100754	Hs.13882	AA454218 Hs.105023 N62375 Hs.102731 AA598947 Hs.36793 W47000 Hs.55950	Hs.62179	AA669055 Hs.73931 N52051 Hs.47408	N20407 Hs.53698 AA488439 Hs.103911
AA41962 AA60977	AA03722 AA44967	AA62118	AA40197 N29860 N32199	H27864 AA628462 AA644587	N59846	AA454218 N62375 AA598947 W47000	R42168	AA66905 N52051	N20407 AA488439
752640 1031966	484874 785745	744360	741891 259891 272327	174627 1032831 845631	289125	795522 290566 898050 325111	30466	854444 282505	264692 843211
GF202 GF202	GF202 GF200	GF202	GF201 GF203 GF201	GF201 GF203 GF204	GF202	GF201 GF202 GF202 GF203	GF203	GF201 GF202	GF203 GF202

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1.25365405		1.6397706	1.9331761		1.78209019	2.10547474								2.57781994		2.37903241								1.79750279	1.87711041			1.81379044	2.43797204
15406.7		15399.23	15389.58		15383.8	15371.57			15360.11	15346.89	15317.65			15288.8		15277.75		15277.29		15276.18	15260.42			15248.99	15239.96			15230.83	15212.13
CTSH					COPEB											SEC24A		SGPL1		AQP1				TAF2N				MCM5	C210RF6
cathepsin H	ESTs, Weakly similar to Similarity to Human ADP/ATP	carrier protein [C.elegans]	ESTs	core promoter element binding	protein	ESTs	Homo sapiens cDNA	FLJ10875 fis, clone	NT2RP4001828	ESTs	ESTs	Homo sapiens mRNA; cDNA	DKFZp434O158 (from clone	DKFZp434O158)	SEC24 (S. cerevisiae) related	gene family, member A	sphingosine-1-phosphate	lyase 1	aquaporin 1 (channel-forming	integral protein, 28kD)	ESTs	TATA box binding protein	polymerase II, N, 68kD (RNA-	binding protein 56)	ESTs	minichromosome maintenance	deficient (S. cerevisiae) 5 (cell	division cycle 46)	frame 6
Hs.76476		Hs.120994	Hs.43213		Hs.4055	Hs.13751			Hs.18851	Hs.176120	Hs.241097			Hs.24135		Hs.211612		Hs.186613		Hs.74602	Hs.48007			Hs.66772	Hs.104864			Hs.77171	Hs.34136
AA487346 Hs.76476		AA708149 Hs.120994			AA416628 Hs.4055	AA699951 Hs.13751			N25240 Hs.108767	AA705306 Hs.119888	AA884762 Hs.125679			AA425770 Hs.21867		H64780 Hs.14574		AA459381 Hs.26827		H24316 Hs.74602	N56942 Hs.48007			AA857343 Hs.66772	AA443724 Hs.104864			AA285155 Hs.77171	N30699 Hs.34136
841470		460792	951100		731292				267458	462829	1467309			773242		238435		810944		51950	280065			1474955	784041			700721	257382
GF200		GF203	GF202		GF202	GF203			GF201	GF204	GF204			GF202		GF202		GF201		GF201	GF204			GF203	GF202			GF203	GF202

1.29144884 1.36621182 1.74803757 1.83243434	1.01008233	1.21511304 2.12047333 1.89892746 1.62641554 2.46424945 1.84673213 2.8276818	2.16981342	2.29618729
15211.13 15205.57 15191.74 15189.97 15155.55	15119.29 15099.64 15098.9	15096.37 15084.55 15078.8 15069.06 15060.69 15047.89 15040.66	14928.54 14924.01 14916.94	14915.26
DRAP1 DOK1 ZYG	GALC AMPD1	D12S2489E FST RU2	CD36L1 INP94A	BDNF
DR1-associated protein 1 (negative colactor 2 alpha) ESTS ESTS ESTS (downstream of tyrosine kinase 1) ZVG homolog	Horno sapiens cDNA FL.20655 fis, clone KAT01590 galadtosylceramidase (Krabbe disease) adenosine monophosphate deaminase 1 (isoform M) DNA segment on Abronosoma 12 (minio 2489	expressed sequence follistatin ESTs ESTs ESTs EST	CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 1 ESTs inositol polyphosphate-4- phosphatase, type I, 107kD	Human Hox5.4 gene fragment brain-derived neurotrophic factor
Hs.118724 Hs.131706 Hs.25063 Hs.12294 Hs.103854 Hs.29285	Hs.239720 Hs.273 Hs.89570	Hs. 74085 Hs. 9914 Hs. 107515 Hs. 61345 Hs. 57874 Hs. 159196 Hs. 114071	Hs.180616 Hs.205024 Hs.32944	Hs.58659 Hs.56023
AA406285 Hs.118724 W38020 Hs.131706 N40951 Hs.28063 H06236 Hs.12294 AA142943 Hs.103854 AA453289 Hs.7257	AA664363 Hs.83642 W85914 Hs.273 AA086476 Hs.89570	AA397819 Hs.74085 AA701860 Hs.9914 H15695 Hs.107515 AA127741 Hs.61345 W67493 Hs.57874 W88720 Hs.59196 AA699313 Hs.14071 F19586 Hs.101255	0 0	W81371 Hs.58659 AA262988 Hs.56023
754538 / 322221 / 277185 44075 195399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 795399 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79539 / 79500 / 79500 / 79500 / 79500 /	868590 / 415698 / 562813 /	725473 434768 49203 490329 343097 417760 433656 42003	~ m . m	347726
GF200 GF203 GF203 GF202 GF201 GF201	GF204 GF200 GF201	GF200 GF203 GF202 GF201 GF202 GF202 GF203	GF201 GF201 GF203	GF202 GF200

Westbrook et al.

Atty Docket No. 2172	1.65703955	2.19951362	1.77197023	1.21986097	1.4643402		1.12622774				
Affy	14897.03	14866.01 14864.6	14860.46 14859	14856.05	14855.53	14843.19	14842.15 14838.54	14810.67	0.50	14805.06	14750.96
		MATR3	TM4SF6 KIAA0703				PSMA1			CACNA11	
APPENDIX A	ESTs FSTs Weakly similar to	HISTONE H1D [H.sapiens] matrin 3	member 6 KIAA0703 gene product Homo sapiens clone 23568,	23621, 23795, 23873 and 23874 mRNA sequences	ESTs, Highly similar to 4- HYDROXYPHENYLPYRUVAT E DIOXYGENASE [H.sapiens] Homo sanions chromosoma	19, cosmid R32184	processoring (prosoning, macropain) subunit, alpha type, 1 EST	Human DNA sequence from clone 967Vez for chromosome 20pt 12-318. Contains the CHGB gene for chromogram B (secretogramin 1, SCG1), a spseudogene similar to part of KIAA0172, the gene for a rovel protein similar to predicted worm, yeast and prant for any worm, yeast and protein should worm, yeast and protein should be a rowed protein similar to predicted worm, yeast and protein should be a rowed protein similar to predicted worm, yeast and protein structure.	plant proteins, calcium channel, voltage-	dependent, alpha 11 subunit Homo sapiens paired	PMX1), mRNA
	Hs.42278 E	Hs.25934 Hs.78825 m	Hs.121068 m Hs.6168 K	2 Hs.12520 2	Hs.166456	Hs.4200	н НS.82159 ty HS.112713 E	19 0 0 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		Hs.125116 d	Hs.30528 (I
	Hs.42278	Hs.25934 Hs.113579	Hs.21637 Hs.6168	Hs.12520	Hs.2899	Hs.4200	R27585 Hs.82159 AA609474 Hs.112713	118.9560	99000	Hs.12823	Hs.49158
	N32071	R52634 N71396	H87106 Hs.2163 AA992668 Hs.6168	R76247	AA010605 Hs.2899	1553640 AA962613 Hs.4200	R27585 AA609474	NOGAE	C+067N	N52765	N66607
et al.	260168	40107 294200	252382 1623210	144747	430314	1553640	134544 1031598	0.604.60	20165	283375	278859
Westbrook et al.	GF202	GF202 GF204	GF202 GF204	GF200	GF203	GF204	GF200 GF202	555001	5	GF201	GF201

Atty Docket No. 21726	1.19163984	1.19278813	2.19175936					1.82083285				1.50478789		2.35424512	2.17573899	2.38728397	1.22513078	1.66679509				1.91832497	1.23357053		1.20778042	2.20335287		07004700	1 38781364	1 0601 4641	1.3001.1
Atty	14730.73	14681.54	14676.79	14674			14654.4	14650.89			14644.19	14643.65	14633.13	14620.12	14611.47	14595.36	14592.11	14589.9		14585.32		14574.05	14557.52		14546.29	14546.16	14545.79	44504.00	14524.30	14514.11	<u>+</u>
	GSTTLp28	DKFZP564M112		DCTD			NSMAF	SK								DKFZP564G013	CBR1	KIAA0431					SPINT2		SF3A1					LI 1172	
APPENDIX A	glutathione-S-transferase like	DKFZP564M112 protein	ESTs	dCMP deaminase	neutral sphingomyelinase (N-	SMase) activation associated	factor	dickkopf-1 like	Homo sapiens mRNA; cDNA	DKFZp434P0626 (from clone	DKFZp434P0626)	ESTs	ESTs	ESTs	ESTs	DKFZP564G013 protein	carbonyl reductase 1	KIAA0431 protein	ESTs, Highly similar to early B-	cell factor [M.musculus]	ESTs, Weakly similar to	KIAA0585 protein [H.sapiens] serine protease inhibitor.	Kunitz type, 2	splicing factor 3a, subunit 1,	120kD	ESTs	ESTs FSTs Wealth similar to	ESIS, Weakly similar to	protein HitsC [in:musculus]	ETI dolliaili colliailiilig 2	[2]
	Hs.11465 Hs 79788	Hs.107942	Hs.12929	Hs.76894			Hs.78687	Hs.40499			Hs.116324	Hs.100688	Hs.119150	Hs.267919	Hs.122707	Hs.15165	Hs.88778	Hs.16349		Hs.185708		Hs.184343	Hs.31439		Hs.21729	Hs.112896	Hs.55961	0.0000	HS.263216	115.207.33	HS.41202
	AA441895 Hs.11465	W76032 Hs.107942	AA400592 Hs.12929	W51951 Hs.77545			AA046107 Hs.95290	AA253464 Hs.40499			AA629324 Hs.116324	H87273 Hs.100688	AA625852 Hs.119150	AA190906 Hs.58111	AA781035 Hs.122707	AA490456 Hs.72217	AA280924 Hs.88778	AA172053 Hs.127576		AA917497 Hs.126716		AA400122 Hs.87562	AA459039 Hs.31439		T72698 Hs.21729	AA620747 Hs.112896	AA284301 Hs.55961		W1548/ HS.10/593	AA/106621 HS.20/33	N51444 HS.47262
ok et al.	774036	345423	743322	340519			376644	669375			743688	220479	745438	613113	1240577	823850	711552	594731		1527066		743220	814378		108667	1049284	324088	0	322652	200497	283348
Westbrook et al	GF200	GF200	GF202	GF201			GF201	GF203			GF204	GF203	GF204	GF202	GF203	GF203	GF200	GF202		GF204		GF202	GF200		GF200	GF202	GF201	0001	GF202	97999	GFZUZ

	1.6568269 1.75759532 2.16276442	1.77763015	1,42646916		2.78989366 1.89301113 1.88378657 1.65971269	1.9358052 1.84061042	
14494.25	14486.92 14479.42 14462.56 14452.67	14451.72 14439.2 14430.67	14408.29	14407.01	14400.29 14399.1 14396.45 14362.78	14357.79 14353.53 14352.03	14344.46
		g АВН	NFATC3	ATP5G1	SMARCD2	PSMA2	2 ZNF42
ESTs, Weakly similar to !!!! ALU CLASS F WARNING ENTRY !!! [H.sapiens] ESTs, Moderately similar to TRANSCRIPTION FACTOR	BTF3 [H.sapiens] ESTs ESTs ESTs	alkylation repair, alkB homolog ABH EST Homo sapiens mRNA for KIAA1140 protein, partal cds	indical factor of activated 1- cells, cytoplasmic 3 ATP synthase, H+ transporting, mitochondrial F0 complex subunit 6 (subunit 9)	isoform 1 SWI/SNF related, matrix associated, actin dependent	Subfamily d, member 2 EST ESTS ESTS	proteasome (prosome, macropain) subunit, alpha type, 2 ESTs	zinc finger protein 42 (myeloid- specific retinoic acid- responsive)
Hs.25661	Hs.93748 Hs.98679 Hs.105282 Hs.36676	Hs.54418 Hs.53672 Hs.131728	Hs.172674	Hs.80986	Hs.250581 Hs.117074 Hs.18585 Hs.42746 Hs.166852	Hs.181309 Hs.204200 Hs.94113	Hs.169832
1035730 AA629092 Hs.25661	AA479954 Hs.111081 AA432127 Hs.98679 AA491247 Hs.105282 AA256461 Hs.36676	AA609609 Hs.54418 H99033 Hs.53672 AA490904 Hs.25600	R38306 Hs.2371	AA046701 Hs.80986	AA478436 Hs.64264 AA677647 Hs.117074 AA425345 Hs.18585 H99829 Hs.42746 H06567 Hs.93530	99 98	AA120779 Hs.106351
1035730	753625 781475 824233 682064	1031747 261453 824533	137457	487373	741067 897259 768619 263084	366104 950464 289865	490387
GF204	GF202 GF202 GF204 GF203	GF201 GF202 GF203	GF203	GF201	GF200 GF204 GF203 GF203	GF204 GF202 GF202	GF201

D. DYDUD		APPENDIX A
	Westbrook et al.	

1.67128671	1.18677611	1.18677611	1.23896977	1.20112865	2.01454874	1.12529223	
14049.34 14000.74 13998.96 13984.21 13974.81	13953.17	13953.17 13947.3	13921.04 13907.51	13902.92	13891.26 13890.51	13886.77	13871.52 13858.54 13855.49 13829.36
CBARA1	ATP6N1A	ATP6N1A KIAA0579		FTCD	SOX13	ATP6F	RASGRP1 RPL29
ESTs ESTs ESTs caclcium binding atopy-related autoantigen 1 ESTs ESTs	ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD)	ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 14 (110/16kD) KIAA0579 protein KIAA0579 protein Homo sapiens DNA El 110006 Es Alono El 110006 Es Alono El 110006 Es Alono El 110006	HEMBA1004972 ESTs formiminotransferase	cyclodeaminase SBV (sex determining region	Y)-box 13 ESTs ATPase, H+ transporting,	lysosomal (vacuolar proton pump) 21kD	RAS guanyl releasing protein 1 (calcium and DAG-regulated) ESTs ribosomal protein L29 ESTs
Hs.105358 Hs.87767 Hs.165428 Hs.277501 Hs.173077	Hs.267871	Hs.267871 Hs.81505	Hs.55014 Hs.30029	Hs.36218	Hs.201671 Hs.133863	Hs.7476	Hs.182591 Hs.50601 Hs.183698 Hs.187824
AA495788 Hs.105358 AA705977 Hs.87767 AA458460 Hs.19566 W74725 Hs.42861 W72555 Hs.58115 AA460266 Hs.22969	AA427472 Hs.73067	AA427472 Hs.118855 AA670389 Hs.81505	AA045286 Hs.55014 AA001709 Hs.30029	W00987 Hs.36218	W81654 Hs.21135 R42543 Hs.100867	AA480826 Hs.7476	AA278633 Hs.110426 W72885 Hs.50601 Al018613 Hs.2401 AA676812 Hs.114441
768366 1239845 809425 344618 345469 796548	770377	770377 878467	487921 428184	296498	347351 30077	810725	703637 344937 1630990 455136
GF203 GF203 GF201 GF201 GF201 GF202	GF200	GF200 GF203	GF201 GF203	GF200	GF204 GF203	GF200	GF204 GF204 GF204 GF204

1,52249976	1.51294229	1.178003	1.18556939	1.26222085		1.18545454	1,000	2.31509315	1.96087722		1.37662751	2.79058183	1,42840725 1,92150027	
13822.11	13820.78	13786.87	13756.79	13745.04 13744.93		13723.29	13/2021	13/09.72	13702.16		13701.14	13691.98	13871.76 13665.88	13662.09
		TBPI 1	GSTM4		_						CYR61			SLC9A3R1
ESTs Homo sapiens mRNA; cDNA DKFZp434M1827 (from clone	DKFZp434M1827) Human clone A9A2BRB6 (CAC)n/(GTG)n repeat-	containing mRNA	glutathione S-transferase M4	ESTs ESTs	ESTs, Moderately similar to rig-	1 protein [M.musculus]	ESIS	ESIS	ESTs	cysteine-rich, angiogenic	inducer, 61	ESTs	Human DNA sequence from clone RP4-2221.5 on chromosome 1934.2-36.11. Contains the gene for importin labba. ("kenyophein"), up to six movel genes and the 5° end of the EIF3S2 gene for the EIF3S2 gene for activity of beta. Contains ESTs, STSs, GSS	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1
Hs.228084 E	Hs.65735	Hs.169078 C	-	Hs.194154 E				_	Hs.42315 E	0	Hs.8867 ir	Hs.124881 E	H8.49797 E HS.112886	s () Hs.184276 is
AA233643 Hs.87170	AA400129 Hs.65735	AA281346 Hs.15334 AA448001 Hs 13993	AA486669 Hs.82891	AA284281 Hs.102376 T99671 Hs.18566		N80769 Hs.25477	AA8/26/9 Hs.12521/	Ŋ	196392 Hs.42315		AA777187 Hs.8867	R51386 Hs.101105	AA401470 Hs.49797 AA620877 Hs.112886	AA425299 Hs.3354
666172 /	743219 /	705188 /		324946 <i>H</i>		_	- -		256680 H		m	39322 F	742590 <i>F</i>	773286 #
GF203	GF202	GF200	GF200	GF201 GF200		GF200	GF204	GFZU3	GF202		GF203	GF203	GF202 GF202	GF201

GF203 GF204 GF204 GF203 GF201 GF201	399513 1470474 1292042 815835 290391 1472479	AA733195 Hs.19385 AA864350 Hs.27628 AA707523 Hs.12002 AA485249 Hs.10927 NG4519 Hs.34650 AA872257 Hs.5324	AA733195 Hs. 19385 AA864350 Hs.27628 AA707523 Hs. 120023 AA85249 Hs. 10927 AA872257 Hs. 5324	Hs.19385 Hs.266933 Hs.120023 Hs.10927 Hs.34650 Hs.5324	ESTs. Highly similar to CG1-58 protein [H.sapiens] hect domain and RLD 2 ESTs Homo sapiens chromosome 19, cosmid R33729 ESTs hypothetical protein FSTs. Weakky similar to	неяс2 СL25022	13653.71 13651.84 13650.88 13602.34 13598.45	1.5780072
GF203	324451	W52104 Hs.79998	W52104 Hs.79995	Hs.172466	ESTS, Weany stilliat to KIAA0775 protein [H.sapiens]	10051280	13588.76	2.05010745
GF202	951068	AA620437 Hs.7921	Hs.7921	Hs. 7921	goign membrane protein of your Homo sapiens mRNA; cDNA DKFZp566E183 (from clone	9021200	13583.69	2.27299428
GF202 GF203 GF200	280291 399138 306806	N47961 AA774606 W24055	N47961 Hs.46794 AA774606 Hs.121682 W24055 Hs.7988	Hs.46794 Hs.121682 Hs.7988	ESTS ESTS ESTS		13566.47 13556.84 13550.15	2.142/3609 1.90610136 1.28099907
GF201	810502	AA457155	AA457155 Hs.25998	Hs.108139	zinc finger protein 212 proteasome (prosome, macropain) subunit, beta type,	ZNF212	13514.15	
GF200 GF203	529861 815036	AA070997 Hs.77060 AA465148 Hs.72402	AA070997 Hs.77060 AA465148 Hs.72402	Hs.77060 Hs.72402	6 ESTs	PSMB6	13507.76 13496.95	1.2841547 2.74520696
GF202 GF200	264400 322561	N21217 W15277	Hs.42961 Hs.76317	Hs.111515 Hs.184014	DKFZP58611023 protein ribosomal protein L31 Homo sapiens mBNA for	DKFZP586I1023 RPL31	13492.53 13490.68	2.05895739 1.48206153
GF202	590338	AA156054	AA156054 Hs.108957	Hs.108957	KIAA1432 protein, partial cds Homo sapiens mRNA; cDNA DKFZp434D1227 (from clone		13488.45	2.25118407
GF202 GF203	32096	R42699 Hs.5107 AA890663 Hs.62402	Hs.5107	Hs.172789 Hs.62402	DKFZp434D1227) p21/Cdc42/Rac1-activated kinase 1 (vaast Ste20-related) PAK1	PAK1	13483.44 13455.02	2.09517629
;								

1.69163243		1.18083991 2.33080907	1.20021579	1.1570323	1.52057652	1.42191725 1.85321878	1.74148842 1.46435458 2.34453415 1.86347634	1.26451206 1.9267746	
13453.2	13444.6	13430.33 13420.59	13404.58	13396.12	13375.21	13366.32 13364.68	13353 13342.22 13340.86 13332.74 13326.31	13293.79 13292.08 13291.38	13272.17 13268.68
	PPAT	TFAP4	C180RF1	SIAH2	DKFZP58611023			SFRS1	IMP DH2
Novel human gene mapping to chomosome 22	phosphoribosyl pyrophosphate amidotransferase transcription factor AP-4 (activating enhancer-binding	protein 4) ESTs	frame 1 seven in absentia (Drosophila)	homolog 2 ESTs. Weakly similar to	GOLGIN-95 [H.sapiens] DKFZP586I1023 protein	ESTS ESTS ESTS, Weakly similar to C44C1.2 nene product	(C.ologans) ESTs ESTs ESTs ESTs	splicing factor, arginine/serine- rich 1 (splicing factor 2, alternate splicing factor) EST	IMP (inosine monophosphate) dehydrogenase 2 ESTs
Hs.25744	Hs.311	Hs.3005 Hs.12807	Hs.153498	Hs.20191	Hs.112145 Hs.111515	Hs.49359 Hs.6546	Hs. 10463 Hs. 86693 Hs. 8688 Hs. 169728 Hs. 99409	Hs.73737 Hs.48486 Hs.116075	Hs.75432 Hs.29302
AA199650 Hs.25744	1472146 AA873575 Hs.311	AA284693 Hs.3005 R60713 Hs.12807	AA489736 Hs.11175	AA029041 Hs.20191	- œ	N67578 Hs.49359 R41450 Hs.6546	AA181149 Hs.10463 AA279628 Hs.88643 AA521103 Hs.8688 W37793 Hs.26342 AA458633 Hs.99409	T65902 Hs.73737 N62212 Hs.48486 AA625764 Hs.116075	AA996028 Hs.75432 N62985 Hs.29302
647420	1472146	713839 42009	823679	470061	795837 855583	285681 30371	625458 704407 826324 321972 813385	80399 290180 745393	1606837 289757
GF203	GF204	GF200 GF202	GF200	GF200	GF202 GF204	GF202 GF202	GF202 GF203 GF203 GF201 GF203	GF200 GF202 GF204	GF204 GF201

Atty Docket No. 2172		1.37257666	1.29007692		2.0225213 1.07754211 1.15146951	1.43848739 1.20759084 1.72647978	2.09243551 2.26326836
Att)	13261.59	13257.79 13233.52 13228.47	13222.43 13222.01 13221.8 13213.46	13208.16	13196.81 13191.88 13191.82 13178.58	13157.5 13154.34 13152.76 13151.9 13149.82	13148.26 13141.73
	TDE1	HSBP1 DKFZP5640123	BAIAP3		PRKDC	SLC4A3	SEC15L
APPENDIX A	tumor differentially expressed 1 heat shock factor binding	protein 1 ESTs DKFZP564O123 protein	ESTS, Weakly similar to cDNA EST EMBL.Z14731 comes from this gene [C.elegans] ESTS BA11-associated protein 3	Homo sapiens mKNA for KIAA1337 protein, partial cds	protein kinase, DNA-activated, catalytic polypeptide EST ESTs	solute carrer tarnily 4, anion exchanger, member 3 exchanger, member 3 ESTs ESTs ESTs ESTs	Homo sapiens cDNA FLJ10880 fis, clone NT2RP4001901 SEC15 (S. cerevisiae)-like
	Hs.272168	Hs.250899 Hs.29032 Hs.11449	Hs.191986 Hs.33719 Hs.101516 Hs.55047	Hs.241419	Hs.155637 Hs.48751 Hs.215113 Hs.9645	Hs.1176 Hs.103110 Hs.160244 Hs.125103 Hs.47011	Hs.67991 Hs.110454
	AA284296 Hs.103071	AA664067 Hs.111818 AA417899 Hs.29032 N50963 Hs.30078	AA776718 Hs.115149 AA421264 Hs.33719 H18444 Hs.101516 N9447 Hs.55047	AA629570 Hs.116738	AA670315 Hs.35726 N63278 Hs.48751 N73201 Hs.47433 R74078 Hs.9645	AA609880 Hs.79105 W57774 Hs.103110 R23222 Hs.23477 AA699707 Hs.125103 N50056 Hs.47011	AA481266 Hs.31443 AA188366 Hs.110454
k et al.	323796	855799 752752 281164	1292847 731019 51097 309638	884727	878333 290142 245806 143227	1031045 340903 131029 433294 282663	815231 625764
Westbrook et al	GF201	GF203 GF203 GF201	GF204 GF202 GF204 GF202	GF204	GF204 GF202 GF200 GF200	GF201 GF202 GF200 GF203 GF201	GF203 GF202

1.26398512 2.27842885	2.62659718	1.73028261 1.91316596 2.21401805	1.09552074	1.24651721	1.09327563
13133.33 13131.49	13116.81 13109.25 13108.22	13106.19 13103.64 13087.84	13070.84 13070.28 13063.69	13052.65	13052 13043.62 13029.67
RELA	PGAM1	ЬРУ	DKFZP586I1023		MAPKAPK2
v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65))	DKFZp434G1726 (from clone DKFZp434G1726 (from clone DKFZp434G1726) phosphoglycerate mutase 1 (brain) ESTs	ESTS, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens] pancreatic polypeptide	Homo sapiens cDNA FLL20V27 fis, done HEP12338 DKFZP59611023 protein EST HOMO sapiens cDNA FLJ11137 fis, done PLACE100438, waaday smillar to ZNO FINGER	PROTEIN 165 mitogen-activated protein kinase-activated protein	kinase 2 ESTs ESTs
Hs.75569 Hs.7446	Hs.97550 Hs.181013 Hs.152250	HS.28399 HS.184604 Hs.178801	Hs.239475 Hs.11515 Hs.104831	Hs.24545	Hs.75074 Hs.182196 Hs.122554
AA443546 Hs.75569 N90704 Hs.54646	AA401386 Hs.97550 AA676970 Hs.74575 AA481486 Hs.105144	AAZE1303 NS.123107 R74480 HS.28399 AA84498 HS.37042 AA398212 HS.97588	AA037815 Hs.95213 H77855 Hs.91352 AA421170 Hs.104831	R63318 Hs.24545	AA455056 Hs.75074 AA142869 Hs.62446 AA775799 Hs.122554
771220 306384	742726 897177 815112	143454 1412398 726628	375863 214331 731091	138550	812251 504396 878272
GF200 GF202	GF202 GF201 GF203	GF200 GF203 GF203	GF201 GF200 GF202	GF200	GF200 GF201 GF204

									1.24890372				1.30425844			2.01732512		2.09433448	1.38739341	2.38986379		1.13411053	2.1990852				2.22056433					1.93059845 1.78429351
	13022.71	13014.99			13007.9		12996.96		12989.24	12988.96			12979.65			12959.46		12953.22	12938.07	12927.44		12917.57	12895.65			12893.3	12886.43		12879.05	1,200/ .04	12861.82	12860.67 12844.55
		COL4A2			SLC16A1		NTRK2		PPIF				PECAM1		ъ-			RPS27		ANXA9						CNK1			DXS1357E		HTR2B	KIAA0015
Homo sapiens mRNA full length insert cDNA clone	EUROIMAGE 566443	collagen, type IV, alpha 2	solute carrier family 16	(monocarboxylic acid	transporters), member 1	neurotrophic tyrosine kinase,	receptor, type 2	peptidylprolyl isomerase F	(cyclophilin F)	ESTs	platelet/endothelial cell	adhesion molecule (CD31	antigen)	ESTs, Weakly similar to	isopentenyl-diphosphate Delta-	isomerase [H.sapiens]	ribosomal protein S27	(metallopanstimulin 1)	ESTs	annexin A9	Homo sapiens clone 24837	mRNA sequence	ESTs	connector enhancer of KSR-	like (Drosophila kinase	suppressor of ras)	ESTs	accessory proteins	BAP31/BAP29	5-hvdroxytryptamine	(serotonin) receptor 2B	EST KIAA0015 gene product
	Hs.157078	Hs.75617			Hs.75231		Hs.47860		Hs.173125	Hs.14060			Hs.78146			Hs.9270		Hs.195453	Hs.22968	Hs.3346		Hs.13531	Hs.172702			Hs.16232	Hs.83286		HS.1813/3	HS.103224	Hs.2507	Hs.45043 Hs.278441
	V30792 Hs.42260	AA430540 Hs.75617			AA043133 Hs.75231		N63949 Hs.47860		105580 Hs.7166	AA029186 Hs.14060			R22412 Hs.78146			R42713 Hs.106518		AA857413 Hs.109940	V30348 Hs.22968	AA425022 Hs.104871		N64669 Hs.13531	AA155574 Hs.72093			AA459278 Hs.16232	AA620401 Hs.83286		AA292226 Hs./9188	14409009 IIS.103224		N40165 Hs.45043 AA706929 Hs.118728
	_	769959			486175 /		289428 N			470035 /			130541 F			32309 F		1475028 /	258101 N	768570 /		290050 N	592200 ₽				950983 ♭		7.55877		_	276361 N 451855 A
	GF201	GF201			GF201		GF201		GF200	GF204			GF200			GF202		GF203	GF203	GF203		GF203	GF202			GF201	GF202	0	GF201	40215	GF201	GF202 GF203

2 28018715	1.20425715		10101010	1.619/000/				1.00892581	1.00892581			1.70742035	1.15982896			1.84004078	1.44910481		1.30245267		1.7494031				
12836 83	12829.12	12010.53	12811.53	12810.95	12810.36	12809.22	12808.15	12768.96	12768.96			12758.2	12748.55	12747.11		12742.08	12736.23	12722.39	12715.85		12709.92	12/03.91		12686.62	
	D1S155E							ZNF161	ZNF161				VPS4	KIAA1107				KIAA0050			AMACR				
Homo sapiens cDNA FLJ10948 fis, clone PLACE1000142, weakly similiar to 3- HYDHOXYBUTYRYL-COA	NRAS-related gene	ESTS Homo sapiens mRNA; cDNA DKFZb434E0516 (from clone	DKFZp434E0516)	ESTS Homo senions mBNA for	KIAA1295 protein, partial cds	ESTs	ESTs	zinc finger protein 161	zinc finger protein 161	ESTs, Weakly similar to	salivary proline-rich protein	precursor [H.sapiens]	vacuolar sorting protein 4	<iaa1107 protein<="" td=""><td>ESTs, Weakly similar to</td><td>unknown [M.musculus]</td><td>ESTs</td><td>KIAA0050 gene product</td><td>ESTs</td><td>alpha-methylacyl-CoA</td><td>acemase</td><td>ESTS</td><td>Homo sapiens mRNA; cDNA DKFZp434P174 (from clone</td><td>DKFZp434P174)</td><td></td></iaa1107>	ESTs, Weakly similar to	unknown [M.musculus]	ESTs	KIAA0050 gene product	ESTs	alpha-methylacyl-CoA	acemase	ESTS	Homo sapiens mRNA; cDNA DKFZp434P174 (from clone	DKFZp434P174)	
H, 0670	Hs.69855	HS.105285	Hs.169817	HS.124266	Hs.26204	Hs.129034	Hs.13849	Hs.167558	Hs.167558			Hs.76277	Hs.234839	Hs.21554		Hs.23650	Hs.270399	Hs.108947	Hs.98684		Hs.128749	HS.46640		Hs.29288	
109470 He RAGE	AA504682 Hs.69855	44491265 HS.105285	O.I	HU5/74 HS.89462	AA131692 Hs.26204	AA776892 Hs.129034	F71325 Hs.13849	AA232647 Hs.6557	AA232647 Hs.83611			AA443936 Hs.76277	W79674 Hs.5195	AA863471 Hs.21554		AA398262 Hs.23650	V95802 Hs.94501	AA918804 Hs.108947	AA432141 Hs.98684		AA453310 Hs.99316	AA481560 Hs.105182		AA676887 Hs.29288	
7 802208		82426/	22	43833	503839	858912 /	110233 T	666377	666377			757143 /	346299 \	1469381 /				1534853 /	781506 /			815297		897135 /	
SC	GF200	GF 204	GF204	GF 200	GF201	GF204	GF204	GF200	GF200			GF202	GF200	GF204		GF203	GF202	GF204	GF202		GF202	GF 204		GF204	

2.5538474			1.70980828	1,75134118	2.34336563	
12685.66 12678.14 12665.59 12658.9		12652.3 12631.3	12622.82 12621.09 12604.74 12600.83	12591.58	12589.46	12582.22 12569.71 12565.52
DEFA1			CRYBA4	AMY2B		KIAA0420
defensin, alpha 1, myeloid- related sequence EST ESTs	Human DNA sequence from clone 71.1 Gontains as probable Zinc Finger protein (seudo)gene, as unknown putative gene, a pseudogene with high similarity to part of artigen Ker7, a putative Chondroline Scultorianslerase	LIKE gene and a K ESTS, ESTS, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	[H.sapiens] crystallin, beta A4 ESTs ESTs	amylase, alpha 2B; pancreatic AMY2B Homo sapiens mRNA; cDNA DKFZA4341143 ffrom clone	DKFZp434143) Homo sapiens cDNA FL_20350 fis, clone HEP19972, lighty similar to	PROTEIN 184 KIAA0420 gene product ESTs
Hs.90918 Hs.50193 Hs.124740 Hs.12065		Hs.154353 Hs.26579	Hs.53644 Hs.57690 Hs.96617 Hs.22248	Hs.75733	Hs.45068	Hs.59053 Hs.129883 Hs.31383
AA128316 Hs.90918 N72150 Hs.50193 W44766 Hs.107175 AA157001 Hs.12065		W47116 Hs.103080 R56808 Hs.26579	H98201 Hs.53644 AA449982 Hs.57690 AA287041 Hs.96617 H29535 Hs.22248	AA454854 Hs.114921	AA207105 Hs.104149	AA055215 Hs.29853 H42894 Hs.117710 H15812 Hs.31383
503468 291129 320865 502405		324664 41225	261163 788764 701602 52957	866608	647985	377246 183103 159535
GF201 GF202 GF201 GF201		GF201 GF204	GF201 GF201 GF203 GF201	GF203	GF203	GF201 GF201 GF204

1.17792786	2.58158086		2.2557782	1.32656893	1.89784336	1.12667693 1.53377084 1.71135722	1.90599186 1.10533857	1.7852208 2.19910338 1.76347411	1.1351905
12562.1	12541.88	12540.28	12527.18	12506.87	12499.89 12498.1 12488.46	12481.22 12478.36 12474.04	12473.19 12447.4 12444.85	12437.47 12423 12419.18	12418.11 12416.44
CD8A	[8]	D6S49E	65	ic) TUBA1 d		· 1 WASF1	KIAA0300	KIAA0987	CKAP1 LOC51209
CD8 antigen, alpha polypeptide (p32)	ESTs, Weakly similar to SNF2alpha protein [H.sapiens] DNA segment on	chromosome 6 (unique) 49 expressed sequence	Homo sapiens cDNA FLJ20519 fis, clone KAT10365	tubulin, alpha 1 (testis specific) TUBA1 Human DNA sequence from intron 22 of the factor VIII gene, Xq28. Contains the end of a 9,586 ropeated region, int2P1-1, involved in many	cases of haemophilia EST ESTs	WAS protein family, member 1 WASF1 ESTs ESTs ESTs, Weakly similar to	GAGE-7 [H.sapiens] KIAA0300 protein ESTs	adenocarcinoma of the lung ESTs EST	cytoskeleton-associated protein 1 RAB9-like protein
Hs.85258	Hs.44143	Hs.88411	Hs.79457	Hs.75318	Hs.98602 Hs.238535 Hs.41272	Hs.75850 Hs.17235 Hs.165384	Hs.43879 Hs.173035 Hs.58217	Hs.103839 Hs.8859 Hs.102617	Hs.31053 Hs.43005
AA443649 Hs.85258	AA447734 Hs.44143	N70057 Hs.97233	AA431196 Hs.121696	AA180912 Hs.75318	AA703660 Hs.98602 AA625860 Hs.116094 N62273 Hs.44603	N59851 Hs.75850 AA664003 Hs.17235 AA620682 Hs.112883	N27023 Hs.43879 AA405458 Hs.70257 W72227 Hs.58217	AA495835 Hs.103839 AA504894 Hs.8859 N47009 Hs.102617	AA504554 Hs.31053 N80848 Hs.43005
771258	813644	297895	782155	612274	450375 745435 290231	284734 855406 1049173	257902 772111 345152	768417 839746 280156	825323 300661
GF200	GF202	GF201	GF202	GF200	GF203 GF204 GF201	GF200 GF203 GF202	GF202 GF200 GF201	GF203 GF202 GF202	GF200 GF201

1 16691293	1.4080512		1.37349492		1.46829794	2.54354024				1.77789529	1.98430915	1.20640267		1.18616912			1.19532571	1.13036503	1.26360411				-1.1312725				1.26654501				1.16273326
12395 27	12394.17		12376.47	12370.39	12359.21	12353.03		12349	12333.75	12325.06	12324.69	12312.08		12305.87			12267.58	12266.06	12239.73			12227.95	12224.3		12208.26	12203.89	12203.41			12200.32	12197.63
				KIAA0026				FUBP1	KIAA0301	KIAA0622		DKFZP586J0619					CYBB	KIAA0019	DKFZP564B163			ITIH4			CHGB	TNG2	CA11				HCCS
Homo sapiens clone 24432	EST	Homo sapiens mRNA for	KIAA1218 protein, partial cds	MORF-related gene X	ESTs	ESTs	far upstream element (FUSE)	binding protein 1	KIAA0301 protein	KIAA0622 protein	ESTs	DKFZP586J0619 protein	Homo sapiens cDNA FI.111289 fis. clone	PI ACE1009621	cytochrome b-245, beta	polypeptide (chronic	granulomatous disease)	KIAA0019 gene product	DKFZP564B163 protein	inter-alpha (globulin) inhibitor	H4 (plasma Kallikrein-sensitive	glycoprotein)	ESTs	chromogranin B	(secretogranin 1)	TCL1-neighboring gene 2	carbonic anhydrase XI	ESTs, Moderately similar to	p53 regulated PA26-12	nuclear protein [H.sapiens]	(cytochrome c heme-lyase)
He 78019	Hs.230619		Hs.114012	Hs.173714	Hs.262061	Hs.55080		Hs.118962	Hs.76730	Hs.11238	Hs.123826	Hs.112184		He 12210			Hs.88974	Hs.278526	Hs.3642			Hs.76415	Hs.205300		Hs.2281	Hs.144519	Hs.22777			Hs.132927	Hs.211571
He 78010	Hs.49946		Hs.119582	4A777926 Hs.121991	4A702094 Hs.114100	Hs.55080		AA676848 Hs.117006	Hs.76730	Hs.26474	4A004946 Hs.123826	4A707004 Hs.112184		He 782			AA463492 Hs.88974	Hs.2475	RG.33			Hs.76415	Hs.13272		Hs.2281	Hs.79645	Hs.22777			Hs.57863	AA281548 Hs.88859
H70034	N70907		H54304	AA777926	AA702094	W37683		AA676848	N24059	R55719	AA004946	AA707004		AAA0572A He 782			AA463492	AA281057 Hs.2475	N69689			N73625	R61311		W37769	R70888	N52089			W95428	AA281548
225056	294321		203022	449498	384252	321905		460111	269374	41029	428298	451364		25,000	1		796984	711826	293715			296123	42666		322148	142579	282587			357778	712577
0000	GF202		GF203	GF204	GF203	GF202		GF204	GF201	GF202	GF202	GF203		CESON			GF200	GF200	GF200			GF201	GF202		GF201	GF201	GF200			GF201	GF200

***********	1.44961104		1.99930912	2.28323887	1.819358			1.6391808	1.24693545	2.30511846			1.08836616		1.80692257	2.27088016		1.52795911	1.91514479	1.64120861	1.6571166		1.74724166	2.01711063		1.11621334		1.35817314	1.89889463	
00707	12194.26		12188.96	12181.81	12169.32		12155.26	12155.06	12146.42	12141.15			12134.88		12116.93	12115.4		12105.58	12089.61	12085.55	12081.25	12076.27	12057.83	12054		12026.25	12012.79	12012.78	11992.92	11968.65
	AAMP							YDD19					nit DPM1		HMGCS1		9	TPX1		DJ167A19.1		KIAA 1078				PPP6C	EIF5A	KIAA0146		
angio-associated, migratory	cell protein Homo sapiens cDNA	FLJ10325 fis, clone	NT2RM2000569	EST	EST	Homo sapiens clone 24870	mRNA sequence	YDD19 protein	EST	ESTs	dolichyl-phosphate	mannosyltransferase	polypeptide 1, catalytic subunit DPM1	3-hydroxy-3-methylglutaryl- Coenzyme A synthase 1	(elqnlos)	ESTs	testis specific protein 1 (probe	H4-1 p3-1)	ESTs	hypothetical protein	ESTs	KIAA1078 protein	ESTs	ESTs	protein phosphatase 6,	catalytic subunit eukaryotic translation initiation	factor 5A	KIAA0146 protein	EST	ESTs
	Hs.8334/		Hs.245342	Hs.59448	Hs.87886		Hs.16561	Hs.25615	Hs.121971	Hs.68829			Hs.5085		Hs.77910	Hs.56006		Hs.2042	Hs.22635	Hs.11923	Hs.112747	Hs.23585	Hs.50847	Hs.22867		Hs.80324	Hs.119140	Hs.278634	Hs.91723	Hs.21452
1,000	AA452988 Hs.83347		AA430511 Hs.87454	W93386 Hs.59448	AA251548 Hs.87886		Al015589 Hs.16561	AA452799 Hs.108946	AA777717 Hs.121971	AA088326 Hs.68829			AA004759 Hs.5085		N62195 Hs.77910	W47416 Hs.56006		AA868278 Hs.2042	AA480980 Hs.22635	AA505141 Hs.11923	AA609666 Hs.112747	AA146963 Hs.23585	AA456822 Hs.50847	H05770 Hs.22867		AA521083 Hs.80324	AA878570 Hs.125392	AA401448 Hs.74670	R43535 Hs.91723	W92233 Hs.21452
7	789011		769944	415110	684798		1636868	788520	449295	511343			429182		290111	324322		1408407	814616	825822	1031820	505433	815558	43829		826459	1492411	742007	32576	358936
000	GF200		GF203	GF202	GF203		GF204	GF203	GF203	GF202			GF200		GF203	GF202		GF203	GF203	GF203	GF202	GF201	GF203	GF203		GF200	GF204	GF200	GF202	GF201

1.40153506	1.14511379	1,96179863 1,22220924 2,11288604 1,72161889	1.75870244		1.60444308
11935.39 11924.39 11899.43	11876.21 11865.4 11865.4	11864.04 11856.1 11854.7 11807.99	11756.42 11746.04 11746.04 11729.4	11700.01	11679.3
UBE2D3	BCKDK DKFZP586I1023 DKFZP586I1023	APG12L	FL/20010 PAGA		
ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5) ESTs	branched chain alpha-ketoacid dehydrogenase kinase DKFZP5861023 protein DKFZP58611023 protein	Apgliz (autopriagy 1z, 5. cerevisiae)-like ESTs ESTs ESTs Human homeobox gene,	complete cds ESTs ESTs ESTs A frautral killer-enhancing factor A) Human DNA sequence from	cohora RPS-1046G13 on chromosome 6q12-13 Contains part of a gene similar to Rattus norvegicus rab3 elector (RIM), ESTs, STSs and GSSs EST, Highly, emiliar to insulin	receptor substrate-s [M.musculus] ESTs, Highly similar to axonemal dynein heavy chain [H.sapiens]
Hs.118797 Hs.105730 Hs.47446	Hs.20644 Hs.111515 Hs.111515	Hs.264482 Hs.90043 Hs.57100 Hs.77823	Hs.74870 Hs.91816 Hs.117407 Hs.181000 Hs.180909	Hs.129190	Hs.121968 Hs.3904
H28023 Hs.113864 AA50462 Hs.105730 N52149 Hs.47446	AA970731 Hs.20644 AA490124 Hs.75355 AA490124 Hs.91370	N72165 Hs.38225 AA233774 Hs.90043 R58948 Hs.57100 AA485216 Hs.77823	AA975010 Hs.74870 AA4A7995 Hs.91816 R448331 Hs.117407 AA460295 Hs.97136 AA775803 Hs.1163	H29290 Hs.3840	AA777710 Hs.121968 N35593 Hs.3904
162975 825297 284379	1573108 839682 839682	291155 666235 41123 815800	1560977 782742 32711 795739 878259	49858	449296
GF204 GF204 GF202	GF204 GF200 GF200	GF203 GF203 GF202 GF203	GF204 GF204 GF204 GF201	GF201	GF204 GF203

1.62206249 1.3716722	1.58301093				11001001	1.55258045	1.67952125	1.30880773				1.29224767			1.6956379											1.60932894
11660.18	11636.73	11617.09	11611.52	11610.09	11609.04	11501.92	11581.73	11573.01	11568.83	11563.7		11560.08	11556.23		11546.47	11542.4			11522.61	11520 57			11514.7		11511.42	11491.46
DKFZP586I1023		GPS2		STF1		KIAAUZ35			TYMS	LOC51313		KIAA0326	HNRPC		PI6								SDHD			PA2G4
P58611023 protein	ESTs G protein pathway suppressor	2 Human clones 23549 and	23762 mRNA, complete cds	osteoclast stimulating factor 1 OSTF1		235 protein	ESTS	ESTS	ylate synthetase	AD021 protein	ESTs	KIAA0326 protein K		6 (placental	oin inhibitor)	ESTs	EST, Weakly similar to	probable protein-tyrosine	kinase receptor [H.sapiens]	HSPC011 [H sapiane]	succinate dehydrogenase	complex, subunit D, integral		ESTs, Weakly similar to 2-19 PROTEIN PRECURSOR	[H.sapiens] proliferation-associated 2G4	
Hs.111515 Hs.21475	Hs.14294	Hs.7301	Hs.87241	Hs.95821	Hs.83115	Hs.6151	HS.11/44/ He 61380	Hs.61304	Hs.82962	Hs.21941	Hs.204081	Hs.6833	Hs.182447		Hs.41072	Hs.119225			Hs.231139	900777	18.4450		Hs.168289		Hs.61265	Hs.5181
Hs.126916 Hs.21475	Hs.14294	AA453458 Hs.7301	AA937220 Hs.87241	4A149226 Hs.103874	N32404 Hs.114616	4A478473 Hs.26505	H2/213 Hs.11/44/	AA425056 Hs.61304	AA663310 Hs.82962	AA187207 Hs.85529	AA879073 Hs.125408	AA128587 Hs.6833	AA455111 Hs.30146		AA410517 Hs.41072	AA420966 Hs.119225		,	AA701961 Hs.114081	A A 723080 Hz 120222	00 118: 120000		AA035384 Hs.108326		AA025434 Hs.61265	AA291135 Hs.12757
R35051 N49378	R26811	AA45345	AA93722	AA14922	W32404	AA47847	H27213	AA42505	AA66331	AA1872C	AA87907	AA12856	AA45511		AA41051	AA42096			AA70196	0000744	7000		AA03538		AA02548	AA29118
136605 277608	132619	795151	1507723	504623	321356	786608	133386	768596	853368	624490	1492512	502909	809835		753862	731229			435944	90000	0.0000		471598		365707	700499
GF202 GF203	GF203	GF201	GF204	GF201	GF204	GF203	GF203	GF203	GF201	GF204	GF204	GF200	GF201		GF200	GF204			GF204	70010	10210		GF201		GF201	GF203

1.19496397	1.24200761	2.16028524	2.33289779	1.6775411 2.25662974	2.003926 1.07915781 1.55676099 2.24758704
11485.8 11482.26 11429.97 11416.55	11410.83 11394.36 11393.84	11384.04 11373.91 11360.71 11347.41	11337.58 11324.95 11320.92 11318.83 11303.64	11286.78	11270.67 11269.1 11265.95 11263.76
PPIC LTA4H	SIAT4C ALDH7 AEBP1	SYNGR1	COL17A1	РТНСН	P84 RPS25 GP2
peptidylprolyl isomerase C (cyclophilin C) leukoriene A4 hydrolase ESTs ESTs ESTs adalytransferase 4C (beta-	garactooladae aphara-i-o sialytransferase) aldehyde dehydrogenase 7 AE-binding protein 1 Homo sapiens mRhd fulli lennth insart cDNA fulli	EURONAGE 39820 synaplogyin 1 SSTs ESTs ESTS ESTS ESTS ESTS ESTS ESTS	DKFZp434D1227) ESTS ESTS Collagen, type XVII, alpha 1 Human clone 137308 mRNA, parlal cds	ESTS parathyroid hormone-like hormone FSTs. Weakly similar to	centaurin beta2 [H.sapiens] nuclear matrix protein p84 ribosomal protein S25 glycoprotein 2 (zymogen granule membrane)
Hs.110364 Hs.81118 Hs.179260 Hs.103014	Hs.75268 Hs.83155 Hs.118397	Hs.113657 Hs.6139 Hs.41055 Hs.55918 Hs.130214	Hs.172789 Hs.178703 Hs.106212 Hs.117938 Hs.159255 Hs.6946	Hs.89626	Hs.4273 Hs.1540 Hs.113029 Hs.53985
AA676404 Hs. 110364 AA465366 Hs.81118 AA418557 Hs.93252 W37338 Hs.103014	AA453898 Hs.75268 N93686 Hs.83155 AA490462 Hs.118397	R38708 Hs. 113657 AA975267 Hs. 6139 AA021546 Hs. 41055 AA455279 Hs. 55918 AA456631 Hs. 130214	N59148 Hs.102717 H56345 Hs.108147 R33856 Hs.106212 H87536 Hs.117938 H87459 Hs.78328 H17081 Hs.6946	32	AA187681 Hs.85550 AA129338 Hs.1540 AA872704 Hs.75577 AA844930 Hs.53985
882459 814095 767346 321837	813751 307069 823851	23461 1558855 364271 810035 811944	287683 203711 136244 252259 252491 47597	796498	625846 564846 1475738
GF201 GF200 GF203 GF201	GF200 GF201 GF200	GF204 GF204 GF203 GF201 GF201	GF202 GF202 GF201 GF201 GF201	GF203 GF203	GF202 GF200 GF203 GF203

1.2396858 2.32681503 1.23629318	1.65391271	1.49512998	1.31652525	2.01580071		1.20503222	1.13984486	1.22816348	2.30887162
11254.04 11243.61 11236.38	11235.55 11223.05 11215.89	11214.03 11211.52 11203.63 11198.65	11188.96 11188.06 11185.17	11176.86	11176.81	11161.97 11159.9 11153.74	11145.92	11139.46	11106.82
CTNNB1 ANXA13	LAMR1 DKFZP586I1023	DKFZP434C245	BECN1 APC	VPS45B	RPS6KB2	D123 CTBP2 ZNF282	REN PTMA) CAPZA1	
catenin (cadherin-associated protein), beta 1 (88KD) morshin A13 EST laminin recentor 1 (67kD)	ribosomal protein SA) DKFZP586I1023 protein ESTs	DKFZP434C245 protein ESTs ESTs ESTs	ESTs beclin 1 (coiled-coil, myosin- like BCL2-interacting protein) adenomatosis polyposis coll adenomatosis polyposis coll	vacuotal protein sorining 435 (yeast homolog) EST, Highly similar to ribosomal protein L7	[H.sapiens] ribosomal protein S6 kinase, 70kD, polypeptide 2	D123 gene product C-terminal binding protein 2 zinc finger protein 282	renin prothymosin, alpha (gene sequence 28)	capping protein (actin filament) muscle Z-line, alpha 1 ESTs, Moderately similar to	transporter ABC1 [H.sapiens]
Hs.171271 Hs.181107 Hs.44939	Hs.181357 Hs.111515 Hs.161542	Hs.59461 Hs.49874 Hs.125232 Hs.161839	Hs.22574 Hs.12272 Hs.75081	Hs.6650	Hs.229237 Hs.103081	Hs.82043 Hs.171391 Hs.171391 Hs.58167	Hs.3210 Hs.250655	Hs.184270	Hs.270507
AA442092 Hs.58464 AA884167 Hs.2776 N39087 Hs.44939	AA485458 Hs.107348 T61071 Hs.10839 N91584 Hs.8782	8 4 5 8	R43279 Hs.22574 AA427367 Hs.12272 N26688 Hs.119041	AA668531 Hs.6650	AA284234 Hs.103081	AA448289 Hs.82043 W86518 Hs.108820 AA457153 Hs.58167	AA455535 Hs.3210 N48162 Hs.22754	AA449037 Hs.82488	H45265 Hs.33249
774754 1468461 276495	811079 83610 303048	462333 811880 1468362 767086	32731 771084 269332	859832	324712	784830 416744 810496	813402	785793	182816
GF200 GF203 GF202	GF203 GF201 GF200	GF204 GF203 GF204 GF202	GF204 GF200 GF204	GF203	GF204 GF201	GF200 GF201 GF201	GF200 GF203	GF200	GF203

Atty Docket No. 2172	2.09319638	1.06271977 2.3460664 1.79050023	1.66381175	1.20803651	1.19693401	1.87940549 1.50335025 1.59361125 1.50308912	1.58401932
Atty	11105.04 11093.99 11088.93	11083.48 11077.81 11065.16	11055.51 11049.19 11038.55 11031.97	11025.27 11021.21 11001.76	10993.87	10987.63 10986.42 10974.65 10963 10962.41	10961.58 10947.41 10944.68 10939.59
	PMS2L12 CLGN	CETIN3 PIM1	KIAA0128	TRDN			MSTP9
APPENDIX A	postmeiotic segregation increased 2-like 12 calmegin ESTs	centrin, EF-hand protein, 3 (CDC31 yeast homolog) pim-1 oncogene ESTs	EST EST KIAA0128 protein; septin 2 ESTs	ESTs triadin apelin; peptide ligand for APJ recentor	ESTs, Weakly similar to testicular tektin B1-like protein [H.sapiens]	UKrZp586F1223) ESTs ESTs ESTS ESTS ESTS ESTS ESTS ESTS	similar to M. musculus MERS and other AHPC/TSA proteins [C elegans] macrophage stimulating, pesudogene 9 EST EST
	Hs.91299 Hs.86368 Hs.156861	Hs.29463 Hs.81170 Hs.49169	Rs.3933/ Hs.29468 Hs.99523 Hs.90998 Hs.108106	Hs.6952 Hs.68731 Hs.181060	Hs.47152	Hs.28540 Hs.274394 Hs.231082 Hs.192644 Hs.55336	Hs.40919 Hs.250826 Hs.116671 Hs.5565
	N93582 Hs.102922 AA778675 Hs.86368 W35416 Hs.94586	~ ~ ~	AA404 149 NS.39337 N73949 HS.29468 AA460289 HS.99523 R76772 HS.90998 AA026356 HS.108106	Al023726 Hs.6952 AA404293 Hs.68731 AA101878 Hs 22793	AA609403 Hs.47152	N59219 Hs.28540 A4455302 Hs.111999 W51835 Hs.103098 H23216 Hs.31962 W15316 Hs.55336	R22945 Hs.107722 T51539 Hs.90568 AA689226 Hs.116671 AA281743 Hs.5565
k et al.	307645 1049033 321751	487425 292726 490779	795308 298281 795723 143966 366414	1654978 758366 489637	743516	288741 810061 325674 51879 322635	131308 72395 856599 712377
Westbrook et al.	GF201 GF202 GF202	GF201 GF200 GF202	GF202 GF201 GF200 GF200 GF204	GF204 GF200	GF202	GF201 GF202 GF202 GF202 GF202	GF203 GF201 GF204 GF203

1.21656132	1.11938869	1.21098939	1.28764639	1.66888758	1.12823605	1.12823605	1.28721005	1.87230194
10925,77 10924.32 10922.22 10917.85 10908.92	10898.23	10852.99	10839.82	10836.43	10830.52	10830.52 10829.06	10824.65 10812.54	10802.19 10801.23 10792.32 10782.57
KIAA0395	MS4A2	RPL32 DKFZP566O084	TFDP2		TOP2A	TOP2A		TM4SF7
Homo sapiens mRNA; cDNA DKTZp4344109) DKTZp4344109) MAA0835 protein ESTs, Highly similar to CGI-38 protein [H.sapiens] ESTs Homo sapiens mRNA; cDNA Homo sapiens mRNA; cDNA DKTZp588N1918 (from clone DKTZp588N1918)	membrane-spanning 4- domains, subfamily A, member 2	ribosomal protein L32 DKFZP566O084 protein	dimerization partner 2) ESTs, Weakly similar to	[C.elegans]	(170kD) topoisomerase (DNA) II alpha	(170kD) ESTs	ESTS ESTS transmembrane 4 sunorfamily	rational Date 1 Superior in the many fraction in th
Hs. 9070 Hs. 167839 Hs. 110453 Hs. 98167 Hs. 169936	Hs.89751	ns.6740 Hs.169793 Hs.11411	Hs.19131	Hs.100843	Hs.156346	Hs.156346 Hs.14518	Hs.169888	Hs.26518 Hs.77542 Hs.22176 Hs.55307 Hs.30579
AA461497 Hs.9070 W47158 Hs.43681 AA045524 Hs.110453 N82944 Hs.4866 AA431428 Hs.98167 AA151553 Hs.22318	N91385 Hs.89751	AA456959 HS.6740 R43544 HS.83343 AA457140 HS.11411	AA465444 Hs.82617	AA489470 Hs.100843	AA504348 Hs.3378	AA504348 Hs.119142 N92359 Hs.14518		AA100696 Hs.26518 N32811 Hs.77542 AA150502 Hs.22176 W04695 Hs.55307 F96455 Hs.30579
795832 324749 487327 278755 782427 503126	306013	810463 810463	814101	897427	825470	825470 308115	66377 32496	490556 259017 491764 320425 197975
GF201 GF201 GF202 GF201 GF201	GF200	GF200 GF201 GF201	GF200	GF202	GF200	GF200 GF201	GF200 GF201	GF201 GF201 GF201 GF202 GF200

Ally Docket No. 2172	1.6509876	1.17099885	1.72883002	2.11324682			1.21626694				1.24531966			2.00344445		1.08295349	2.00474349	1.28345177				1.19673222							1.67308959	-1.2698013		1.248849		
Auy	10776.9	10769.04	10738.97	10732.46			10721.55			10714.29	10700.02			10691.19		10685.88	10681.57	10673.26	10668.48	10659.38		10656.32	10651.48	10645.5		10638.26	10607.11		10605.3	10594.5	10594.23	10579.54	10574 20	100/4:38
		UNC119					ATP6S1				CDC25B					KLK3			DKFZP586I1023	NRP2		TGFBR2	PIR121			TANK				DKFZP564M182		TUBBS		TARD
APPENDIX A	Homo sapiens mRNA for KIAA1340 protein, partial cds	unc119 (C.elegans) homolog	EST	EST	ATPase, H+ transporting,	lysosomal (vacuolar proton	pump), subunit 1	Homo sapiens mRNA; cDNA	DKFZp586H0924 (from clone	DKFZp586H0924)	cell division cycle 25B	Acetylcholinesterase {14-E5	doman} [human, tumor cell	lines, Genomic, 847 nt]	kallikrein 3, (prostate specific	antigen)	ESTs	ESTs	DKFZP586I1023 protein	neuropilin 2	transforming growth factor,	beta receptor II (70-80kD)	p53 inducible protein	ESTs	TRAF family member-	associated NFKB activator	ESTs	ESTs, Weakly similar to	/prediction	DKFZP564M182 protein	ESTs	tubulin, beta, 5	peroxisome proliferative	activated receptor, della
	Hs.51743	Hs.81728	Hs.98844	Hs.46642			Hs.6551			Hs.106390	Hs.153752			Hs.157124		Hs.171995	Hs.105000	Hs.170266	Hs.111515	Hs.17778		Hs.82028	Hs.258503	Hs.217754		Hs.146847	Hs.268690		Hs.240763	Hs.20760	Hs.156984	Hs.108014		HS.106415
	AA700099 Hs.118785	4A457199 Hs.81728	AA435945 Hs.98844	Hs.46642			AA488715 Hs.75696			Hs.43268	AA448755 Hs.75779			Hs.89881		4A490981 Hs.1548	4A449090 Hs.105000	AA040043 Hs.44552	AA996104 Hs.8693	4A156964 Hs.17778		4A487034 Hs.82028	Hs.4282	Hs.118841		4A134814 Hs.79076	Hs.24277		4A608632 Hs.30134	AA705999 Hs.129849	4A885221 Hs.125625	Hs.108014		Hs.106415
	AA70009	AA45719	AA43594	N49619			AA48871			N24914	AA44875			N63940		AA49098	AA44909	AA04004	AA99610	AA15696		AA48703	H09818	R43523		AA13481	R28303		AA60863	AA70599	AA88522	N74524		N33331
retal.	435776	838389	730543	277785			841689			270017	786067			293924		824568	785674	485858	1635874	502536		841149	46896	32777		502486	134682		950770	1239877	1468727	291756		270626
Westbrook et al.	GF203	GF200	GF202	GF202			GF200			GF201	GF200			GF203		GF200	GF203	GF200	GF204	GF204		GF200	GF201	GF204		GF201	GF201		GF202	GF203	GF204	GF203	į	GF201

1.16834117	1.69431783	1.61675435	1.24248965			-1.0532725		2.44947849 1.65462377	1.64716739
10571.05 10569.42 10555.61 10553.7 10538.25	10530.42	10529.2 10517.08	10516.31	10513.06	10501.67	10487.87		10467.79 10462.34	10447.51 10447.1 10437.6
USP9X CA2 TNNI2 ZNF278	REG1B		SURF5 I		KCNB1				DNAI1
ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) carbonic anhydrase II roppnin 1, skeletal, fast ESTs zinc finger protein 278	regenerating islet-derived 1 beta (pancreatic stone protein, pancreatic thread protein)	Homo sapiens cDNA FLJ20419 fis, clone KAT02435 ESTs	surfeit 5 ESTs, Weakly similar to neural F box protein NFB42	[R.norvegicus] potassium voltage-gated channel. Shab-related	subfamily, member 1 Homo sapiens mRNA; cDNA DKF7n564M113 (from clone	DKFZp564M113)	ESTs, Moderately similar to RNA polymerase I associated	factor [M.musculus] ESTs dvnein. axonemal.	informediate chain 1 ESTs EST
Hs.77578 Hs.155097 Hs.83760 Hs.105293 Hs.27801	Hs.4158	Hs.11184 Hs.24211	Hs.78354	Hs.65709	Hs.84244	Hs.205678		Hs.24884 Hs.104073	Hs.112667 Hs.160690 Hs.95313
N26828 Hs.43861 H23187 Hs.7883 AA181334 Hs.83760 AA504777 Hs.105293 AA449718 Hs.27801	AA844864 Hs.4158	AA43435 Hs.107277 AA464200 Hs.24211	AA459247 Hs.78354	AA284184 Hs.89312	AA069770 Hs.84244	AA167550 Hs.51811		AA176812 Hs.24884 AA488351 Hs.104073	AA609218 Hs.112667 AA625861 Hs.32214 AA054554 Hs.95313
257109 51865 611532 825856 785941	1412300	770289	814460	324220	382457	609188		611206 843150	1031478 745437 489462
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	1.19035156	1.21986796	2.51662286				1.05940073	1.93658908				2.52392365	1.31723655				1.69251213	1.12705516				-1.033849	2.00328141	1.01071241		1.21219107		1.25056431		1.71922755		2.03448037		
	10436.39	10426.17	10418.27		10410.57		10406.71	10402.67				10399.84	10396.9			10389.37	10377.76	10376.04			10362.55	10353.47	10349.7	10334.21	10324.12	10317.24		10309.03	10306.85	10300.99	10283.19	10274.31	10 02001	10270.61
	RARRES1	器	KIAA0517		C180RF1		SGK									DBCCR1		PRSS2				EDNRB			AF020591			PEX13					מאממס	GPHKZL
retinoic acid receptor responder (tazarotene	induced) 1	phosphorylase kinase, beta	KIAA0517 protein	chromosome 18 open reading	frame 1	serum/glucocorticoid regulated	kinase	ESTs	ESTs, Weakly similar to !!!!	ALU SUBFAMILY J	WARNING ENTRY !!!!	[H.sapiens]	ESTs	deleted in bladder cancer	chromosome region candidate	-	ESTs	protease, serine, 2 (trypsin 2)	Homo sapiens cDNA	FLJ20094 fis, clone	COL04320	endothelin receptor type B	ESTs	EST	zinc finger protein	ESTs	peroxisome biogenesis factor	13	EST	ESTs	ESTs	ESTs	G protein-coupled receptor	Kinase z (Drosopniia)-like
	Hs.82547	Hs.78060	Hs.12372		Hs.153498		Hs.159640	Hs.8941				Hs.6853	Hs.6189			Hs.6090	Hs.55902	Hs.241561			Hs.29700	Hs.82002	Hs.101515	Hs.46923	Hs.142634	Hs.268883		Hs.115240	Hs.116087	Hs.14633	Hs.22571	Hs.183380	2000	Hs.32959
	N94424 Hs.82547	AA476263 Hs.75345	AA464935 Hs.12591		N56872 Hs.102703		82	N59553 Hs.8941				AA417994 Hs.6853	W33011 Hs.22228			H10959 Hs.22263	AA233892 Hs.55902	AA284528 Hs.2048			AA708627 Hs.29700	H28710 Hs.82002	AA504253 Hs.101515	N49267 Hs.46923	AA629926 Hs.48878	R98774 Hs.36014		R16849 Hs.115240	AA625844 Hs.116087	H17012 Hs.14633	R43269 Hs.22571	AA456286 Hs.30794		N23898 Hs.32959
	309583	772951	838889		277463		840776	248669				767456	321706			47037	666707	713685			506509	49665	825404	280362	884683	200873		128783	745418	50569	32515	813148	000110	255333
	GF200	GF200	GF202		GF201		GF200	GF203				GF202	GF200			GF201	GF202	GF200			GF204	GF200	GF203	GF202	GF204	GF200		GF200	GF204	GF203	GF201	GF202		GF201

Atty Docket No. 2172			1.28090596		1.46750269		1.74863533		1 08550534	1.55800364		1.29488177	1.95898427			1.20599053		1.44049901		0.00000	25.25529152	2.16374656	1.89774439			1.85167921	
Afty	10263.65 10263.65 10263.63	10233.01	10226		10220.68		10210.37		10205.55	10200.2		10198.18	10164.09	10147.57		10141.26		10137.21		10133.51	10125.5	10114.39	10107.51		10106.06	10095.68	
	STK10 KRT13		DKFZP434B168		SMARCA1		COX6C					SCAM-1				HSF2				POLR2E			ABHGAP6		ADRB2	KIAA0849	
APPENDIX A	serine/threonine kinase 10 keratin 13 ESTs	ESTs	DKFZP434B168 protein SWI/SNF related, matrix	associated, actin dependent	subfamily a, member 1	cytochrome c oxidase subunit	Vic	ESTs, Weakly similar to !!!!	ENTRY III (H saniens)	ESTs	vinexin beta (SH3-containing	adaptor molecule-1)	ESTs	ESTs	heat shock transcription factor	2	ESTs, Highly similar to DNAJ PROTEIN HOMOLOG MTJ1	[M.musculus]	polymerase (RNA) II (DNA	directed) polypeptide E (25kD) POLR2E	ESIS	ESTs Des GTDess potimoting protoin	niio airase activatiig proteii 6	adrenergic, beta-2-, receptor,	surface	KIAA0849 protein	
	Hs.16134 Hs.74070 Hs.44158 Hs.31709	Hs.49031	Hs.48604		Hs.152292		Hs.74649		Hs 93961	Hs.49397		Hs.33787	Hs.47312	Hs.36567		Hs.158195		Hs.13015		Hs.24301	HS.13/0//	Hs.47223	Hs 250830		Hs.2551	Hs.18827	
	AA044263 Hs.16134 W60057 Hs.94751 W72692 Hs.44158 AA025631 Hs.31709		8 Hs.48604		AA496809 Hs.1061		AA121158 Hs.17801		3 Hs 93961			ន្ត	_	4 Hs.36567		AA250730 Hs.826		AA449438 Hs.13015		Ω		7 Hs.47223	AA495981 Hs 102778			9 Hs.18827	
		_	N80458					-	B26163	_		-	_	H51434							_	N51297			_	R62469	
ok et al.	486386 342008 345838 366233	340835	292654		897667		511718		132140	286657		453183	280567	179572		669443		785571		469369	282104	283070	768489		241489	36584	
Westbrook et al.	GF204 GF201 GF201 GF201	GF201	GF200		GF200		GF202	5	GF200	GF202		GF203	GF202	GF204		GF200		GF202		GF201	GFZUZ	GF202	GF203		GF201	GF202	

1.48196508 1.4807689 1.4807689 1.98683124 1.1790464 1.152589708 1.32180962 1.32180962 1.16075139	1.15059932 1.46912057 1.13479519
10095.5 10092.28 10068.18 10066.03 10056.03 10051.64 10049.13 10039.84 9994.685 9994.685 9997.7483 9967.265 9967.265 9967.265 9967.265 9967.265	9923.074 9919.529 9915 9901.437
TEDP1 KIAA0318 EMP2 MPHOSPH9 MPHOSPH9 KIAA0973 KIAA0973	PWP1
ESTS. ESTS, Highly similar to CGI-25 ESTS ESTS ESTS ESTS ESTS ESTS EST EST Transcription factor Dp-1 KAAA318 protein meltineliar membrane protein optimeliar to allematively spilical membrane protein optimeliar to summan optimeliar to signal peptideaes/SUBLINIT glycine C-acetyltransferase (2-marine-3-kerboturyrate-CoA ligase) KIAAA0973 protein KIAAA0973 protein KIAAA0973 protein KIAAA0973 protein KIAAA0973 protein ESTS ESTS ESTS ESTS ESTS	nuclear phosphoprotein similar to S. cerevisiae PWP1 ESTs emerges and then sapiens cDNA FLJ1089 fis, clone NTZRP4002296 bromodomain adjacent to zinc finger domain, 2A
Hs.104985 Hs.7236 Hs.529748 Hs.59773 Hs.101681 Hs.73353 Hs.65746 Hs.27091 Hs.16704 Hs.27099 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489 Hs.27489	Hs.172589 Hs.21594 Hs.12457 Hs.277401
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782838 753021 381062 381062 382704 322704 322708 304975 109863 44798 244739 24739 725489 307094 739625 739625 739625 739625 739625 739625 739625 739625	843069 503581 53265 417509
GF202 GF202 GF203 GF202 GF202 GF201 GF201 GF201 GF204 GF204 GF206 GF206 GF206 GF206 GF207 GF206 GF206 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207 GF207	GF200 GF201 GF203 GF200

1,19198793 1,7149843 1,72629058 1,3592578	1.15980508 1.40968433 2.14966051	1.12347841 1.13413208 1.9446643	1.7351467	1.17952366 2.4026082 2.15706305 1.59277649 2.52317956 1.20539282 -1.238135 2.27182749
9895.317 9892.806 9885.046 9868.24 9868.24 9867.356 9897.356	9854.601 9842.232 9836.805 9834.323 9820.832	9798.836 9780.894 9779.989	9764.44 9764.023 9758.832 9751.245 9745.28	9742.015 9734.966 9721.263 9713.377 9703.731 9684.191 9682.47
DKFZP566K023	ALTE HBS1L	CST3 UBE2I	CBFB RPS6	APOD ZNF212 DKFZP566B0846
Homo sapiens mRNA; cDNA DKFZp434H2121 (from clone DKFZp466K023 protein ESTs EST ESTS ESTS	ESTs Ac-like transposable element ESTs ESTs ESTs HBS1 (S. cerevisiae)-like	oystatin C (amyloid angiopathry and cerebral hemorrhage) uloquitin-conjugating enzyme E2I (homologous to yeast UBCs) ESTs core-briding factor, beta	subunit ribosomal protein S6 ESTs ESTs	apolipoprotein D ESTs ESTs ESTS ESTS ESTS ESTS ESTS ESTS
Hs.33104 Hs.19999 Hs.55185 Hs.104348 Hs.47660 Hs.106313 Hs.31712	Hs. 105904 Hs. 9933 Hs. 94642 Hs. 167836 Hs. 191385 Hs. 221040	Hs.135084 Hs.84285 Hs.188691	Hs.179881 Hs.241507 Hs.8687 Hs.107233 Hs.98295	Hs. 75736 Hs. 108139 Hs. 22488 Hs. 98936 Hs. 85950 Hs. 112644 Hs. 269475
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754148 491615 309119 684562 814547 22987 267696	645284 855029 323404 136188 435690 950926	949938 841292 1031580	624754 781459 811785 815096 767281	159608 740748 773402 757386 665033 1031346 1031582
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1.69823159 1.09390457 1.46494938 1.01576911 1.72556627	-1.0237729 1.116074 2.09777366	1.19783525		1.52327488	1.78048091 2.73029953	1.72529052	1.10350801
9653.42 9652.667 9646.896 9641.226 9640.562 9638.757 9635.776	9632.121 9616.91 9609.892 9608.74	9607.712	9602.282	9593.017	9567.894 9565.229 9550.451	9525.712	9514.323
DKFZP434G1017 DAD1 KIAA1089 KIAA1067	ZNF193 TONDU	PSMA3	CLPTM1 CREB3	EYA3 EVI2B	KIAA0459	CEPT1	NEDD4
hypothetical protein defender against cell death 1 KIAA1099 protein KIAA1097 protein ESTs EST	ESTs, Weakly similar to ESTs, Weakly similar to PUTATIVE PRE-MRNA SPLCING FACTOR RNA HELLOASE IH sapiens] Zinc finger protein 193 TONDU ESTs	proteasome (prosome, macropain) subunit, alpha type, 3	cleft lip and palate associated transmembrane protein 1 cAMP responsive element binding protein 3 (luman) eves absent (Drosobnila)	homolog 3 ecotropic viral integration site 2B	ESTs EST KIAA0459 protein	ESTs choline/ethanolaminephosphot ransferase	neural precursor cell expressed, developmentally down-regulated 4
Hs.107376 Hs.26890 Hs.267811 Hs.243901 Hs.128450 Hs.61696	HS.7174 HS.96448 HS.9030 HS.68846	Hs.167106	Hs.106671 Hs.173422	Hs.46925 Hs.5509	Hs.77855 Hs.236223 Hs.28169	Hs.46668 Hs.125031	Hs.1565
AA400195 Hs.107376 AA455281 Hs.82890 AA456139 Hs.57442 N75473 Hs.106053 W85651 Hs.128450 AA131678 Hs.61696 AA609002 Hs.11626	AA118610 Hs.7174 AA282188 Hs.96448 AA700322 Hs.9030 AA700328 Hs.6848	AA465593 Hs.82308	AA005140 Hs.100439 AA461304 Hs.3753	N49272 Hs.114415 AA159620 Hs.5509	AA044906 Hs.77855 R43020 Hs.22307 H15653 Hs.28169		AA442095 Hs.1565
742783 810039 796357 299162 416325 504111	767387 668182 460666 511210	814246	429060	280365	488706 31972 49291	280327	774751
GF202 GF200 GF202 GF201 GF203 GF201	GF202 GF200 GF200 GF200	GF200	GF201	GF203	GF202 GF203 GF203	GF202 GF201	GF200

1.19573842	20000120:1	-1.9533877 1.05431798	1.05431798			1.19905012	1.8481064		1.30101529	2.34259617	
9512.675	9502.093	9490.584 9489.806	9489.806 9488.104 9487.328	9474.509	9474.431	9472.9 9448.578	9447.872 9439.535	9427.111	9422.907	9415.476 9415.4	9411.156
KIAA0871	S100A1	PRG1 DKFZP58611023	DKFZP58611023	ASMTL		EIF48	-		CD58		ACCN3
Homo sapiens clone 25056 mRNA sequence KIAA0871 protein Homo sapiens mRNA; cDNA DKFZp434M082 (from clone	DKFZp434M08Z) S100 calcium-binding protein A1	proteoglycan 1, secretory granule DKFZP586I1023 protein	DKFZP586I1023 protein ESTs	acetylserotonin O- methytransferase-like Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-	containing mRNA eukaryotic translation initiation	factor 4B ESTs	ESTs ESTs ESTs, Weakly similar to cDNA EST yk481g5,5 comes from	this gene [C.elegans] CD58 antigen, (lymphocyte	function-associated antigen 3) ESTs, Weakly similar to cDNA EST yk484g1.3 comes from	this gene [C.elegans] ESTs amiloride-sensitive cation	channel 3, testis
Hs.106127 Hs.7972	Hs.31774 Hs.251702	Hs.1908 Hs.111515	Hs.91564	Hs.6315	Hs.8068	Hs.93379 Hs.22270	Hs.266076 Hs.189916	Hs.128060	Hs.75626	Hs.55608 Hs.249185	Hs.98547
5	H46221 Hs.31774 AA425934 Hs.89840	AA278759 Hs.1908 AA490124 Hs.75355	AA490124 Hs.91370 R44173 Hs.91564	AA427398 Hs.6315	AA074535 Hs.8068	R28424 Hs.23383 R43352 Hs.22270	15	AA181506 Hs.128060	0	W42541 Hs.55608 W92947 Hs.59383	AA428361 Hs.98547
795750	178268	703581	34243 34243	771056	366042	133180	71825	611510	490368	323117 356949	773610
GF201 GF200	GF203 GF201	GF200	GF201	GF201	GF201	GF200	GF202 GF204	GF204	GF200	GF201 GF202	GF204

1.62658221 1.22663604 1.21794515	1.10417059	1.10417059	-1.0441366	1.01190895	1.17493966	1.16227136		-1.0136952
9393.448 9385.862 9373.696	9373.393	9373.393	9372.809	9358.732 9357.991	9352.233	9336.613	9329.566	9323.453
FPR1	, ATP6N1A	, ATP6N1A		PRCC KIAA0467	CRABP2	HNRPH1		TJP3
Homo sapiens mRNA; cDNA DKFZp434B231 (from clone DKFZp434B231) ESTs formyl peptide receptor 1	ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD)	ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (10/116kD)	ESTs, Weakly similar to OHF YNL240c [S.cerevisiae] papillary renal cell carcinoma	(translocation-associated) KIAA0467 protein	cellular retificio acid-binality protein 2 beteroreneous puclear	ribonucleoprotein H1 (H) Homo sapiens cDNA El 11161 fis clone	PLACE1007021	occludens 3)
Hs.267445 Hs.99816 Hs.753	Hs.267871	Hs.267871	Hs.22158	Hs.9629 Hs.11147	Hs.183650	Hs.245710	Hs.7111	Hs.25527
W47667 Hs.109907 R78539 Hs.98816 AA425249 Hs.753	AA427472 Hs.73067	AA427472 Hs.118855	AA707853 Hs.22158	AA488233 Hs.9629 N95780 Hs.94500	AA598508 Hs.86358	W96114 Hs.83573	AA044846 Hs.7111	AA402040 Hs.25527
324358 144878 773236	770377	770377	413056	877644 308497	897770	358457	488707	741919
GF202 GF200 GF200	GF200	GF200	GF203	GF200 GF201	GF200	GF200	GF201	GF203

1.54658885 1.42642249 .37975775 .31150883 1.11627667 13575564 .94680245 .32117751 3209.654 9207.906 9201.628 3263.125 9252.617 9242,659 9236,979 9236,424 9225.962 9219.909 9310.233 9295.742 9277.478 3211.857 321.657 DKFZP56611024 DKFZP566E104 **KIAA0247** MASP1 ICAM1 FRDA S dodecenoyl-Coenzyme A delta Chondroitin 6-Sulfotransferase intercellular adhesion molecule ESTs, Weakly similar to weak clone 71L16 on chromosome outative gene, a pseudogene mannan-binding lectin serine protease 1 (C4/C2 activating Human DNA sequence from with high similarity to part of 1 (CD54), human rhinovirus somerase (3,2 trans-enoylpseudo)gene, an unknown Kp11. Contains a probable component of Ra-reactive similarity to TPR domains Coenzyme A isomerase) DKFZP566I1024 protein antigen KI-67, a putative DKFZP566E104 protein KIAA0247 gene product Zinc Finger protein LIKE gene and a K Friedreich ataxia C.elegans] eceptor actor) **ESTS** ESTS ESTS ESTS ESTS Hs.168383 4s.177930 4s.104050 1s.189834 4s.154353 4s.227152 Hs.55040 4s.117361 Hs.55158 Hs.89466 4s.78605 1s.94680 4s.14407 1s.82426 4s.95998 AA284109 Hs.103085 AA480865 Hs.104050 AA405800 Hs.89466 AA699983 Hs.117361 Hs.55158 4s.55040 AA455291 Hs.14407 Hs.82426 Hs.51061 Hs.74887 AA398073 Hs.97500 AA425001 Hs.78605 AA284112 Hs.94680 AA443853 Hs.30123 AA253413 Hs.95998 N37689 R77293 181199 194362 N63733 241365 322123 309486 742115 324333 810062 435719 726523 814537 324762 292894 145112 768358 369419 784093 GF201 GF200 GF203 GF204 GF201 GF204 GF203 GF203 GF202 GF202 GF202 GF200 GF201 GF201 GF201

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GF203	796623	AA461460 Hs.88663	Hs.88663	Hs.88663	Homo sapiens cDNA FLJ10545 fis, clone NT2RP2001675		9188.018	1.12574524
			=		Human DNA sequence from clone RP4-622L5 on chromosome 1934.2-36.11. Contains the gene for importin alpha 7 (karyopherin), up to six novel genes and the 5 end of the EIFSS2 gene for eukaryotic translation initiation charges 3 beta. Contains ESTs, per 20.		0186 283	1 91067 <u>45</u> 0
GF200 GF203	111391 262540	T85191 H99316	Hs.15866 Hs.30127	Hs.15866 Hs.30127	51.58, GSS hypothetical protein long fatty acyl-CoA synthetase	HSPC226	9181.115	1.63323435
GF201 GF201 GF204	757268 277163 1031047	AA426087 N40939 AA609881	AA426087 Hs.14945 N40939 Hs.44162 AA609881 Hs.116863	Hs.14945 Hs.112110 Hs.193077	2 gene PTD007 protein ESTs, Moderately similar to TFII-I protein [H.sapiens]	KIAA0837 PTD007	9173.792 9173.792 9153.729	
GF202 GF204	627687 1467686	AA196287 AA885397	AA196287 Hs.124158 AA885397 Hs.125642	Hs.135 Hs.156997	gamma-glutamyttransterase 1 GGT1 ESTs Homo sapiens mRNA; cDNA DKF2p564H172 (from clone	GGT1	9136.108	1.29791112
GF204 GF202	868378 279616	AA634108 N48302	AA634108 Hs.102017 N48302 Hs.46852	Hs.192810 Hs.46852	DKFZp564H172) EST	9	9114.313	1.4754223
GF201 GF201 GF202 GF202 GF204	299342 452374 811010 504332 221786	N75572 Hs.1086 AA700876 Hs.572 AA485365 Hs.1270 AA131921 Hs.7103 H92192 Hs.2831	V75572 Hs.108687 AA700876 Hs.572 AA485365 Hs.12705 AA131921 Hs.71030 H92192 Hs.28310	Hs.15202 Hs.572 Hs.12705 Hs.214368 Hs.28310	chimerin (chimaerin) 2 orosomucoid 1 ESTs ESTs	CHNZ ORM1	9105.305 9095.35 9075.021 9062.258	1.7330752
GF200	760224	AA425139	AA425139 Hs.98493	Hs.98493	X-ray repair complementing defective repair in Chinese hamster cells 1	XRCC1	9060.034	1.2571784

DOBOTYDB DYDEDI

APPENDIX A

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			1.37305266				1.13619134				1.25907515	1.18233934				1.6535528	1.98924583	1.5024787	1.12580851	1.85892112		1.13232146	1.24119303	1.36990773	1.11276449		1.12583024
	9027.113	9026.4	9024.495		9014.272		9014.024	8994.723			8985.906	8983.892			8973.974	8972.07	8967.191	8966.847	8960.275	8947.572	8947.382	8938.489	8932.057	8913.83	8913.761		8910.183
							TFRC				CACNA1D							CGI-51			CTSB	KIAA0878	KIAA0082	CYC1	CTSS		MADH4
Homo sapiens cDNA FLJ10432 fis, clone NT2RP1000470, weakly similar p PUTATIVE ATP- DEPENDENT RNA HELICASE T26G10.1 IN	CHROMOSOME III	ESTs	ESTs	Human BTK region clone ftp-3	mRNA	transferrin receptor (p90,		ESTs	calcium channel, voltage-	dependent, L type, alpha 1D		ESTs	Homo sapiens mRNA; cDNA	DKFZp762L106 (from clone	DKFZp762L106); partial cds	ESTs	EST	CGI-51 protein	ESTs	ESTs	cathepsin B	KIAA0878 protein	KIAA0082 protein	cytochrome c-1	cathepsin S	MAD (mothers against decapentabledic, Drosophila)	homolog 4
	Hs.143187	Hs.42251	Hs.102533		Hs.278857		Hs.77356	Hs.184185			Hs.23838	Hs.28803			Hs,3903	Hs.99384	Hs.59192	Hs.4877	Hs.238645	Hs.54925	Hs.249982	Hs.188006	Hs.154045	Hs.697	Hs.181301		Hs.75862
	AA464741 Hs.6355	AA779841 Hs.122118	N36992 Hs.102533		AA679345 Hs.75927		AA029889 Hs.90335	AA705798 Hs.119919			H29256 Hs.23838	AA034501 Hs.28803			W32509 Hs.100127	AA455012 Hs 99384	W88693 Hs.59192	AA424675 Hs.98296	AA677968 Hs.117096	AA278858 Hs.54925	W47179 Hs.70576	AA620379 Hs.51652	AA504534 Hs 79142	AA865265 Hs.127322	AA236164 Hs.81356		AA456439 Hs.75862
	810613		273648		866874		469952	_			49630	471372			321488	811943	417715	767236	430751	703541	324205	950968	825293	1455394	687875		788421
	GF201	GF204	GF202		GF201	3	GF200	GF204			GF200	GF200			GE201	0000	GE202	GF203	GF203	GF203	GF201	GE202	GESON	DE203	GE200) j	GF200

					1.51177736		1.30969169			1.26067178	1.3858836				1.24218451	2.12880759		1.27111465	1.81522512	1.37777272			1.53599808		2.29705499		1	-1.0006517 1.04893499
	8908.935 8900.545		8894.734		8893.313	8888.829	8888.814			8887.743	8880.704		8870.446		8861.158	8858.97	8856.402	8849.572	8836.348	8824.812			8821.333	8809.855	8805.789	8803.162	8795.303	8792.17 8791.604
			ZNF137				LUM						ZNF33A		PSEN1											RUVBL2		
Homo sapiens mRNA; cDNA DKFZp586L1722 (from clone	DKFZp586L1722) ESTs	iger protein 137 (clone		Homo sapiens cDNA FLJ20371 fis, clone	HEP19701		umican	ESTs, Moderately similar to	HNF3/FH TRANSCRIPTION FACTOR GENESIS	[M.musculus]		zinc finger protein 33a (KOX		presenilin 1 (Alzheimer	ie 3)	Ts.		2	Is	ĪS	Homo sapiens mRNA; cDNA	OKFZp434B225 (from clone	DKFZp434B225)	ESTs	ıs	RuvB (E coli homolog)-like 2 RI Homo sapiens clone 23551	mRNA sequence	_s L
ŖĀ	Hs.8518 DKI		Hs.151689 pH	훈급	Hs.267566 HE	Hs.7890 ESTs	Hs.79914 lum	ES	HN	Hs.56213 [M.			Hs.70617 31)			Hs.172932 ESTs	Hs.238615 EST	Hs.126412 ESTs	Hs.119957 ESTs	Hs.5723 ESTs	로	ž	Hs.4746 DK	Hs.250465 ES	Hs.24250 ESTs	Hs.6455 Ru Hol		Hs.112906 EST Hs.6799 ESTs
	AA459310 Hs.8518 B42796 Hs 22223		AA043458 Hs.359		AA621018 Hs.112837	N49774 Hs.7890	AA453712 Hs.79914			N57731 Hs.56213	H61684 Hs.37986		AA700419 Hs.70617		4A403083 Hs.3260	AA160080 Hs.42269	4A670270 Hs.116701	331512 Hs.24358	4A788772 Hs.119957	N55087 Hs.5723			H41496 Hs.7271	AA459674 Hs.99492	AA424517 Hs.24250	AA976843 Hs.6455	W47134 Hs.12445	AA620794 Hs.112906 W47254 Hs.6799
	810923 A		486623 A		1056198 A	282404 N	813823 A			341201 W	208940 H		460584 A		727390 A	593658 A	1032712 A	135240 R	1240394 A	245485 N			192593 H	795564 A	767075 A	1588331 A		1055497 A 324255 V
	GF201	2	GF201		GF202	GF201	GF200			GF202	GF200		GF201		GF200	GF202	GF204	GF200	GF203	GF200			GF203	GF201	GF203	GF204	GF201	GF202 GF200

	1.13632784		1.25546149 1.17011614 1.78680156			1.27084389	1.18464248			2.04522433	1.195368 1.89843692
8780.663	8780.316 8773.428	8769.579	8760.265 8754.18 8743.231	8742.506 8740.493 8722.769	8721.512 8720.187	8710.486	8701.94	8698.095	8697.609	8696.617	8690.455 8689.43 8683.889
MYBL1	MEA	3PR56	PTDSS1	MAG	GCHFR	CTSB	ARHE	FACL3	DDX8P1		FXYD1
v-myb avian myeloblastosis viral oncogene homolog-like 1 MYBL1 Homo sapiens cDNA	FLJ20812 fis, clone ADSE01316 male-enhanced antigen	G protein-coupled receptor 56 GPR56	phosphatidylserine synthase 1 PTDSS1 EST ESTs	myelin associated glycoprotein MAG ESTs ESTs GTP cyclohydrolase I	rotein	isin B	nily,	atty-acid-Coenzyme A ligase, ong-chain 3	DEAD/H (Asp-Glu-Ala-Asp/His) box binding protein 1 DDXBP1 SSTS, Weakly similar to	E04Fo.z. gene product [C.elegans] FXYD domain-containing ion	ransport agained (phospholemman) ESTs
Ns.2537	Hs.90964 / Hs.278362 r	Hs.6527	Hs.77329 Hs.101281 Hs.21550	Hs.1780 Hs.108264 Hs.15641	Hs.83081 f		Hs.6838	Hs.268012	Hs.75251	Hs.208987	Hs.160318 Hs.122713 Hs.27947
1526789 AA911236 Hs.2537	N74272 Hs.90964 AI025120 Hs.118244	AA775249 Hs.6527	H28984 Hs.77329 R61390 Hs.101281 R40449 Hs.21550	R42831 Hs.79247 AA404260 Hs.108264 W63789 Hs.15641	AA074446 Hs.83081 W86423 Hs 108645	AA598950 Hs.84898	W3/306 HS.3/045 AA443302 Hs.6838	H29215 Hs.25747	R43509 Hs.75251	AA400189 Hs.97786	H57136 Hs.95510 AA399237 Hs.122713 H14376 Hs.27947
1526789	298592 1631747	878571	49920 37883 28611	32444 758355 342211	525799	898035	322051 784593	49944	32565	742780	204686 726438 48525
GF204	GF203 GF204	GF204	GF200 GF203 GF203	GF201 GF201 GF201	GF201	GF200	GF200	GF201	GF201	GF202	GF201 GF202 GF203

1.65063593		1.68410934				2.39736552	1.39619216	0,00000	1.22638043	2.13916263	1.43400555			2.19264611	
8681.888 8675.877	8675.181 8670.197	8664.655	8663.761			8662.993	8647.416	8638.117	8636./48	8635.452	8627.219	8619.772		8617.336	8617.051
	RAGB	MUT					EPS15				MY06				C9ORF3
ESTs ESTs Homo sapiens BAC clone	NH0121A08 from 7p14-p13 GTP-binding protein ragB methylmalonyl Coenzyme A	mutase Homo sapiens mRNA; cDNA DKFZp434K0614 (from clone	DKFZp434K0614); partial cds Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3'	part of a gene for a novel KIAA0279 LIKE EGF-like domain containing protein	(similar to mouse Celsr1, rat MEGF2), a novel gene for a protein similar to C. elegans	B0035.16 a	epidermal growth factor receptor pathway substrate 15 EPS15	ESTs	ESTs	ESTS	myosin VI	ESTs, Moderately similar to	Homo sapiens mRNA for	KIAA1321 protein, partial cds chromosome 9 open reading	rame 3
Hs.116661 E Hs.98138 E	Hs.13467 N Hs.50282 C	Hs.155212 n H	Hs.108903		. .	Hs.122552 E	Hs.79095	N			Hs.22564	cc		Hs.24336	Hs.18075
AA669081 Hs.116661 AA412446 Hs.98138	Hs.13467 Hs.50282	Hs.7853	N20237 Hs.108903			AA463508 Hs.103293	4A490223 Hs.79095	AA884749 Hs.125677	Hs.44392	Hs.94535	N49895 HS.46980 AA028987 Hs.118483	He 97104	13.0.61	Hs.103018	AA485743 Hs.18075
AA669081 AA412446	H16803 N73499	AA232575 Hs.7853	N20237			AA463508	AA490223	AA884749	N32847	W15296	N49895 AA028987	Aleeson	060000	W37999	AA485748
854461 730100	50772 295857	666349	264609			797001	823943	1467300	259275	322615	243656 470216	005,460	202400	322219	811149
GF204 GF202	GF204 GF201	GF203	GF201			GF202	GF200	GF204	GF202	GF202	GF200	6	פוס	GF202	GF201

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	1.24723743	-1.2117187	1.80294232	1.21313625		1.17273779	1.32067531	1.27522039 2.05977047	2.26218308
8615.822	8586.641 8575.13	8565.763	8541.103	8540.037 8538.348	8537.538 8488.086	8453.043	8452.701	8451.226 8449.921	8449.152 8448.155
M17S2		8,500		MMP7				CHC1L	COX7C LOC51057
membrane component, chromosome 17, surface marker 2 (ovarian carcinoma antigen CA125) Homo sapiens CDNA	ADSE01247 ESTs ESTs, Highly similar to			.e. 7	ES1S, riginy annual to HSPC003 [H.sapiens] ESTs ESTs, Weakly similar to !!!! ALU SUBFAMILY J	[H.sapiens] ESTs, Weakly similar to neuronal voltage-gated calcium channel gamma-2	subunit [H.sapiens] chromosome condensation 1-	like ESTs cytochrome c oxidase subunit	VIIc hypothetical protein
Hs.277721	Hs.213640 Hs.103316	Hs.278222	ns.zuszso Hs.12457	Hs.2256 Hs.184598	Hs.25635 Hs.268728	Hs.30036	Hs.90207	Hs.27007 Hs.94122	Hs.3462 Hs.13475
AA676470 Hs.94471	AA418826 Hs.60350 AA495904 Hs.103316		H3111/ HS.23/20 R44163 Hs.91414	AA031513 Hs.2256 AA464728 Hs.87430	AA875936 Hs.25635 R56769 Hs.52200	AA016300 Hs.30036	N64379 Hs.94159	AA495766 Hs.89433 N62780 Hs.94122	AA629719 Hs.3462 AA131885 Hs.13475
882511 AA	767985 AA 768432 AA		1/961/ H5		1492238 AA 41103 R5	361255 AA	290213 N6	768316 AA 289594 N6	884480 AA 504358 AA
GF201	GF202 GF203	GF200	GF202	GF200 GF201	GF204 GF201	GF203	GF202	GF200 GF202	GF202 GF201

	1.05695816	1.29274333	1.15708578			1 87891646			2.36574485			1.27886549				1.23389467		1.39509335	1 14349045	1.10323248		1.1941594	
•	8440.416	8433.608 8430.948	8427.389		8395.392	8393.605			8373.27			8371.293		8367.542		8366.904		8358.895	8345 422	8337.771	8335.86	8327.587	8316.698
		ATP1B3	E1E9B9													CRADD			POGERR			KIAA0874	
APPENDIX A	ESTs	ATPase, Na+/K+ transporting, beta 3 polypeptide EST	eukaryotic translation initiation factor 2B, subunit 2 (beta,	Homo sapiens mRNA; cDNA DKFZp434M196 (from clone	DKFZp434M196)	ESTs	Homo saniens mBNA: cDNA	DKFZp761N0823 (from clone	DKFZp761N0823)	ESTs, Highly similar to supported by GENSCAN	prediction and spliced EST	[H.sapiens]	FLJ20150 fis, clone	COL08263	containing adaptor with death	domain	Homo sapiens mRNA; cDNA DKFZp761G1211 (from clone	DKFZp761G1211)	platelet-derived growth factor	receptor, pera porypeptide	ESTS	KIAA0874 protein	ESTs
	Hs.38959	Hs.76941 Hs.117120	700027	1000	Hs.14898	Hs.47261	HS.5/35		Hs.61809			Hs.46744		Hs.108502		Hs.155566		Hs.3532	11- 704 44	HS./6144	Hs.8241	Hs.27973	Hs.13743
	Hs.38959	AA489275 Hs.76941 AA678375 Hs.117120		HS./4130	AA625752 Hs.14898	Hs.47261	HS.5/35		Hs.94307			Hs.46744		Hs.55588		Hs.90863		Hs.99628	107.70	HS./6144	Hs.24941	Hs.27973	Hs.13743
	N23717	AA489275 AA678375		H80304	AA625752	N52782	AA465529 HS.5/35		W23546			N57487		W37680		R37937		R70769		1129CH	R80603	AA425782	W04645
7 di ai.	255295	842894		18/200	745387	283405	814964		295514			277346		321908		24032		142551		40643	300466	768940	320343
Westproon et al.	GF202	GF200		GF200	GF204	GF201	GF203		GF200	;		GF203		GF201		GF200		GF200		GF200	GF203	GF203	GF201

1.32471817	1.1061032	2.32328872 1.26174768 1.75176666 1.92378901	1.1986266 1.37653836 1.37811269	1.30124165	1.12548104 1.53238972 1.4835194 1.18344435	1.2392197
8314.801 8314.33	8312.946 8305.62	8301.904 8298.218 8297.439 8283.595	8282.707 8280.787 8280.787	8278.759	8277.325 8270.577 8266.11 8263.334 8243.071 8242.961	8239.617
HMG4	ЕРНВ2	B2M KIAA0706	T Storage	2	901	RPL30
high-mobility group (nonhistone chromosomal) protein 4 EST ESTs, Weakly similar to reverse transcriptase	[M.musculus] EphB2 ESTs, Weakly similar to similar to Glutachoxin, Zinc	IC.elegans) Deta-z-microglobulin KIAA0706 gene product ESTs ESTs, Weakly similar to !!!! WARNIN' J WARNIN' J WARNIN' G WARNIN' J	[H.sapiens] EST ESTs ESTs tryroid receptor interacting	protein 13 Homo sapiens clone 24554 unknown mRNA Homo sapiens cDNA FLJ10630 fis, clone	NT2RP2005622 Humo sapiens cDNA FLJ20382 fis, clone HEP14524 EST ESTS GSTs grancalcin	ribosomal protein L30
Hs.19114 Hs.98852	Hs.105265 Hs.125124	Hs.21536 Hs.75415 Hs.139648 Hs.3994	Hs.35009 Hs.44780 Hs.107510	HS.30212 HS.104788	Hs.22595 Hs.14791 Hs.45048 Hs.269001 Hs.189172 Hs.79381	Hs.111222
AA670197 Hs.19114 AA435978 Hs.98852	AA491209 Hs.105265 W72792 Hs.127469	R4404 Hs.21536 AA670408 Hs.75415 AA165679 Hs.32602 N45129 Hs.3994	N63753 Hs.35009 N36083 Hs.44780 H15396 Hs.107510	AA625651 HS.30212 AA446446 HS.104788	AA479106 Hs. 22595 AA282273 Hs. 14791 N40177 Hs. 45048 H79558 Hs. 29198 R44739 Hs. 79381	AA775364 Hs.111222
878640 730589	824054 345103	34641 878798 593215 282935	292966 272918 49435	781036	753940 712950 276396 239615 743306 34140	878681
GF204 GF202	GF204 GF202	GF202 GF203 GF202 GF203	GF200 GF202 GF202	GF203	GF202 GF203 GF202 GF201 GF201 GF201	GF203

1.14728653 1.60610319 1.23694616	1.22203419	1.0100927	1,23652446	1.16670478	1.7 8 597279 1.2254772	1.09684583
8237.328 8229.37 8216.922	8206.035 8198.057 8195.144 8193.702	8188.929 8185.619 8182.263 8176.688 8168.409	8161.297 8159.517 8151.208	8146.486	8127.004 8122.643 8121.875 8120.284	8113.979
	TRAP240 UBQLN2 SEEK1	KIAA0329 DKFZP434J154	PSEN2 SLC6A1	СГТН	RPS23	P85SPR
Homo sapiens cDNA FLJ20001 fis, clone ADKA01273 ESTs Homo sapiens mRNA; cDNA DKFZp4341162 (from clone DKFZp4341162)	thyroid hormone receptor- associated protein, 240 kDa subunit ubiquiin 2 SEEK1 protein	ES18 KIAA0329 gene product DKFZP434J154 protein ESTs ESTs	presentiin 2 (Alzheimer disease 4) solute carrier family 6 (neurotransmitter transporter, GABA), member 1	ESTs Clathrin assembly lymphoid- myeloid leukemia gene ESTs, Weakly similar to X- linked retinopathy protein	[H.sapiens] ribosomal protein S23 ESTs ESTs PAK-interacting exchange	factor beta
Hs.172382 Hs.268956 Hs.5605	Hs.11861 Hs.4552 Hs.91600 Hs,48800	Hs.8861 Hs.11711 Hs.226372 Hs.57836 Hs.10727 Hs.261700	Hs.25363 Hs.2682 Hs.6019	Hs.107384 Hs.7885	Hs.118269 Hs.3463 Hs.47130 Hs.112942	Hs.172813
R98074 Hs.35815 H65839 Hs.38422 H82325 Hs.5605	ε 4	W/2293 Hs.8861 H75699 Hs.11711 AA975243 Hs.13778 W/22557 Hs.57836 R26404 Hs.10727 AA401612 Hs.38239	AA152294 RG.60 H46254 Hs.2682 AA630006 Hs.6019	H05939 Hs.107384 R59062 Hs.117517	W37880 Hs.118269 N73091 Hs.53842 N50853 Hs.47130 AA621062 Hs.112942	AA457036 Hs.75136
206781 R98 210565 H65 240033 H82		345032 W73 233078 H75 1588431 AA6 345332 W73 132248 R26		43679 H05 41929 R55	322186 W3 291974 N7: 280957 N5(815530 AA
GF200 GF200 GF200	GF201 GF204 GF202 GF201	GF202 GF204 GF201 GF201	GF200 GF201 GF203	GF203 GF200	GF203 GF201 GF201 GF202	GF200

	1.5481614	1.11664349	1.19759657	1.18730451	1.63233812	-1.0233737 1.14205924	1.63031611 1.64008096 1.44327983	1.36728353
8111.015	8109.569 8088.848	8080.958	8077.717	8067.765	8059.938	8058.217 8057.116 8052.789	8050.739 8031.793 8026.515	8017.067 8008.087 7998.59
NPR2		ALAS2	UBE4A	MADD	SLC25A17	HE4	KIAA0432	KIAA0117
natriuretic peptide receptor B/guanylate cyclase B (atrionatriuretic peptide receptor B) receptor B HOMS, cDNA Homo sapiens mRNA; cDNA DKFZD6548076 (from clone DKFZD6548076)	DKFZp564B076) ESTs aminolevulinate, delta-, synthase 2.	anemia) ubiquitination factor E4A	(homologous to yeast UFD2) MAP-kinase activating death	domain solute carrier family 25 (mitochondrial carrier; peroxisomal membrane	protein, 34kD), member 17 epididymis-specific, whey-acidic protein type, four-disulfide core; putative ovarian	carcinoma marker ESTs ESTs ESTs. Weakly similar to	butyrophilin [H.sapiens] ESTs KIAA0432 gene product Homo sapiens mRNA; cDNA	DKFZp434C136 (from clone DKFZp434C136) ESTs KIAA0117 protein
Hs.78518	Hs.252317 Hs.252317	Hs.79103	Hs.75275	Hs.82548	Hs.62245	Hs.2719 Hs.70704 Hs.100890	Hs.181223 Hs.55560 Hs.155174	Hs.6567 Hs.122115 Hs.174135
1632011 AA994689 Hs.78518	R82802 Hs.126272 AA460950 Hs.104538	AA410346 Hs.79103	AA447528 Hs.75275	AA282445 Hs.82548	AA446906 Hs.62245	AA451904 Hs.2719 R96941 Hs.70704 AA779892 Hs.100890	AA706311 Hs.119955 W37815 Hs.55560 N74285 Hs.6998	W74352 Hs.11582 AA779811 Hs.122115 AA448533 Hs.2358
	796110	753346	782587	712848	784253	786675 200402 1 1034699	3 1240160 2 321993 3 298612	345047 1 1034596 782618
GF204	GF203 GF201	GF200	GF200	GF200	GF202	GF200 GF200 GF204	GF203 GF202 GF203	GF200 GF204 GF200

1.25234211	1.20753372 1.2357175	1.16518093			1.61288522			1.89597845		1.35029526		
7990.361 7989.401 7988.855	7986.817 7981.757	7970.227 7966.511	7951.868 7951.468	7939.393	7936.859	7935.935	7933.063	7923.876	7920.306	7918.234	7914.189	7912.29 7907.604 7906.021
TPD52L2	GOSR2 TMOD	KIAA0996 KIAA0097		CUL4B			UTRN		LSAMP	CFLAR		PMSCL2 DKFZP586L2024
ESTs, Weakly similar to c29 [M.musculus] tumor protein D52-like 2 ESTs goldi SNAP receptor complex		KIAA0996 protein KIAA0097 gene product	Homo sapiens cDNA FLJ20511 fis, clone KAT09708 ESTs	cullin 4B ESTs, Weakly similar to myosin phosphatase target	subunit 1 [H.sapiens] Homo sapiens cDNA FLJ11100 fis, clone	PLACE1005550 utrophin (homologous to	DNA	DKFZp434K0172) limbic system-associated	membrane protein CASP8 and FADD-like	cDNA	DKFZp434D024) polymyositis/scleroderma	autoantigen 2 (100kD) ESTs DKFZP586L2024 protein
Hs.55412 Hs.154718 Hs.160550	Hs.100651 Hs.170453	Hs.60177 Hs.76989	Hs.134406 Hs.98260	Hs.155976	Hs.12185	Hs.38114	Hs.17401	Hs.121073	Hs.26479	Hs.195175	Hs.97823	Hs.75584 Hs.168672 Hs.58419
Hs.55412 Hs.19650 Hs.24407	R22156 Hs.103061 AA410680 Hs.78517	AA447525 Hs.60177 AA598942 Hs.76989	T82457 Hs.13206 AA629282 Hs.98260	AA780712 Hs.122696	AA676768 Hs.12185	AA454607 Hs.38114	AA676840 Hs.104252	N47542 Hs.118028	AA933871 Hs.26479	RG.36	AA453520 Hs.97823	AA487064 Hs.75584 N64426 Hs.48164 W81546 Hs.58419
W73634 R06309 R31575	R22156 AA410680	AA447526 AA598942	T82457 AA629283	AA780712	AA676768	AA454607	AA67684(N47542	AA93387	N94588	AA45352	AA48706 N64426 W81546
344595 126221 135654	130773 723986	782581 898032	22278	882694	897033	811590	460114	280888	1536967	309776	795424	841179 294281 347661
GF201 GF200 GF200	GF200 GF200	GF201 GF200	GF204 GF204	GF204	GF203	GF201	GF201	GF203	GF204	GF200	GF201	GF201 GF201 GF201

Atty Docket No. 2172	1.82364822	1.42009111	1.07430657	1.20403111	1.55301348	1.17284935	1.19285781		2 1 205/1276	2.29297864					2.05748332	1.51288985				1.3958074		-1.0578524	1.39364909			1.22887189	1.83318733		1.28035194	1.71347846	
Atty	7903.768 7901.706	7898.191	7894.841	7885.209	7880.652	7879.803	7875.128	7873.206	7050 495	7868.699				7868.045	7864.086	7860.754	7858.593			7857.249		7856.672	/854.315		/846.429	7845.026	7820.456	/818./13	7818.423	7813.634	7812.096
		DKFZP586H2123	PTD010		NPM3		STX5A		1/1000	Second					REV1		NCL			EGFR		I IL13RA1			SLC29A2	KIAA0268				CHN2	KIAA0960
APPENDIX A	EST ESTs	DKFZP586H2123 protein	PTD010 protein	ESTs nucleophosmin/nucleoplasmin.		ESTs	syntaxin 5A	ESTs	proprotein conventase	Subtilisiri/kexiri type 3 EST	Homo sapiens HMT-1 mRNA	for beta-1,4	mannosyltransferase,	complete cds	REV1 protein	ESTs	nucleolin	epidermal growth factor	receptor (avial) erguniopiasuo lenkemia viral (v-erb-b)	oncodene homolog)	(6)	interleukin 13 receptor, alpha 1 IL13RA1	ESTs solute carrier family 29	(nucleoside transporters),	member 2	KIAA0268 protein	ESTs	EST	ESTs	chimerin (chimaerin) 2	KIAA0960 protein
	Hs.230617 Hs.206710	Hs.55044	Hs.182470	Hs.128629	Hs 90691	Hs.48419	Hs.154546	Hs.35198		HS.94376 Hs.44469				Hs.44592	Hs.110347	Hs.169908	Hs.79110			Hs 77432	101	Hs.250911	Hs.179912		Hs.32951	Hs.241552	Hs.29692	Hs.116706	Hs.49210	Hs.15202	Hs.29900
	N62867 Hs.48652 N72009 Hs.69081	86	_	N55187 Hs.109335	AA447561 Hs 99118	AA435990 Hs.48419	4A452374 Hs.75923	W15305 Hs.35198		AA399377 HS.21630 N33323 Hs 44469				4A454579 Hs.105024	V51427 Hs.54032	194746 Hs.94483	V90109 Hs.118127			B35665 He 77.432		4A485453 Hs.52794	4A458934 Hs.23645		4A402891 Hs.32951	4A429602 Hs.78862	4A424813 Hs.29692	AA670355 Hs.116706	AA446001 Hs.49210	AA599311 Hs.77860	N92895 Hs.29900
ok et al.	289647 N62			245583 N55	782617 AA			322461 W1:		726479 AAS				809521 AA	_	_	302933 N9C			197017 B3		811067 AA	814432 AA		741958 AA	_	-	878409 AA	781004 AA	1091543 AA	_
Westbrook et al	GF202	GF202	GF200	GF202	CE200	GF202	GF200	GF201		GF203	2			GF201	GF202	GF202	GF201			0000	00715	GF203	GF203		GF201	GF200	GF203	GF204	GF202	GF203	GF201

ntegrin, alpha M (complement

1.36923216 2.55799015 2.46651665 1.67847756 1.20648133 1.07047443 1.38964683 1.26680586 .09583828 2.16415989 1.6585438 7619.915 7669.641 7610.611 610.408 7603.996 7639.243 624.872 7624.092 7620.156 662.986 662.714 7661.34 7639.332 628.677 7625.377 671.921 669.89 644.69 7.644.7 KIAA0637 PLAGL2 U3-55K ABCA1 ITGAM NASP NMT AK2 Human Chromosome 16 BAC component receptor 3, alpha; also known as CD11b (p170), nuclear autoantigenic sperm oleiomorphic adenoma genecalcium-activated potassium channel rSK2 [R.norvegicus] amily A (ABC1), member 1 alternatively spliced product using exon 13A [H.sapiens] ATP-binding cassette, submacrophage antigen alpha U3 snoRNP-associated 55clone CIT987SK-A-61E3 N-myristoyltransferase 1 ESTs, Weakly similar to <IAA0637 gene product</p> protein (histone-binding) ESTs, Highly similar to Homo sapiens cDNA FLJ20772 fis, clone adenylate kinase 2 oolypeptide) kDa protein COL06053 ESTs ESTS ESTS ESTS ESTS ESTS ike 2 ESTS 4s.111039 4s.114970 1s.243886 **Is.114970** 4s.154104 Hs.181634 4s.247150 Hs.153768 Hs.109259 Hs.211562 4s.167942 4s.171811 4s.172631 4s.13604 4s.17975 Hs.98280 Hs.98023 Hs.9925 4s.9567 AA134771 Hs.114970 AA448910 Hs.111039 AA461317 Hs.115577 AA418000 Hs.98280 AA704187 Hs.19649 AA179161 Hs.73562 AA054704 Hs.16314 Hs.83833 Hs.47417 Hs.42672 AA644128 Hs,68875 AA486182 Hs.17975 AA453518 Hs.98023 AA521292 Hs.19067 AA608716 Hs.9925 4A436187 Hs.1763 AA456413 Hs.9567 N32907 Hs.7954 AA465355 Hs.6297 H09730 N52078 99766H 767449 827168 460899 321605 842760 754406 488115 282561 263836 788386 796328 795407 309228 845415 814086 950891 85371 502463 15464 GF202 GF203 GF203 GF203 GF202 GF202 GF203 GF202 GF201 GF200 GF201 GF201 GF201 GF203 GF201 GF204 GF200 GF201

Atty Docket No. 21 /2/		-1.0999661	1.07248429	1.35308481	2.13594034 1.34989082			2.10967575 1.77492988	1.80318203 -1.0515509	1.97455669
Atty	7585.59 7583.181 7571.937 7570.011	7552.526	7536.346 7531.811	7530.268 7528.71	7523.271 7522.843	7521.21	7517.546	7516.146 7513.193	7506.929 7498.419	7490.776
	KIAA1014		RHEB2	DRPLA CD72		PTPN2		ATP2B1	EIF4EBP3	MOF
APPENDIX A	n DNA	N I ZRP2000369 ESTs Ras homolog enriched in brain	2 ESTs dentatorubral-pallidoluysian	atrophy (atrophin-1) CD72 antigen Homo Sapiens mRNA, partial cDNA sequence from cDNA	selection, DCR1-16.0 ESTs	protein tyrosine phosphatase, non-receptor type 2 Human DNA sequence from clone 717M23 on chromosome 20 Contains a novel gene, ESTs, STSs,	GSSs and CpG Islands ATPase, Ca++ transporting,		eukaryotic translation initiation factor 4E binding protein 3 ESTs member of MYST family histone acet/l transferases.	h
		Hs.173374 F Hs.125229 F	Hs.177507 2 Hs.47289 I	Hs.169488 (Hs.116481 (Hs.66185 Hs.141269	Hs.82829	Hs.29846	Hs.78546 Hs.24945	Hs.106711 Hs.106728	Hs.42343
	AA485425 Hs.48919 AA488062 Hs.7149 AA872279 Hs.6834 AA707617 Hs.120299	AA431438 Hs.15855 H95140 Hs.125229	AA482117 Hs.91185 AA011100 Hs.47289	H08642 Hs.3143 AA812996 Hs.116481	AA496916 Hs.66185 AA417900 Hs.4296	AA428195 Hs.82829	N40959 Hs.107266	AA262804 Hs.78546 AA450334 Hs.24945	AA196275 Hs.25711 W80964 Hs.106728	N63425 Hs.109406
ketal.	60.10	782460 AA 256513 HS	756401 AA 359684 AA	45291 HG	897485 AV 752754 AV	773567 AA	277208 N	685626 Av 785540 Av	627630 Av 347224 W	277956 N
Westbrook et al.	GF201 GF201 GF204 GF204	GF201 GF203	GF203 GF201	GF200 GF203	GF202 GF203	GF201	GF201	GF203 GF203	GF202 GF200	GF202

			1.23981774	1.15584229		901010000	2:30042130						1.0452452			1.27850449	1.43386579	2.02029103	1.4145573					
	7489.634	7483.712 7478.462	7478.301	7468.29		7466.861	7447.996			7447.14			7439.59		7435.364	7434.432	7432.667	7429.095	7419.561	7419.105	7412.795		7409.286	/402.0//
	LOC51251		H.	NR2F6											AKAP4	TIP-1		KIAA0607	EXTL3				0.7	0 I
APPENDIX A	hypothetical protein Homo sapiens mRNA; cDNA DKFZp434L0435 (from clone	DKFZp434L0435) ESTs	serine threonine protein kinase NDR nuclear receptor subfamily 2.		ESTs, Moderately similar to transcription repressor protein	PRDI-BF1 [H.sapiens]	ESI FSTs	Homo sapiens mRNA; cDNA	DKFZp434B2328 (from clone	DKFZp434B2328); partial cds FSTs Moderately similar to IIII	ALU SUBFAMILY SX	WARNING EIN HY !!!!	[H.sapiens] ESTs	A kinase (PRKA) anchor	protein 4 AF	Tax interaction protein 1 TI		_	exostoses (multiple)-like 3 E)	ESTs	ESTs	Homo sapiens mRNA; cDNA DKFZp434P1530 (from clone	DKFZp434P1530)	ubiquitin carrier protein EZ-C UBCH IO
	Hs.55189	Hs.145513 Hs.33263	Hs.8724	Hs.239752		Hs.116328	HS.20/250 Hs 115033			Hs.55565			Hs.184596 Hs 120170	2	Hs.97633	Hs.12956	Hs.98842	Hs.94653	Hs.9018	Hs.6729	Hs.12292		Hs.125511	Hs.93002
	AA427715 Hs.55189	AA777268 Hs.121905 N73301 Hs.33263	AA521346 Hs.8724	AA666180 Hs.67619		AA694500 Hs.120344	N95322 HS.55134	2000 1 13:11 2000		W72972 Hs.55565			N23134 Hs.43329	000001118:150110	AI025520 Hs.97633	AA434504 Hs.12956	AA435936 Hs.98842	N35489 Hs.94653	AA706935 Hs.9018	W32375 Hs.6729	R39899 Hs.12292		တ္သ	R80790 Hs.113725
	770997	448591 292068	826135	859422		1276486	308105	27004		344854			266849	2000	1643144	770884	730544	272169	451871	321330	26842			146882
	GF201	GF204 GF201	GF200	GF202		GF204	GF202	50		GF201			GF203	102 20	GF204	GF200	GF202	GF202	GF203	GF201	GF204		GF204	GF204

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1.74251999	1.22177034	1.00836558 1.07009941				1./56/6243	1.23497834		1.09832073	1.53797802	-1.2513976
7394.604	7383.094	7382.977 7375.238 7367.562	7366.289	7358.784	7353.93	7353.472	7342.518	7342.12	7334.498	7332.038	7328.066
		A2LP	ZNF74	L1CAM		KIAA0923	PRKCB1	DIO3			PTK7
Homo sapiens mRNA; cDNA DKFZp762D096 (from clone DKFZp762D096); partial cds Homo sapiens mRNA; cDNA PKFZp434N1526 (from clone	DKFZp434N1526) ESTs, Weakly similar to RAR- RESPONSIVE PROTEIN	TIG1 [H.sapiens] ataxin 2 related protein FSTs	Zinc finger protein 74 (Cos52) L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs) syndrome, spastic	paraplegia 1) ESTs, Highly similar to WWP2	n.sapiensj EST	ESTs KIAA0923 protein	orotein kinase C, beta 1 delodinase, iodothyronine,	ype III ESTs, Weakly similar to putative protein RFX-Bdelta4	H.sapiens] ESTs, Weakly similar to TRANSFORMATION- SENSITIVE PROTEIN IEF	SSP 3521 [H.sapiens]	PTK7 protein tyrosine kinase 7 PTK7
Hor DKI Hs.54320 DKI Hor DKI	Hs.22937 DKI ES' REI	Hs.109276 TIG1 [Hs.43509 ataxin Hs.218260 ESTs				Hs.204828 EST Hs.22587 KIA		Hs.49322 type ES put	Hs.113165 [H.s ES TR TR SE	Hs.20242 SS	Hs.90572 PT
Hs.54320	Hs.22937	Hs.94667 Hs.43509 Hs.90088	Hs.3057	Hs.42923	R66082 Hs.98978 AA625955 Hs.116109	R83017 Hs.33345	Hs.77202	Hs.49322	AA700625 Hs.113165	AA497041 Hs.20242	Hs.90572
N73011	R63172	W47077 Hs.94667 AA029963 Hs.43509	AA629838 Hs.3057		R66082 AA625955	R83017	AA479102 Hs.77202	N67048	AA700625	AA497041	AA453789 Hs.90572
291891	137971	325070 470179 795397	884790	269787	140174 745466	194401	753923	296032	433522	823582	813742
GF202	GF200	GF200 GF200	GF201	GF201	GF201 GF204	GF200	GF200	GF201	GF203	GF203	GF200

GF202	418197	W90364 Hs.38894	Hs.38894	ESTs KIAA0112 protein: homolog of		7327.234	1.31151542
GF200	562867	AA100612 Hs.71827	Hs.71827	yeast ribosome bigenesis regulatory protein RRS1 spastic paraplegia 7,	KIAA0112	7323.985	2.38577594
GF204 GF201	1256737 364555	AA876165 Hs.125327 AA022601 Hs.5386	Hs.78497 Hs.203213	parapregin (para and complicated autosomal recessive) ESTs Homo sapiens mRNA; cDNA	SPG7	7311.439 7299.476	
GF201 GF204	327461 1632216	W20438 Hs.55406 Al005330 Hs.19845	Hs.5306 Hs.25615	DKFZp586F1122 (trom clone DKFZp586F1122) YDD19 protein	YDD19	7288.178 7286.526	
GF201	744800	AA64448 Hs.19718	Hs.19718	protein tyrosine phosphatase, receptor type, U	PTPRU	7281.838	
GF203 GF201	148444 882497	H12320 Hs.79194 AA676604 Hs.76512	Hs.79194 Hs.173714	binding protein 1 MORF-related gene X ESTs, Weakly similar to rab-	CREB1 KIAA0026	7280.688 7280.332	1.28924771
GF203	42872	R61883 Hs.24970	Hs.24970	related GTP-binding protein [H.sapiens] Homo sapiens cDNA FLJ10808 fis, clone NT2PP4000879, weakly		7279.738	1.96154347
GF201	771254	AA443582 Hs.89991	Hs.59838 He 64638	similar to UBIQUITIN- ACTIVATING ENZYME E1		7276.284	1.8835105
GF201	770898		Hs.98806	hypothetical protein Homo sapiens mRNA; cDNA	FLJ20485	7260.06	
GF202	281614	N48000 Hs.102627	Hs.140945	DKFZp586L141)		7257.248	2.30167682
GF202	322676	W15495 Hs.109765	Hs.129781	frame 5	C210RF5	7256.871	1.5092056
GF201	884355	AA629542 Hs.82318	Hs.82318	WAS protein family, member 3 WASF3	WASF3	7249.975	

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7234.515	7229.008	7228.32	7220.331	7219.42		7215.442	7205.73		7204.979	7204.449			7198 975	7198.374			7194.893	7189.166	7106 469	700.405	7183.176	7180.946	7173.813		7158.791
СЯНВР		LTBP4		INBPI		стѕр			ALOX5AP	AEBP1				EPHB6			PTEN	HELLS		SHAAI		PFKM			
corticotropin releasing hormone-binding protein Hormo sapiens cDNA Hormo sapiens cDNA Lazboob fis, clone KAT06223, highly similar to AF132944 Horno sapiens CGI-	39 protein mRNA atent transforming growth	4	ESTs	neterogeneous nuclear	mal	/I protease)	ESTs	arachidonate 5-lipoxygenase-		•	ESTs, Weakly similar to !!!!	ALU SUBFAMILY SX WABNING ENTBY IIII	Walling Element		phosphatase and tensin	homolog (mutated in multiple	advanced cancers 1) F	.ల	sitol	attachment		phofructokinase, muscle	EST	Homo sapiens mRNA; cDNA DKFZp564N072 (from clone	DKFZp564N072)
Hs.115617	Hs.128791	Hs.85087	Hs.188837	He 9730		Hs.79572	Hs.47939	-	Hs.100194	Hs.118397			Uo 50050	Hs.3796			Hs.10712	Hs.278409	:	HS.4/42	Hs.164679	Hs.75160	Hs.143548		Hs.26118
AA700862 Hs.115617	AA464166 Hs.77294	AA732832 Hs.118124	AA679219 Hs.119495	0676 3H 801760 A		AA485373 Hs.9946	Hs.47939		Hs.100194	AA490684 Hs.9633			020000 IIo E0050	AA609284 Hs.3796			Hs.10712			AA455301 HS.4742	AA780997 Hs.122717	AA099169 Hs.75160	Hs.94682		Hs.26118
AA700862	AA464166	AA732832	W46617 AA679218	A A 0.074 O.	200	AA485373	N55266		H02307	AA490684			14/0.4004	AA609284			W37864	W25169		AA45530	AA78099	AA09916	W49559		H10397
452345	810343	399390	323263 866716	1940505	00000	811028	245768		151201	823851			100000	1031552			322160	308633		810059	1240538	489626	324811		47080
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-			7127,429 1.09578856	7119.721	7103.977		7096.389 1.50458187	7089 571			7061.801		7056.034 1.33665449		7047.553 1.39825077			/03/.11 1.20/00622			/ 036.583	1000 000		7017.171 1.43125668		7014.22 -1.2320143	7012.69			7009.72 1.30189651	
CLDN4		KIAA0136	RLF	GKP2	WHN	Sign	7007-00	LOCS1201										BLXCIC			PYGL	0000	מילט			NFATC4					
claudin 4 ESTs	ESTs	KIAA0136 protein rearranged L-myc fusion	eouenbes	glycerol kinase pseudogene 2	Werner syndrome	YDD IS protein	ESTs	rec ribosomal protein S97a	ESTs, Weakly similar to ZINC	FINGER PROTEIN 83	[H.sapiens]	ESTs	ESTs	Homo sapiens mRNA for for	histone H2B, clone pjG4-5-14	DEAD/III (Asp-diu-Aia-	Asp/HIS) box polypeptide 18	(Myc-regulated)	phosphorylase, glycogen; liver	(Hers disease, glycogen	storage disease type VI)	quinoid dihydropteridine	reductase	EST	nuclear factor of activated T-	cells, cytoplasmic 4	ESTs	Homo sapiens mRNA; cDNA	DKFZp434G1919 (from clone	DKFZp434G1919); partial cds	
Hs.5372 Hs.246858	Hs.45203	Hs.70359	Hs.13321	Hs.98008	Hs.150477	HS.25615	Hs.55938	Hs.5943	19:05:		Hs.121417	Hs.17301	Hs.99070		Hs.20418		:	Hs.100555			Hs.771	:	HS./5438	Hs.244531		Hs.77810	Hs.30085			Hs.7256	
AA430665 Hs.5372 N62272 Hs.48502	N50928 Hs.109279	N73634 Hs.70359	R26070 Hs.13321		N64051 Hs.48920		W46341 Hs.55938	AA461174 Hs.5943	NA623032 118:0237		AA776810 Hs.121417	N95558 Hs.17301			N71982 Hs.20418			R08935 Hs.100555			AA147640 Hs.83568		H38198 HS./5438	AA461090 Hs.124826		AA394127 Hs.77810	AA705470 Hs.30085			AA702737 Hs.23235	
770388 290229	281100	289143	132122	743077	285544	743749	323806	796806	170110		1291658	308495	781300		290841			127925			505573		23//6	796155		725649	462237			383961	
GF201 GF202	GF202	GF200	GF200	GF201	GF201	GF204	GF202	GF201	GIZO		GF204	GF201	GF202		GF203			GF200			GF201		GF200	GF202		GF203	GF204			GF203	

				1.73891042		1.67270406	-1.3366664			1.88134579	1.52163548			1.06226627		2.26712669		1.26120342	1.376494			1.01454093	2.23068978		1.17225187		1.35578603		1.3592871	2.13383745				1.76806055
	7003.361	6999.573	6993.555	6985.837		6983.92	6958.401			6930.908	6926.665			6924.465	6923.791	6920.292	6917.482	6908.185	6907.772			6902.59	6903.203		6898.241	6893.739	6890.954		6888.413	6887.13	6886.321	6884.471		6882.951
	MVK	CSNK1E				HOMER-2B								DXF68S1E		YDD19	FFD1	DKFZP586I1023	CLK2			CDC2L5			BRF2	KIAA0627					LBP-9	IL10RA		
mevalonate kinase (mevalonic	aciduria)	casein kinase 1, epsilon	ESTs	ESTs	Homer, neuronal immediate	early gene, 2	EST	Homo sapiens mRNA; cDNA	DKFZp434N1928 (from clone	DKFZp434N1928)	ESTs	DNA segment, numerous	copies, expressed probes	(GS1 gene)	ESTs	YDD19 protein	EH domain containing 1	DKFZP586I1023 protein	CDC-like kinase 2	cell division cycle 2-like 5	(UIUIIII IESIEI ASC-I CIAICA CCII	division controller)	ESTs	butyrate response factor 2	(EGF-response factor 2)	KIAA0627 protein	EST	ESTs, Highly similar to CGI-	149 protein [H.sapiens]	ESTs	LBP protein	interleukin 10 receptor, alpha	ESTs, Weakly similar to ORF	YNL227c [S.cerevisiae]
	Hs.130607	Hs.79658	Hs.183653	Hs.268273		Hs.93564	Hs.47567			Hs.8817	Hs.132721			Hs.78991	Hs.58646	Hs.25615	Hs.155119	Hs.111515	Hs.73986			Hs.59498	Hs.99154		Hs.78909	Hs.108614	Hs.112956		Hs.189658	Hs.11090	Hs.114747	Hs,327		Hs.131887
	H08205 Hs.75138	Al022854 Hs.26201	AA134753 Hs.29347	W37422 Hs.109850		AA426025 Hs.93564	N52876 Hs.47567			H24940 Hs.8817	R16241 Hs.100862			AA278240 Hs.78991	W81432 Hs.58646		0	R28397 Hs,23851	AA283062 Hs.73986			AA489042 Hs.59498	AA448170 Hs.99154		AA480880 Hs.78909	AA447599 Hs.94192	AA621246 Hs.112956		AA481443 Hs.5481	N40188 Hs.102550	AA865554 Hs.114747	AA437226 Hs.327		AA159825 Hs.131887
	45600	1650615	502364	322024		757244	283619			160609	53391			703479	347586	23136	323917	133130	713080			824937	782769		814576	782700	744564		756553	276412	1470131	757440		593457
	GF201	GF204	GF201	GF202		GF202	GF202			GF203	GF203			GF200	GF201	GF202	GF201	GF200	GF200			GF203	GF202		GF200	GF201	GF202		GF203	GF202	GF204	GF201		GF203

	2.11587534		2.28030198		2.21382882		1.40311621									1.46444214	1.67233668	-2.5086967	2.41967308	1.66442702		1.09872172		1.74022251		1.82339397	1.15747988	1.46349124		1.30269306	1.48530461	1.6626691
	6880.651	6873.339	6869.591	6866.271	6857.482		6856.843		6845.054							6843.869	6841.618	6831.878	6830.477	6826.575	6825.45	6823.87	6823.169	6817.869	6810.902	6810.784	6809.85	6804.894	6804.64	6803.577	6790.298	6777.484
					DKFZP564M182		IGFBP6		SEC24A										RPL39			PCM1							ICA1	PIG3		
ECTs Highly similar to	HSPC039 protein [H.sapiens]	EST	ESTs	EST	DKFZP564M182 protein	insulin-like growth factor	binding protein 6	SEC24 (S. cerevisiae) related	gene family, member A	Homo sapiens cDNA	FLJ11323 fis, clone	PLACE1010362, weakly	similar to 1-	PHOSPHATIDYLINOSITOL	PHOSPHODIESTERASE	PRECURSOR (EC 3.1.4.10)	ESTs	ESTs	ribosomal protein L39	EST	ESTs	pericentriolar material 1	ESTs	ESTs	EST	EST	ESTs	ESTs	islet cell autoantigen 1 (69kD) quinone oxidoreductase	homolog	ESTs	EST
	Hs.226799	Hs.116250	Hs.42574	Hs.105723	Hs.20760		Hs.274313		Hs.211612							Hs.25625	Hs.94109	Hs.187658	Hs.177461	Hs.26651	Hs.105728	Hs.75737	Hs.97714	Hs.61957	Hs.156945	Hs.43542	Hs.44247	Hs.22557	Hs.167927	Hs.50649	Hs.99621	Hs.48703
	AA399264 Hs.78067	AA628431 Hs.116250	H98777 Hs.42574	AA504131 Hs.105723	AA452802 Hs.91244		AA478724 Hs.1477		R78521 Hs.100985							R49708 Hs.25625	ιO	AA398364 Hs.97615	N76229 Hs.40128		_	AA164439 Hs.75737	AA431430 Hs.97714	AA214559 Hs.61957	AA884386 Hs.125574	N24597 Hs.43542	AA424589 Hs.44247	AA490935 Hs.22557	AA491302 Hs.90	AA668595 Hs.50649	AA464707 Hs.99621	N63062 Hs.48703
	726488	1032798	261664	825232	788526		753620		144925							38542	412989	726693	244911	38027	825622	594743	782433	683151	1461724	267273	767191	824001	824659	859359	810235	284724
	GF203	GF204	GF202	GF204	GF202		GF200		GF201							GF203	GF203	GF203	GESON	GF203	GF204	GF200	GF201	GF203	GF204	GF202	GF203	GF203	GF201	GF200	GF202	GF202

2.12996404	1.19141227	1.49467328	1.1744001 1.06387659 2.04479861		1.61871529	-1.0669181 1.23901732 1.57739365 1.81265024	2.28759613
6766.228 6759.375	6759.101 6756.517 6751.74	6749.974 6728.839	6724.898 6717.237 6715.162 6714.725	6712.443	6702.026	6695.577 6688.765 6682.196 6663.16	6656.358 6647.156
	BRE DKFZP7271051 KRT6B	KIAA1035	FOLR1 RPL21	TFAP2A	KIAA0118	SDHB	EXTL2
Horno sapiens mRNA; cDNA DKFZp781C169 (from clone DKFZp761C169); partial cds ESTs brain and reproductive organ-expressed (TNFRSF1A expressed (TNFRSF1A)	≣	lar to	3	transcription factor AF-2 alpha (activating enhancer-binding protein 2 alpha)	EST, Highly similar to KIAA0972 protein [H.sapiens] KIAA0118 protein ESTs, Highly similar to CGI-85	protein [H.sapiens] succinate dehydrogenase complex, subunit B, iron sulfur (Ip) ESTs ESTs	EST exostoses (multiple)-like 2
Hs.71252 Hs.30082	Hs.80426 Hs.239370 Hs.111758	Hs.4190 Hs.21542	Hs.118048 Hs.73769 Hs.125998 Hs.184108	Hs.18387	Hs.98151 Hs.184627	Hs.20824 Hs.64 Hs.98072 Hs.24790	Hs.112611 Hs.61152
AA521472 Hs.73435 AA004760 Hs.30082	AA47082 Hs.80426 AA479910 Hs.25598 AA936779 Hs.127117	AA026686 Hs.101820 N50785 Hs.13269	N48070 HS.118048 R24635 Hs.73769 AA889801 Hs.125998 AA464034 Hs.75467	N63770 Hs.89743	AA412491 Hs.98151 W37481 Hs.29860	AA521414 Hs.20824 AA463565 Hs.64 AA410301 Hs.98072 AA59839 Hs.24790	AA608894 Hs.112611 W31725 Hs.54579
826226 / 428309 /	739993 / 772912 / 1486118 /	366579 / 283871	281730 F 131839 F 1460832 / 810617 /	293032	730504 /	797016 754455	1048650 320797
GF203 GF201	GF200 GF201 GF204	GF201 GF203	GF202 GF200 GF204 GF200	GF201	GF202 GF201	GF203 GF200 GF203 GF203	GF202 GF201

	1.67381365		1.59594153		1.64488956	1.24110273		00000	1.13583003				1.12800143	1.63722269			1.2208681	1.68742608					1.83376828	1.56079075		-1.05/0962		0 11060016	2.11002010	1 2126701	2
	6644.222 6635.43		6630.051		6629.354	6624.904	6624.476	6620.337	9920.299				6616.333	6613.295			6611.986	6611.548		6607.328		6604.138	6603.406	6599.998		6591.729		100 0010	6576.082	6579 609	2000
	KCND1		KCNAB3				DKFZP586M1824											KIAA0580		MAP3K11	8		RPL35A			PPP1H7				DTNIS	
potassium voltage-gated channel, Shal-related	subfamily, member 1 ESTs	potassium voltage-gated channel, shaker-related	subfamily, beta member 3	ESTs, Moderately similar to unnamed HERV-H protein	[H.sapiens]	ESTs	DKFZP586M1824 protein	ESTs	ESTs	ESTs, Weakly similar to	similar to M. musculus MER5	and other AHPC/TSA proteins	[C.elegans]	ESTs	Human clone KDB1.2	(CAC)n/(GTG)n repeat-	containing mRNA	KIAA0580 protein	mitogen-activated protein	kinase kinase kinase 11	ESTs, Highly similar to CGI-63	protein [H.sapiens]	ribosomal protein L35a	ESTs	protein phosphatase 1,	regulatory subunit 7	ESIs, Highly similar to	secreted apoptosis related	protein 1 [H.sapiens] FSTs	C activities	reliculori s
	Hs.55276 Hs.259737		Hs.24379		Hs.220505	Hs.99338	Hs.25882	Hs.42454	Hs.61555				Hs.40919	Hs.104838			Hs.75456	Hs.22572		Hs.89449		Hs.19513	Hs.179666	Hs.107537		Hs.36587		:	Hs.31386 Hs 17803	20070	HS.252831
	W02729 Hs.109744 AA485088 Hs.7489		AA416665 Hs.24379		N94488 Hs.55054	AA453623 Hs.99338		N26758 Hs.42454	AA029428 Hs.61555				AA489015 Hs.23445	AA470079 Hs.104838			R21506 Hs.75456	AA193671 Hs.22572		R80779 Hs.89449		R05506 Hs.119626	AA873351 Hs.9020	W46783 Hs.12263		AA459572 Hs.36587		;	AA449300 Hs.31386	110013 113.17.02	AA056148 HS.1944
	327112 815737		731014		309895	795456	436364	269570	366795				824916	730406			130156	666110		146868		125193	1471829	324596		814508			785866	2000	380851
	GF204 GF203		GF202		GF202	GF202	GF204	GF201	GF202				GF203	GF202			GF200	GF202		GF201		GF204	GF203	GF203		GF200			GF202	10210	GF200

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1 18710081	10001.0	1.20328486	1.34401497	1.0764/613	1.27/04/8/			1.78302784		1.21224558	1.06747499				1.0488431	1.13912272	1.19396787	1.37626033		1.30197562	1.48933478	1.25975205	1.78570192
5573 263	000.0.700	6570.537	6565.288	6564.113	6556.358	020000	6537.435	6537.427		6535.482	6535.313		6535.071	6523.897	6518.498	6514.194	6505.245	6504.719	6502.071	6499.655	6496.87	6494.333	6491.722
S GPW	OMING	SPON1	PROCR		RBM10		NR112						FARSL		RPS4X	COPE		PA26			KIAA0829	ERF	
uridine monophosphate synthetase (orotate phosphoribosy) transferase and contidine-5-	decarboxylase) spondin 1, (f-spondin)	extracellular matrix protein protein C receptor, endothelial	(EPCR)	ESTs	RNA binding motif protein 10	ESTS nuclear receptor subfamily 1,	group I, member 2	EST	ESTs, Weakly similar to	[H earline]	FST	phenylalanine-tRNA	synthetase-like	EST	ribosomal protein S4, X-linked RPS4X coatomer protein complex,	subunit epsilon	EST n53 requisited PA26 nuclear	profein	ESTs	ESTs	TBP-interacting protein	Ets2 repressor factor	ESTs
! !	Hs.205/	Hs.5378	Hs.82353	Hs.31005	Hs.154583	Hs.165096	Hs.118138	Hs.99032		C3C3CC 011	Hs 93692		Hs.23111	Hs.116214	Hs.75344	Hs.10326	Hs.48388	He 14125	Hs.42530	Hs.180461	Hs.184786	Hs.110906	Hs.271682
	AA426227 Hs.2057	AA427924 Hs.5378				N72204 Hs.43517	AA699679 Hs.118138	AA443930 Hs.99032		10000 Ho 100044	AA497030 HS.105241		W96450 Hs.23111	AA628210 Hs.116214	AA888182 Hs.75344	AA776942 Hs.10326	N59450 Hs.48388	AAAA7661 He 14125	V67678 Hs.42530		119300 Hs.28410	4A419231 Hs.110906	182330 Hs.40364
	760344 /	773495 /	-	~	_	291231 N	446892	-			89736		358643	1055666	1492147	858979		013584				755593	240050
	GF200	GF203	GF200	GF203	GF200	GF201	GF204	GF202		000	GFZ0Z	202	GF201	GF204	GF203	GF203	GF202	0000	GF201	GF200	GF202	GF203	GF200

1.39038548	2.5830097 1.79702027	1.29753586 -1,1880928	2.0007994		1.12444683	1.72099727	1.16233247 2.34356026 1.48472977 1.22943377
6491.333 6487.987	6484.91 6481.873 6466.422 6457.93	643.536 6438.536 6438.536	6398.088	6394.676	6385.453	6380.174	6373.03 6369.845 6366.333 6364.891 6357.852
	KIAA0016 TSG101	KIAA0068			PRSC1	PTPRE	SDC4
Homo sapiens mRNA; cDNA DKFZp586N012 (from clone DKFZp586N012) ESTs translocase of outer mischondrial membrana 20	_	KIAA0068 protein ESTs	ESTS EST EST EST EST EST ALU SUBFAMILY SO WARNING ENTRY !!!!	[H.sapiens] Human BRCA2 region, mRNA sequence CG006	(legumain) Homo sapiens mRNA; cDNA DKFZp564G163 (from clone	DKFZp564G163) protein tyrosine phosphatase, receptor type, epsilon polypeptide syndecan 4 (amphialycan,	ryudocan) ESTs ESTs ESTs
Hs.12702 Hs.44257	Hs.75187 Hs.48507 Hs.99210 Hs.118910	Hs.77257 Hs.129010 Hs.14545	Hs.102942 Hs.228548	Hs.26612 Hs.110630	Hs.18069	Hs.91393 Hs.31137	Hs.252189 Hs.121587 Hs.48754 Hs.48333 Hs.141461
AA173611 Hs.12702 AA476253 Hs.44257	AA644550 Hs.75187 N62301 Hs.48507 AA449121 Hs.99210 AA670215 Hs.118910	AA446316 HS.1097 AA598583 HS.77257 AA490109 HS.129010	AA453537 NS.107063 N95476 HS.102942 R22306 HS.80545	R58982 Hs.26612 W80632 Hs.110630	8	H75578 Hs.91393 AA464542 Hs.31137	AA148736 Hs.72082 T91080 Hs.5255 N63286 Hs.48754 AA704508 Hs.48333 N48872 Hs.46543
595637 772952	845441 290370 785851 878744	897840 839641	310054 130843	41243 415529	760298	232899	504763 112565 290162 451092 279536
GF202 GF202	GF201 GF202 GF202 GF201	GF200 GF202	GF202 GF200	GF204 GF201	GF200	GF200	GF200 GF201 GF202 GF203 GF203

	1.34171389		1.62158853	1.16235017 1.64969606	0000010	1.74377858	1,22435388 1.60026662 1,4641877 2,45504372	1.08829975	
6343.485	6340.228	6339.457	6339.319	6334.272	6316.838	6311.699	6305.106 6302.262 6299.527 6296.717	6281.915	6268.318 6266.58
C210RF33	VAMP4 KIAA0869	3	ATR				1 IL13RA1	COL1A1	
ES1 (zebrafish) protein, numan homolog of vesicle-associated membrane	protein 4 KIAA0869 protein Homo sapiens cDNA FLJ10307 fis, clone	NT2RM2000259 ataxia telangiectasia and Rad3	elated Homo sapiens mRNA; cDNA DKFZp762A227 (from clone	DKFZp762A227) ESTs	ESTS ESTS ESTS, Weakly similar to GEF-	2 protein [H.sapiens]	interleukin 13 receptor, alpha 1 IL13RA1 ESTs EST EST. MUSUBFAMILY SP ALU SUBFAMILY SP AMARNING ENTRY !!!	[H.sapiens] collagen, type I, alpha 1	ESTs, Highly similar to KIAA0776 protein [H.sapiens] ESTs
E9 Hs.182423 hu	Hs.21543 pr Hs.21543 Kl Hc	Hs.55024 N	Hs.77613 re H DI	8 2	HS.98701 E. HS.9879 E. HS.131925 E. E.	Hs.121849 2	Hs.250911 in Hs.10263 ES Hs.47299 ES Hs.48830 ES Hs.48830 ES	Hs.271914 [H Hs.172928 cc	E: Hs.98846 KI Hs.125549 E:
AA025421 Hs.78859	Hs.102664 Hs.21543	AA455138 Hs.55024	AA453176 Hs.54404	Hs.107286 Hs.42011	AAZSUGST HS:99701 T55407 HS:9879 AAG25673 HS:119337	: Hs.7081	AA411324 Hs.67878 157773 Hs.10263 151601 Hs.4729 N63609 Hs.48830	AA608729 Hs.53409 R48844 Hs.118485	AA625809 Hs.98846 AA884114 Hs.125549
AA025421	N51629 R43798	AA455138	AA453176	N76193 H95086	AA290631 T55407 AA625673	AA460542 Hs.7081	AA411324 T57773 N51601 N63609	AA608729 R48844	AA625809 AA884114
365883	280490 35300	809879	788109	284592 243317	73436 745367	796650	755037 79217 281545 289071	950924 153646	744923 1468921
GF201	GF203 GF203	GF201	GF202	GF200 GF200	GF203 GF201 GF204	GF202	GF200 GF202 GF202 GF202	GF202 GF204	GF204 GF204

1.70333333	2.07200549	1.24441267	-1.4079896	1.47481743	-1.0100198		-1.1083304	2.19474574		1.64208421	1.3515041	
6258.176 6246.573 6239.44	6235.016 6231.484	6226.239	6216.735	6215.124 6208.081	6203.817		6199.046	6198.447	6196.829	6186.776 6184.833	6181.752 6179.224 6177.707	
in SLC4A2 FOG2	PRKG1	LAMP1			FOXG1B		or BCRP1				SNRPA1 ZNF265	
solute carrier family 4, anion axchanger, member 2 (erythrocyte membrane protein band 3-like 1) Friend of GATA2 EST	dependent, type I ESTs vsosomal-associated	membrane protein 1 ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	[H.sapiens] Homo sapiens mRNA for	KIAA1341 protein, partial cds ESTs	iorkhead box G1B	Breakpoint cluster region protein, uterine leiomyoma, 1;	barrier to autointegration factor BCRP1 ESTs, Weakly similar to	R10D12.12 [C.elegans] ESTs, Moderately similar to	unknown [H.sapiens] Homo sapiens mRNA; cDNA DKFZp434C0814 (from clone	DKFZp434C0814) ESTs small nuclear	A' EST zinc-finger protein 265	
Hs.79410 b Hs.106309 F	Hs.2689 CHS.267992 E	Hs.150101	Hs.241569	Hs.44268 Hs.44705	_			Hs.110853	Hs.178949	Hs.194110 Hs.99427	Hs.80506 Hs.116026 Hs.194718	
Hs.112452 Hs.106309 Hs.59358	AA668959 Hs.2689 H91121 Hs.93270	Hs.75175	AA487192 Hs.51527	AA598567 Hs.44268 N35222 Hs.44705			AA035095 Hs.10488	AA126799 Hs.110853	AA680272 Hs.116654	AA757406 Hs.57315 AA456435 Hs.99427	AA122272 Hs.80506 AA620893 Hs.116026 AA452256 Hs.5117	
W45518 R49439 W92715	AA6689 H91121	H29077	AA4871	AA5985	R44020		AA0350	AA1267	AA6802	AA7574 AA4564		
323577 38347 418337	854401 241179	49710	841280	898195	33051		471742	490548	869164	395410 788405	490772 1055573 786592	
GF201 GF203 GF202	GF201 GF200	GF200	GF202	GF202	GF200		GF203	GF202	GF204	GF204 GF203	GF201 GF204 GF203	

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Westbrook et al	et al.			:	APPENDIX A		Atty	Atty Docket No. 21726
GF201	277066	N39584	Hs.17404	Hs.17404	ESTs colony stimulating factor 2 receptor, beta, low-affinity		6152.618	
GF200	704020	AA279147	AA279147 Hs.89425	Hs.265262	(granulocyte-macrophage) nucleolar autoantigen (55kD) similar to rat synaptonemal	CSF2RB	6146.782	1.3741591
3F200	347434	W81191	Hs.83574	Hs.207251	complex protein	SO65	6145.483	1.762202
GF203	825719	AA504834		Hs.165404	ESTs		6144.46	1.14691552
GF203	309469	N94357	V94357 Hs.25127	Hs.25127	ESTs pp1		6142.008	1.56225265
3	70000			8	solute carrier family 25 (mitochondrial carrier;			
GF200	842784	AA48630E	AA486305 Hs.78713	Hs.78713	phosphate carrier), member 3		6133.056	1.03173017
GF202	266597	AA149987	AA149987 Hs.24500	Hs.274407	protease, serine, 16 (thymus)	PRSS16	6132.945	1.60928186
			0000		Homo sapiens cDNA		6139 407	-1 0726048
3F203	739227	AA421100	4A421100 HS.9096	HS:9096	FLJZU4/3 IIS, CIONE NA LO/ USZ		6124.57	1 05111865
GF200	131307	R23058	423058 Hs.106082	HS.268685	ESIS		0104:043	1.03111003
GF203	383967	AA70274C	AA702740 Hs.114140	Hs.263414	ESTs		6123.597	1.06393009
GF203	825356	AA504492	AA504492 Hs.50144	Hs.278242	tubulin, alpha, ubiquitous	K-ALPHA-1	6115.31	1.2999272.1
GF204	28373	R37362	Hs.21351	Hs.21351	ESTs transmembrane 4 superfamily		6115.2	
000	793070	0007000	7000 UC 2007	Le 9997	member 1	TM4SF1	6112.034	1.19888315
GF204	844881	AA773744	AA773744 Hs.121679	Hs.121679	ESTs		6110.819	
3F200	43198	H12903	Hs.709	Hs.709	deoxycytidine kinase nuclear transcription factor Y,	DCK	6109.979	1.22582097
GF203	665393	AA195042	AA195042 Hs.85978	Hs.84928	beta	NFYB	6108.984	1.43675842
3F201	262334	H99394	Hs.40339	Hs.40339	ESTs		6108.59	
GF204	1472585	AA872311	AA872311 Hs.126205	Hs.9754	activating transcription factor 5 ATF5	S ATF5	6107.258	
3F201	261667	Н98780	Hs.40290	Hs.40290	ESTs Homo sapiens mRNA; cDNA DKFZp434J1027 (from clone		6105.782	
GF201	34326	R44953	Hs.22908	Hs.22908	DKFZp434J1027); partial cds kinesin-like 5 (mitotic kinesin-		6103.048	
GF202	50080	H17934	Hs.70230	Hs.270845	like protein 1)	KNSL5	6101.324	2.26633543

1.17371061	2.16464978		1.11541493	1.08662597 1.72460228	1.13530029	1.98431955	2.44245895 1.5745252 1.41298905	1.62558761	1.02636125 1.33374693
6082.132 6081.64 6079.446	6076.83 6076.736	6073.457 6072.404	6068.058	6064.089	6060.586	6055.671	6049.348 6047.164 6037.642 6037.527	6036.505	6036.4 6022.053 6017.378
YDD19		тнро	PCANAP7	MLL			CASP4		SILV
YDD19 protein ESTs ESTs	ESTS ESTS thrombopoletin (myeloproliferative leukemia virus onoogene ligand,	development factor) EST prostate cancer associated	protein 7 myeloid/lymphoid or mixed- lineage leukemia (trithorax	(Drosophila) homolog) ESTs Homo sapiens mRNA; cDNA DKF7A434C)R14 (from clone	DKFZp434C0814) Homo sapiens cDNA FLJ10479 fis. clone	NT2RP2000120 caspase 4, apoptosis-related	cysteine protease ESTs ESTs ESTs	ESTs, Weakly similar to cDNA EST EMBL: D75506 comes from this gene [C.elegans] FYN oncogene related to	SRC, FGR, YES silver (mouse homolog) like ESTs
Hs.25615 Hs.48793 Hs.26720	Hs.13329 Hs.115278	Hs.1166 Hs.116148	Hs.27495	Hs.199160 Hs.118531	Hs.194110	Hs.5268	Hs.74122 Hs.54632 Hs.23272 Hs.206833	Hs.66915	Hs.169370 Hs.95972 Hs.46542
AA084517 Hs.7602 AA443823 Hs.48793 AA045527 Hs.26720	AA018460 Hs. 13329 AA629532 Hs. 115278	AA479058 Hs.1166 AA626279 Hs.116148	AA418020 Hs.27495	AA701046 Hs.10293 AA052966 Hs.118531	AA460675 Hs.31748	AA424834 Hs.5268	AA287122 Hs.48391 N90541 Hs.54632 AA427625 Hs.23272 W42450 Hs.94624	AA504357 Hs.66915	N22980 RG.21 N67770 Hs.95972 AA210699 Hs.46542
546600 784064 487333	362424	754034 745065	767475	397432 509964	796239	768170	701819 306180 770801 323041	825467	267431 291448 682749
GF200 GF202 GF204	GF203 GF204	GF201 GF204	GF203	GF203 GF202	GF202	GF202	GF203 GF202 GF201 GF202	GF203	GF200 GF201 GF203

-1.0115024	1.6707517	-1.2240656	1.46998775	1.31149002	1.99055352		1.06374657		1.24538502		1.54307875			
6007.489 6007.149 6002.703	5999.108	5989.688 5987.864	5987.465 5983.2	5967.896 5963.229	5962.931	5958.473	5955.19	5953.536	5944,113 5944.039		5942.154	5935.927	5933.77 5933.431	5932.718 5931.634 5920.923
NBEA	KIAA0846	C210RF56					PTK2B	TIMM8B					LIPA	KRT4
neurobeachin ESTs EST	KIAA0846 protein chromosome 21 open reading	frame 56 ESTs	ESTs ESTs	ESTs ESTs	ESTs, Weakly similar to !!!! ALU CLASS F WARNING ENTRY !!!! [H.sapiens]	ESTs	protein tyrosine kinase 2 beta translocase of inner mitochondrial membrane 8	(yeast) homolog B Homo sapiens mRNA; cDNA DKFZp762L137 (from clone	DKFZp762L137); partial cds ESTs	ESTS, Moderatery Similar to NY-REN-25 antigen	[H.sapiens] Homo sapiens clone 24758	mRNA sequence lipase A, lysosomal acid, cholesterol esterase (Wolman	disease) ESTs	ESTs keratin 4 ESTs
Hs.3821 Hs.45119 Hs.43933	Hs.24024	Hs.116107 Hs.13248	Hs.12284 Hs.67709	Hs.237691 Hs.44193	Hs.205021	Hs.122643	Hs.20313	Hs.268561	Hs.180780 Hs.270863		Hs.15301	Hs.185807	Hs.85226 Hs.47269	Hs.4947 Hs.3235 Hs.59138
AA775279 Hs.4799 N41052 Hs.45119 N27366 Hs.43933	AA465095 Hs.59876		R38548 Hs.101049 AA411685 Hs.67709	AA704572 Hs.59783 N30562 Hs.44193			R85257 Hs.20313	W04502 Hs.107130	AA906997 Hs.110327 AA398902 Hs.51251		R61337 Hs.15301	H58250 Hs.107368	AA630104 Hs.85226 AA010221 Hs.47269	AA485084 Hs.110462 AA629189 Hs.3235 AA005115 Hs.59138
878630 277283 255897	815013	327495 41819	22867 753376	383767	230509	378399	180298	320146	1521977 726983		42681	204536	854701 430231	815750 1035889 429185
GF204 GF201 GF202	GF203	GF202 GF204	GF204 GF203	GF203 GF202	GF200	GF204	GF200	GF201	GF204 GF203		GF202	GF201	GF201 GF201	GF204 GF201 GF201

1.4798953 1.65398867 1.29679513	1.4270798 1.95031739	1.29091134	1.03830976	-1.3188491	1.13956952	1.55625326	1.9340375	1.37636006	1.12764653
5920.525 5918.865 5916.769 5915.993 5915.825	5908.176 5907.761	5906.683 5903.324 5895.055	5893.183 5887.902	5884.542	5882.765	5878.416	5871.44	5870.155	5866.013 5865.189
CTF1	IFITM2	GUCY1B3	ILF2 RNAC		CSRP3				
ESTS ESTS cardiotophin 1 ESTS interferon induced	transmembrane protein z (1- 8D) ESTs guandate exclase 1 soluble	granjrate cyclase ;, sociolo; beta 3 EST ESTs	factor 2, 45kD RNA cyclase homolog Homo sapiens mRNA for TBARID nordein (TRARID)	gene)	cysteine and glycine-rich protein 3 (cardiac LIM protein) CSRP3 Homo sapiens cDNA El 11309 fis chane	PLACE1010076	ESTs, Moderately similar to KIAA0454 protein [H.sapiens] Homo sapiens mRNA for	KIAA1321 protein, partial cds Homo sapiens mRNA; cDNA	DKFZp434L1021); partial cds ESTs
Hs.98564 Hs.185030 Hs.109520 Hs.25537 Hs.49703	Hs.174195 Hs.97781	Hs.77890 Hs.227985 Hs.45061	Hs.75117 Hs.113052	Hs.26320	Hs.83577	Hs.28005	Hs.105235	Hs.24336	Hs.5392 Hs.103012
AA430629 Hs.98564 R02166 Hs.13972 N71770 Hs.109520 AA884403 Hs.25537 W32096 Hs.49703	AA862371 Hs.117444 AA40092 Hs.97781	AA457178 Hs.77890 R40129 Hs.101177 N50515 Hs.45061	H95638 Hs.114312 AA453591 Hs.14077	N34876 Hs.32087	AA195959 Hs.83577	AA191512 Hs.28005	AA486407 Hs.105235	AA788805 Hs.34795	AA125869 Hs.13398 W35362 Hs.103012
770969 124719 290689 1461737 321434	1455976 743261	838359 30095 280692	242952 795213	276617	627939	626640	842871	1240431	502762 321637
GF201 GF200 GF203 GF203 GF201	GF203 GF202	GF200 GF203 GF201	GF203 GF201	GF203	GF200	GF202	GF202	GF203	GF201 GF202

		1.04402092	1.20972803	1.50988315	1.39684169		1.47682081	-1.060155			1.15423078		1.20381854				1.92590391		3000011	1.1506806
5863.504	5851.221 5850.012	5848.517	5843.61	5840.989	5829.459		5824.568	5824.508	5824.362	5821.816	5821.281	5815.753	5804.881		5803.377	5795.803	5783.865	5779.081	100	5//4.224
SLC11A2		IL18BP		NACA	CRYAB				DKFZP586I1023	IF141	ARPC1A				GAD2	LOC54103	RPL5			CHGA
solute carrier family 11 (proton- coupled divalent metal ion transporters), member 2 Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone	DKFZp586E1120) ESTs	interleukin 18 binding protein ESTs, Moderately similar to	histone H2B [H.sapiens] nascent-polypeptide-	polypeptide FSTs	crystallin, alpha B	ESTs, Weakly similar to alternatively spliced product	using exon 13A [H.sapiens]	ESTs	DKFZP586I1023 protein interferon-induced protein 41,	30kD actin related protein 2/3	complex, subunit 1A (41 kD)	ESTs	ESTs	glutamate decarboxylase 2 (pancreatic islets and brain,	65kD)	hypothetical protein	ribosomal protein L5	ESTs	chromogranin A (parathyroid	secretory protein 1)
Hs.57435	Hs.100292 Hs.17733	Hs.278593	Hs.188762	Hs.146763 Hs 77114	Hs.1940		Hs.109259	Hs.112742	Hs.111515	Hs.241510	Hs.90370	Hs.261931	Hs.102914		Hs.170808	Hs.12969	Hs.180946	Hs.46812		Hs.172216
Hs.50332	AA134696 Hs.100292 AA035730 Hs.17733	AA777410 Hs.122537	AA610040 Hs.112721	AA664241 Hs.75791	AA504943 Hs.1940		AA405533 Hs.109259	AA609651 Hs.112742	AA773187 Hs.6176	Hs.84296	AA490209 Hs.90370	AA625990 Hs.116114	Hs.102914		Hs.1668	Hs.12969	AA496838 Hs.118781	Hs.46812		Hs.106247
N73680	AA134696 AA035730	AA777410	AA610040	AA664241	AA504943		AA405533	AA609651	AA773187	R54613	AA490206	AA625990	N93176		R44005	T66902	AA496838	N48075		R36264
289229	502413	449043	1032048	855620	839736		772410	1031791	845774	154493	823930	745493	304846		33643	66373	897596	281733		137158
GF201	GF201	GF203	GF202	GF202	GF200		GF202	GF202	GF204	GF201	GF200	GF204	GF202		GF201	GF201	GF200	GF201		GF200

1.26297476		1 1 201 0000	2.2228286	1.70534859		1.3626884		-1.2620469	1.2475118		1.0613995	1.934/89/2		1.23904545	2.02899491		1.35423758
5771.28		5769.501	5764.168	5759.409		5750.543	5750.322	5749.954	5748.036	5745.31	5734.837	5727.379	5726.843	5717.206	5713.953	5713.705	5712.598
≣		BMPR2				_	MAN1B1		CX3CR1		r Q H2BFQ		se LNPEP	EFNB3		NPM1	FDPS
ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!	bone morphogenetic protein receptor, type II	serine/threonine kinase)	ESTS	EST	ubiquinol-cytochrome c	reductase (6.4kD) subunit mannosidase, alpha, class 1B,	nember 1	ESTs chemokine (C-X3-C) receptor	1 ESTs, Weakly similar to R26660_1, partial CDS	H.sapiens]	H2B histone family, member Q H2BFQ	ESTs	leucyl/cystinyl aminopeptidase LNPEP	ephrin-B3	ESTs nucleophosmin (nucleolar phosphoprotein B23,	numatrin) famesyl diphosphate synthase (famesyl pyrophosphate synthetase,	geranyltranstransferase)
E A V V V		٠.	HS.499/3 E			Hs.8372 n		Hs.28773 E	Hs.78913 1	Hs.19223		Hs.103277 E	Hs.166733 le	-	Hs.258828 E	Hs.173205	Hs.77393
AA486571 He 105696		Hs.53250	HS.49973 He 57812	Hs.48344		Hs.107450	Hs.4814	AA426065 Hs.28773	Hs.78913	AA670391 Hs.19223	AA456695 Hs.2178	AA001834 Hs.103277 AA521427 Hs.105527	Hs.30877	AA485795 Hs.26988	Hs.49182	AA669758 Hs.66709	Hs.77393
44486571		N20203	W61905	N59234		R46837	AA446899 Hs.4814	AA426065	N51278	AA670391	AA456695	AA001834 AA521427	H08816	AA485795	N66348	AA669758	T65907
0000	266040	264556	294512	289480		36607	784260	757234	283023	878764	813149	427978 826155	45284	811088	285370	884301	80410
CESO	202	GF201	GF200	GF202		GF200	GF201	GF202	GF200	GF204	GF200	GF202 GF204	GF201	GF200	GF202	GF201	GF200

Westbrook et al.	ok et al.			APPENDIX A		Atty	Atty Docket No. 21 /26/9
GF202	487330	AA045518 Hs.3830	Hs.3830	KIAA0893 protein transforming growth factor	KIAA0893	5712.072	1.38993483
GF202	811848	AA454619 Hs.25511	Hs.25511	beta 1 induced transcript 1	TGFB111	5710.659	1.42241143
GF204 GF204	586742 451256	AA130669 Hs.16420 AA780059 Hs.118379	Hs.16420 Hs.192003	Npw38-binding protein NpwBP LOC51729 ESTs	, LOC51729	5703.168 5702.729	
				branched chain aminotransferase 2,			
GF201	756490	AA436410 Hs.101408	Hs.101408	mitochondrial	BCAT2	5701.403	
GF201	810064	AA455292 Hs.89125	Hs.89125 Hs.84469	ESTS		5695 152	
GF201	324494		Hs.78846	heat shock 27kD protein 2	HSPB2	5684.058	
GF204	447417	AA702339 Hs.119542	Hs.119542	ESTs		5679.18	
GF200	203551	H56033 Hs.36089	Hs.167576	ESTs		5673.218	1.86038378
				glucocorticoid receptor DNA			
GF201	291363	N72276 Hs.29020	Hs.102548	binding factor 1	GRLF1	5667.367	
GF201	487436	AA043360 Hs.16291	Hs.16291	ESTs		5667.327	
GF204	489351	AA058341 Hs.34635	Hs.251967	ESTs		5665.185	
				Homo sapiens unknown			
GF204	25778	R37265 Hs.106266	Hs.7540	mRNA		5664.412	
				contactin 2 (transiently			
GF201	28510		Hs.2998	expressed)	CNTN2	5663.218	
GF201	46977	H10372 Hs.101237	Hs.227997	EST		5660.381	
GF202	784218	AA446867 Hs.48297	Hs.48297	DKFZP586C1620 protein	DKFZP586C1620	5660.03	1.49214683
				guanine nucleotide-binding			
200	1002	A A 4 O 4 4 0 0 0 0 0 0 0 0 0 0 0	192000	protein G(I)/G(O) gamma-z	GNG9	5850 788	
GFZU	14/500	AA131400 US.Z3173	18.23/0/	Minde	GINGE	2000	* 0 4044544
GF202	742904	AA405815 Hs.1212/6	Hs.1212/6	ESTS Homo sabiens mRNA: cDNA		9657.19	1.64211311
				DKFZp586H051 (from clone			
GF202	123735	R01179 Hs.112536	Hs.47986	DKFZp586H051)		5654.333	1,54126785
GF201	869450	-	Hs.179943	ribosomal protein L11	RPL11	5650.493	
GF201	260138	N32056 Hs.44227	Hs.44227	heparanase	HPSE	5640.117	

1.1334496		2.34879539	1.16606666		1.4449536		-1.1401009	1.45224139		4 10600100		1.40180065		1,4453476			
5639.347		5636.712	5636.066		5632.984	5632.374	5629.325	5623.714		5617 040	5610.434	5608.528		5603.841	5589.767	5586.875	5585.817
PPP2R1A		KIAA0946								Tacad					LOC51706		
protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	KIAA0946 protein; Huntingtin	interacting protein H ESTs, Highly similar to putative glycolipid transfer	protein [H.sapiens] Homo sapiens cDNA FLJ10259 fis, clone	HEMBB1000947, highly similar to Homo sapiens clone HAW100 putative	ribonuclease III mRNA	ESTs	ESTs	ESTs	dolichyl-	alphosphooligosacchande-	ESTs	ESTs	ESTs, Highly similar to PEROXISOME ASSEMBLY	FACTOR-2 [H.sapiens]	(B5R.1)	ESTs Forta Highly similar to	cols, rigiliy siriliat to unknown [H.sapiens]
Hs.173902		Hs.4014	Hs.233495		Hs.49163	Hs.131833	Hs.105613	Hs.61803		12000-11	Hs.97628	Hs.88414		Hs.83714	Hs.5508	Hs.250349	Hs.194581
AA427688 Hs.85243		W67243 Hs.57860	AA449847 Hs.99230		AA459956 Hs.49163	H15560 Hs.131833	AA478478 Hs.105613	AA126832 Hs.61803		72000 -11	AA629116 Hs.97628	AA504505 Hs.88414		AA465385 Hs.83714	W84612 Hs.11567	AA782306 Hs.124207	AA625810 Hs.127488
770027		343429	788667		796409	49296	786603	502063		10.44.00	1035759	825366		814115	356835	857545	744925
GF200		GF202	GF203		GF202	GF204	GF203	GF202		000	GF204	GF203		GF203	GF201	GF204	GF204

		1.13063577		1.76257407		2.23398769		1,75003931	-1.0651256	1.8802054 1.02650391	1.17543302	1.32374945 1.06495746 1.08883675	-1.0392398
-	5582.858	5577.052	5573.231 5572.658	5566.03	5565.151	5556.888	5555.85	5548.854	5546.318	5544.894 5543.387	5539.837	5538.757 5538.102 5533.121	5528.931
		PSCD1			FKBР9		WHSC2				JTV1	HMGCS1	FLJ20748
Homo sapiens cDNA FLJ20155 fis, clone COL08754, highly similar to ACSA_ECOLI ACETYL-	COENZYME A SYNTHETASE pleckstrin homology, Sec7 and coiled/coil domains	1(cytohesin 1) Homo sapiens mRNA, complete cds, WD-repeat like	sequence ESTs	EST FK506-binding protein 9 (63	kD) ESTs, Weakly similar to ZINC FINGER PROTEIN 177	[H.sapiens] Wolf-Hirschhorn syndrome	candidate 2 Homo sapiens cDNA FLJ20287 fis, clone	HEP04390 FSTs	ESTs Homo sapiens agrin precursor	mRNA, partial cds ESTs	JTV1 gene 3-hydroxy-3-methylglutaryl- Coenzyme A synthase 1	(soluble) ESTs ESTs	hypothetical protein
	Hs.14779	Hs.1050	Hs.31714 Hs.123465	Hs.99506	Hs.8762	Hs.22744	Hs.21771	Hs.26369 Hs 94812	Hs.112087	Hs.273330 Hs.43880	Hs.258730	Hs.77910 Hs.49111 Hs.74832	Hs.91973
	AA455146 Hs.14779	AA480859 Hs.1050	N50962 Hs.31714 AA620614 Hs.123465	AA459917 Hs.99506	AA488087 Hs.107481	AA283932 Hs.22744	AA629195 Hs.116311	Hs.26369		AA458878 Hs.111481 N27028 Hs.43880	4A486430 Hs.77613	Hs.110409 3 Hs.49111 4 Hs.74832	_
	AA4551	AA4808	N50962 AA62061	AA4599	AA4880			H98630	AA4014	AA458878 N27028	AA4864	T56013 W04206 W15284	R65573
	809894	814546	281162	795627	840697	700677	1035911	261518	743161	810801	842906	73252 296754 322586	139376
	GF201	GF200	GF201 GF204	GF202	GF201	GF203	GF204	GF203	GF202	GF202 GF202	GF200	GF202 GF200 GF202	GF200

1.63412739 1.22634406	1.3230717	1.57662354	1.06586194	-1.1173879	2.27 120031	1.30015119	-1.3580578	2.14700244	1.07756254	1.32148647	1.26883265	1.1624927					2.25734398	1.07438258	0000	2.08204728
5528.552 5523.637 5522.348	5519.766 5517.219 5513.339	5504.193 5500.963	5500.865	5499.17	5494.553	5494.37	5493.864	5492.131	5483.893	5483.633	5474,499	5474.077		5471.042	5466.751	5461.543	5460.988	5460.449	5460.342	5453.901
L10RB			PCOLN3				DCN	DKFZP564G0222	DIO2	AKAP6		TSPAN-3						ZNF294		
interleukin 10 receptor, beta ESTs ESTs Homo sapiens chromosome 5, BAC clone 203013 (LBNL	H155), complete sequence ESTs ESTs	ESTs ESTs procollagen (type III) N-	endopeptidase EST, Highly similar to ADP- RIBOSYLATION FACTOR-	LIKE PROTEIN 2 [H.sapiens]	ESTs	ESTs	decorin	DKFZP564G0222 protein deiodinase, iodothyronine.	type II A kinase (PRKA) anchor	protein 6	ESTs	tetraspan 3	ESTs, Weakly similar to sperm tail protein Mst98Cb	[D.melanogaster]	ESTs	ESTs	ESTs	zinc finger protein 294	ESTs	ESI
Hs.173936 Hs.50145 Hs.91954	Hs.167399 Hs.144998 Hs.97819	Hs.26102 Hs.9572	Hs.183138	Hs.121996	HS.59525 Hs.268170	Hs.100830	Hs.76152	Hs.13370	Hs.154424	Hs.89666	Hs.22245 Hs.26070	Hs.100090		Hs.22047	Hs.98995	Hs.103070	Hs.99027	Hs.111286	Hs.14891	Hs.46995
52 33	H16743 Hs.4965 H22916 Hs.20050 AA400718 Hs.97819	AA024604 Hs.124976 AA609785 Hs.9572	N27227 Hs.57302	-	W9425/ HS.59525 H99771 Hs.4086		N72931 Hs.47453	AA463457 Hs.13370	R62242 Hs.13037		H10348 HS.22245 AA452116 HS.26070	AA287196 Hs.100090		AA863204 Hs.127060	AA460328 Hs.98995	AA284275 Hs.103073	Q	N89877 Hs.54549	က္သ	N49958 Hs.46995
842860 286548 377728	50114 51710 753139	365085 1031967	261971	449510	358/33 263846	26259	245899	811790	139766	40844	46647 786530	713647		1455740	795788	323867	788554	305585	809918	282716
GF200 GF202 GF201	GF201 GF204 GF203	GF202 GF204	GF200	GF203	GF202	GF202	GF200	GF202	GF200	GF200	GF203	GF200		GF204	GF201	GF201	GF203	GF202	GF201	GF202

-1.2092477	1.21388019 -1.6268657 1.33892367 1.57109956 2.11148745	1.22727056	1.1599318 1.1599318 1.28500257	1.27715128	-1.0291585 1.95367239 1.19230786
5445.282 5439.184	5434.26 5432.366 5430.582 5429.735 5418.308	5415.127	5408.195 5401.328 5401.328 5396.863 5391.324 5389.656 5387.269	5384.125 5383.51 5370.61	5369.167 5368.132 5356.424 5353.091
	TCEA2	RSC1A1	ACCN2 KIAA0973 KIAA0973 ELA1 DKFZP564F0923 ATP7B	СDН2	CLK1 KIAA0263
Homo sapiens cDNA FLJ10024 fis, clone HEMBA1000636 ESTs	A anisotropico i congrandi i c	regulatory soluter carrier protein, family 1, member 1 NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase)	an influence account of the characteristic o	cadherin 2, N-cadherin (neuronal) ESTs ESTs Homo sapiens cDNA	r Luzoo Iz iis, uorie ADSE01316 CDC-like kinase 1 ESTs KIAA0263 gene product
Hs.182698 Hs.22410	Hs.80598 Hs.97626 Hs.33245 Hs.61151 Hs.7065	Hs.239459 Hs.8248	Hs.274361 Hs.227489 Hs.227489 Hs.21 Hs.25524 Hs.20279 Hs.34999	Hs.161 Hs.13821 Hs.179925	Hs.90964 Hs.2083 Hs.46663 Hs.74579
AA147928 Hs.26252 AA437225 Hs.22410	AA412500 Hs.80598 AA398422 Hs.97626 AA733022 Hs.33245 AA022625 Hs.61151 H05818 Hs.7065	H02439 Hs.30309 AA406535 Hs.8248	AA479629 Hs. 87220 AA479629 Hs. 115747 AA478629 Hs. 80285 AA845015 Hs. 21 AAA975710 Hs. 86849 AA029722 Hs. 20279 N26536 Hs. 84999	W49619 Hs.161 AA463639 Hs.13821 N68864 Hs.92184	T91047 Hs.126785 H75547 Hs.2083 N47075 Hs.46663 AA634464 Hs.74579
505344 757437	730149 726894 399112 364406 44253	151251	1635320 739625 739625 1412412 1589017 366778	325182 811837 293438	112495 232973 280308 743880
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		1,12992845	1.81064687 1.4500232	1.22659789	-1.2826042 -1.1227672 1.8485918 1.13073649		1.21937574	1.31727512
5350.606	5342.469	5342	5341.956 5318.978	5318.372 5312.217	5306.19 5305.451 5294.299 5290.703 5281.829	5275.254	5269.842 5269.842 5266.888	5251.366
		TLE1		АРР	DAZL		FDFT1 FBP1	
ESTs ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ MADDIMIC ENTEY !!!	[H.sapiens] transducin-like enhancer of	Spile 1, normolog of crosophina E(spt) ESTs, Weakly similar to KERATIN, TYPE I	[H.sapiens] EST amyloid beta (A4) precursor	Protein (protease neximal), Alzheimer disease) ESTs Homo sapiens mRNA; cDNA	DNFZp434P228) ESTs ESTs deleted in azoospermia-like	protein phosphatase, EF hand calcium-binding domain 1 farnesyl-diphosphate	farnesyltransferase 1 ESTs fructose-bisphosphatase 1	ESTs
Hs.99804	Hs.193133	Hs.28935	Hs.8834 Hs.114475	Hs.177486 Hs.30029	Hs.108972 Hs.94854 Hs.13021 Hs.73078 Hs.124011	Hs.211589	Hs.48876 Hs.163564 Hs.574	Hs.20799
Hs.99804	Hs.12004	Hs.28935	Hs.39516 Hs.114475	Hs.103045 Hs.118070	AA046618 Hs. 108972 AA029697 Hs. 94854 AA463237 Hs. 13021 AA774538 Hs. 73078 W38026 Hs. 124011	Hs.99234	AA679352 Hs.48876 R43678 Hs.12317 AA699427 Hs.574	Hs.20799
R66526	T70032	T61445	N95112 N65971	W42849 H85437	AA046618 Hs. 10897 AA029697 Hs. 94854 AA463237 Hs. 13021 AA774538 Hs. 73078 W38026 Hs. 12401	H18855	AA679352 Hs.4887 R43678 Hs.1231 AA699427 Hs.574	H81275
141208	80912	79898	293845 293798	323371 220069	376697 366746 797062 1343980 322242	51064	866882 22845 433253	239524
GF204	GF201	GF200	GF200 GF203	GF201 GF203	GF202 GF201 GF202 GF203 GF203	GF201	GF201 GF202 GF201	GF200

ESTs, Weakly similar to PREGNANCY ZONE

	1.35169405	1.08402603				-1.0211756				1.65319962			1.70607308				1.23345519	1.05569585												1 10120055	00000
	5242.738	5241.016	5240.775	5239.677		5237.953	5234.717	5233.794		5229.53	5228.256		5217.476	5210.144	5203.741		5202.183	5199.377											5196.697	5105.043	0100.045
				NPHP1		PRND	GSTA4	KIAA0414			KIAA0775		TNFSF10		GDI2		PLCB3	JUNB												9776	NINK.
PROTEIN PRECURSOR	[H.sapiens]	ESTs	EST	nephronophthisis 1 (juvenile)	prion gene complex,	downstream	glutathione S-transferase A4	KIAA0414 protein	ESTs, Weakly similar to	T08D2.6 [C.elegans]	KIAA0775 gene product	tumor necrosis factor (ligand)	superfamily, member 10	ESTs	GDP dissociation inhibitor 2	phospholipase C, beta 3	(phosphatidylinositol-specific)	jun B proto-oncogene	Human DNA sequence from	clone RP1-39G22 on	chromosome 1p32.1-34.3.	Contains the 3' part of the RLF	gene for rearranged L-myc	fusion sequence (ZN-15	related zinc finger protein), a	novel gene, the ZMPSTE24	gene for yeast zinc	metalloproteinase STE24	homolo	ESI	pyruvate Kinase, muscie
	Hs.110080	Hs.69504	Hs.120358	Hs.75474		Hs.121281	Hs.169907	Hs.127649		Hs.66309	Hs.94790		Hs.83429	Hs.122709	Hs.56845		Hs.37121	Hs.198951											Hs.98952	Hs.238760	HS.198281
	AA600184 Hs.110080	AA490478 Hs.69504	AA719026 Hs.120358	W44768 Hs.103030		W76645 Hs.58272	AA152347 Hs.19657	AA702698 Hs.7289		R24222 Hs.102446	H18424 Hs.94790		R68721 Hs.80174	AA682221 Hs.122709	N20593 Hs.62419		AA846573 Hs.37121	T99236 Hs.89792											AA626247 Hs.98952	AA776308 Hs.121848	AA1883/8 Hs.54602
	950355	823890	1292544	320871		345342	504791	448098		131566	50879		139226	1293112	264146		1404396	122428											745523	453718	625/86
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-1.1705427	1.18874003	1.29844433	1.2010517 2.00494476	2.42041782 1.48380226	1.3938033	-1.5498382		1.13330616	1.31712638
5182.701 5180.294	5177.676 5167.548	5164.725	5144.275 5140.532	5132.024 5130.023	5127.705 5117.507	5114.472 5114.147 5108.238	5101.938	5101.436 5089.075	5088.538 5087.98
	SCYA19		WNT5A		IRF2	SCYA5 LOC51238 LOC51583	COL6A2	TUBA2	G1P3
Homo sapiens mRNA; cDNA DKFZp586C0224 (from clone DKFZp586C0224) EST small inducible cytokine	subfamily A (Cys-Cys), member 19 EST	ESTs, Weakly similar to KIAA0872 protein [H.sapiens] ESTs wingless-type MMTV integration site family, member integration site family, member	5A EST ESTs Weakly similar to	C56C10.3 [C.elegans] ESTs	interferon regulatory factor 2 ESTs small inducible cytokine A5	(RANTES) hypothetical protein RIG-like 7-1	ESTS collagen, type VI, alpha 2	Homo sapiens mRNA; cDNA DKFZp434G0812 (from clone DKFZp434G0812); partial cds tubulin, alpha 2	interieron, alpha-rinduciole protein (clone IFI-6-16) ESTs
Hs.5884 Hs.23963	Hs.50002 Hs.112683	Hs.6479 Hs.188497	Hs.152213 Hs.46878	Hs.164478 Hs.60374	Hs.83795 Hs.97752	Hs.241392 Hs.18778 Hs.4909	Hs.118078 Hs.4217	Hs.130885 Hs.98102	Hs.265827 Hs.169142
Hs.5884 Hs.23963	AA680186 Hs.50002 AA609295 Hs.112683	Hs.6479 Hs.17206	Hs.52273 Hs.46878	H73321 Hs.102219 AA010253 Hs.60374	W33021 Hs.109841 AA401342 Hs.97752	AA486072 Hs.69744 AA485424 Hs.18778 AA425947 Hs.4909	4A775409 Hs.118078 4A633747 Hs.109897	T85902 Hs.16027 AA426374 Hs.98102	AA448478 Hs.46569 H09749 Hs.22610
N67822 R46794	AA68018 AA60929	R40481 T97640	W49672 N56888	H73321 AA01025	W33021 AA40134	AA48607 AA48542 AA42594	AA77540 AA63374	T85902 AA42637	AA44847 H09749
291623 36480	430465 1031551	27817 121625	324901 277487	232586	321739 742564	840753 811038 760299	878111 857640	112494 757489	782513 46453
GF201 GF203	GF201 GF202	GF202 GF200	GF200 GF202	GF200 GF202	GF201 GF202	GF202 GF201 GF200	GF204 GF201	GF200 GF201	GF200 GF201

	1.34686127		1.17874789 1.37429234 1.21508371	1.6532/924	1.24432537	1.27109033	1.23858768	-1.0330201 1.91547551 -1.127033	1.97696153 1.56470148 1.1276155
	5083.577	5076.052	5070.997 5067.099 5067.023	5064,115 5051.242	5045.814	5044.466 5038.508	5038.174 5032.913 5030.592	5027.19 5022.644 5019.229 5011.735	5009.75 5004.588 4994.79 4991.956 4986.34
		VBP1	RPS15A		EIF2S3 RPL34	SSR3 LOC51582	MYRL2	EIF4B	DKFZP586I1023
APPENDIX A	Homo sapiens cDNA FLJ11006 fis, clone PLACE1003045 ESTs	ESTs von Hippel-Lindau binding protein 1	ESTs ribosomal protein S15a ESTs	ESTs ESTs eukaryotic translation initiation factor 2, subunit 3 (gamma,	52kD) ribosomal protein L34 signal sequence receptor, gamma (translocon-	associated protein gamma) antizyme inhibitor myosin regulatory light chain 2,	smooth muscle isoform ESTs FSTs	eucaryotic translation initiation factor 4B ESTs ESTs ESTs	Horno sapiens cDNA FLJ11090 is, clone PLACE1005308 DKTZP58811023 protein ESTs ESTs
	Hs.49344 Hs.95612	Hs.9291 Hs.198307	Hs.17865 Hs.2953 Hs.99121	Hs.39132 Hs.12708	Hs.211539 Hs.250895	Hs.28707 Hs.223014	Hs.9615 Hs.114120 Hs.177982	Hs.93379 Hs.50078 Hs.24740 Hs. 176675	Hs.238039 Hs.11515 Hs.229116 Hs.87440 Hs.110470
	AA171718 Hs.49344 AA074677 Hs.95612		N71442 Hs.17865 AA872341 Hs.2953 AA447592 Hs.99121	AA448390 Hs.39132 AA151994 Hs.12708	5	R67592 Hs.112192 R67562 Hs.10325	4A877166 Hs.9615 4A702432 Hs.114120 4A400414 Hs 97795	N3426 Hs.26076 N71769 Hs.50078 R34314 Hs.24740 N33555 Hs.42168	0 0 1
	•			781342 AA4 505199 AA1		141153 R67 141959 R67	1473274 AA8 447918 AA7		
WestDioon et al.	GF202 GF200	GF201 GF201	GF200 GF203 GF202	GF202 GF201	GF200 GF204	GF204 GF200	GF203 GF204	GF203 GF203 GF203 GF203	GF202 GF204 GF202 GF201 GF201 GF202

1.16160582 -1.0709131	1.73497444 1.72793064	1.17348684 1.18480898	-1,16778	1.12750989	1.85266686		1.15184654 -1.1144814 1.14602226	1.24001569	1.01617533	2.27447008
4983.954 4982.511 4981.827	4981.803 4973.533 4970.434	4969.298 4969.186	4964 83	4964.691	4962.358	4961.795	4960.942 4958.609 4954.009	4953.416 4952.844 4952.516	4951.421 4949.255 4946.382	4944.69
96-I9O	UBP1	LAMB1						C220RF4 RCE1		SS8
io de la companya de	Joseph Direction of December 1971 LBP-1a) LSTs		ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	n.saprensj ESTs ESTs, Moderately similar to	CGI-14 protein [H.sapiens] Human clone 23548 mRNA	sequence ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	[H.sapiens] ESTs ESTs chromosome 22 open reading	tse RCE1	420	protease, serine, 8 (prostasin) PRSS8
ESTs ESTs CGI-96 protein	(LBP-1a) ESTs	ESTs laminin, beta 1 ESTs	ESTs, Weakly similar I ALU SUBFAMILY J WARNING ENTRY IIII	ESTs ESTs ESTs, Modera	CGI-14 protei Human clone	sequence ESTs, Moderately simi ALU SUBFAMILY SQ WARNING ENTRY IIII	[H.sapiens] ESTs ESTs chromosome	frame 4 prenyl protein proteas ESTs Homo sapiens cDNA	OVARC1000420 ESTS ESTS	protease, ser
Hs.104372 Hs.68784 Hs.239934	Hs.28423 Hs.7124 Hs.85004	Hs.98631 Hs.82124 Hs.108226	70078	Hs.55953	Hs.271845	Hs.71848	Hs.191716 Hs.70945 Hs.96557	Hs.20017 Hs.55613 Hs.194444	Hs.19039 Hs.188992 Hs.41241	Hs.75799
R22087 Hs.23330 AA147439 Hs.68784 AA458973 Hs.6444	4A443722 Hs.28423 349120 Hs.7124	AA429806 Hs.98631 AA446251 Hs.82124 H90296 Hs.108226	2000 JU	HS.55953	AA460695 Hs.25543	Hs.71848	AA479055 Hs.105630 AA599102 Hs.70945 AA292655 Hs.96557	Al005114 Hs.20017 W38024 Hs.114619 AA788648 Hs.123997	H83094 Hs.19039 AA676813 Hs.124878 W37448 Hs.41241	AA872020 Hs.75799
R22087 AA14743 AA45897	AA443722 R49120	AA42980 AA44626 H90296	Leogo	M46575	AA46069	R38161	AA47906 AA59910 AA29266	AI005114 W38024 AA788648	H83094 AA676813 W37448	AA8720
130756 591671 810878	784035 38493	780942 774471 240678	2000	324111	796712	23548	754021 950470 701766	1626279 322240 1240304	198874 455138 321902	1475659
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2.12403022	-1.1268805	1.02492669		1.51741306		1.52390726				1.16778343				1.29698629				-1.1141508		1.17984201				1.55066314				1.78365586	1.31116781	1.8672154	-1.3471818				-1.0062324	
4941.414	4937.641	4928.668	4928.05	4922.208	4920.72	4912.917				4909.765	4900.896			4898.808		4892.368		4891.792	4891.023	4889.201	4888.048			4878.922	4876.256	4876.147		4875.972	4875.883	4874.391	4872.849	4872,666	4871.217		4869.792	
					ZNF263						RPS13							GRB2			KIAA1018					KIAA0876		LTBP3							SFRS9	
EST	EST	ESTs	ESTs	ESTs	zinc finger protein 263	ESTs	ESTs, Weakly similar to !!!!	ALU SUBFAMILY SX	WARNING ENTRY !!!!	H.sapiens]	ibosomal protein S13	ESTs, Moderately similar to	yrosine phosphoprotein SLP-	76 [H.sapiens]	Homo sapiens mRNA for	<iaa1375 cds<="" p="" partial="" protein,=""></iaa1375>	growth factor receptor-bound	protein 2	ESTs	ESTs	<iaa1018 p="" protein<=""></iaa1018>	Homo sapiens cDNA	FLJ10656 fis, clone	VT2RP2006038	ESTs	KIAA0876 protein	atent transforming growth	actor beta binding protein 3	EST	EST	ESTs	EST	ESTs	splicing factor, arginine/serine-	ich 9	
	_		Hs.44243 E	_	Hs.182528 zi	Hs.100595 E	ш	∢	>	Hs.17946 [l	Hs.165590 ri	ш	₽	Hs.260872 7	_	Hs.9663 K	-	Hs.6289 p	-	_	Hs.5400 K	T	ш.	Hs.12255 N	_	Hs.24174 K	_	Hs.238839 fa	Hs.98647 E	Hs.129804 E	Hs.112208 E	Hs.116928 E	Hs.58636 E	-	Hs.77608 ri	
Hs.59478	AA610071 Hs.112813	Hs.48518	Hs.101148	Hs.34399	4A421783 Hs.56808	AA489200 Hs.100595				Hs.17946	AA629641 Hs.76783			Hs.47588		Hs.126559		AA449831 Hs.78711	Hs.4952	Hs.28501				Hs.12255	Hs.31066	Hs.24174		4A447782 Hs.106709	4A430040 Hs.98647	AA453993 Hs.112119	AA620697 Hs.112208	AA663895 Hs.116928	4A045278 Hs.58636		AA490721 Hs.77608	
W93579	AA610071	N62340	R39765	R91271	AA421783	AA489200				N92085	AA629641			N52958		R82991		AA449831	H29620	R64153	AA156859			N47993	H17789	AA431721		AA447782	AA430040	AA453993	AA620697	AA663895	AA045278		AA490721	
357209	1031086	290416	26164	195139	739090	825011				293437	857243			283715		187055		788654	52865	139883	502496			281590	50141	782233		813825	781106	795254	1049185	906696	487082		824041	
GF202	GF202	GF202	GF204	GF200	GF201	GF203				GF200	GF201			GF200		GF204		GF200	GF201	GF200	GF201			GF203	GF201	GF201		GF202	GF202	GF202	GF202	GF204	GF201		GF200	

1.356425	1.03111538 1.25245308 1.02858515 1.02161651	1.13684676 1.7899317 1.22523828	1.37996638	1.32722315 1.32722315 -2.1176387
4860.789 4858.588 4856.013	4854.418 4841.229 4840.874 4838.835	4835.479 4835.479 4835.403 4830.146	4828.225 4827.789 4826.449 4826.449 4826.166 4807.147	4805.305 4805.189 4802.977
	ATP7A KIAA0005	PSMD2 DKFZP434P106 VRK1 RPS6KB1	ACTN3 NIFIE14	BAP1 BAP1
ESTs EST ESTs ATPase, Cu++ transporting,	• –	A Trass, 2 DKFZP434P106 protein 1 DKFZP434P106 protein 1 Thousand protein 56 kinase 1 Thousand protein 56 kinase 7 Okto, polypeptide 1 Tokno saplens mINA; cDNA	`	Underlant carboxy-renning in Underlant carboxy-renning in Underlant carboxy-termine in Underlant carboxy-termine in Vidoriase) ESTs. Weakly similar to coding region determinant binding protein [M.musculus]
Hs.21703 Hs.118517 Hs.93698	Hs. 606 Hs. 12772 Hs. 155291 Hs. 124984	Hs.74619 Hs.236522 Hs.48269 Hs.86858	Hs. 186547 Hs. 1216 Hs. 15422 Hs. 9234 Hs. 14280 Hs. 14280	Hs.106674 Hs.106674 Hs.231535
315779 Hs.21703 AA045369 Hs.118517 H53073 Hs.93898	AA236141 Hs.606 AA481281 Hs.98356 AA463591 Hs.77493 H05072 Hs.124984	AA455193 Hs.74619 AA460274 Hs.24479 AA112979 Hs.48269 AA425446 Hs.86858	AA400198 Hs.93753 AA196000 Hs.1216 AA705034 Hs.15422 AA485368 Hs.9234 NB7747 Hs.88963 AB4776 Hs.116705	H09065 Hs.106674 H09065 Hs.7577 N27637 Hs.109019 AA634543 Hs.116851
53371 487903 202395	687820 815251 773922 43405	809992 796549 530545 773319	742789 628357 461463 810989 417223 415810 878355	46154 46154 255651 743948
GF203 GF204 GF201	GF200 GF203 GF200 GF203	GF200 GF203 GF201 GF200	GF202 GF200 GF204 GF201 GF201 GF201 GF201	GF200 GF200 GF202 GF204

1.28684594	1.11209044	1.62139018	1.12875248	-1.0981839	1.04813633 1,46829708 1.66943111 2.12374919
4790.82 4778.308	4778.21 4775.086 4773.634 4763.762 4763.475 4757.713	4750.46 4747.183 4746.569	4742.725 4735.895 4734.226 4732.978	4732.85 4732.21 4722.372 4721.352 4717.912	4716.973 4711.149 4710.877 4710.875 4709.64
	YES1 AF3P21 CTNS KIAA0290		EIF2B2 VEGFB	EPAS1 GSS	DKFZP564O1863
ESTs ESTs v-ves-1 Yamaquchi sarcoma	viral oncogene homolog 1 EST SH3 protein ESTs cystinosis, nephropathic FSTs cystinosis, nephropathic FSTs	EST EST EST eukaryotic translation initiation factor 28 subunit 2 fheta	Jakob Jakobalin Z (Jeda, 199kD) vascular endothelial growth factor B EST EST EST EST Andothelial DAS domain	enflorite IT-AS contain protein IESTs ESTs. Highly similar to CGI- 111 protein [H.sapiens] ESTs glutathione synthetase glutathione synthetase plutathione synthetase CKI-AS-AS-AS-AS-AS-AS-AS-AS-AS-AS-AS-AS-AS-	DKFZp434D2472); partial cds ESTs Horno sapiens clone 24606 mRNA sequence ESTs ESTs DKFZP564O1863 protein
Hs.55800 Hs.245931	Hs.194148 Hs.105310 Hs.102929 Hs.24305 Hs.64837 Hs.96485 Hs. 68753	HS.26733 HS.22688 HS.116161	Hs.170001 Hs.78781 Hs.46651 Hs.46996	Hs.8136 Hs.12787 Hs.11085 Hs.267491 Hs.82327	Hs.112645 Hs.68665 Hs.17481 Hs.94881 Hs.99487
Hs.55800 Hs.19897	Hs.75680 Hs.105310 Hs.102929 Hs.24305 Hs.64837 Hs.96485	M836/0 H8:38/33 V62263 H8:48501 R61780 H8:22688 AA626364 H8:116161	H92556 Hs.114291 AA630120 Hs.78781 V47003 Hs.46651 V49962 Hs.46996	AA777910 Hs.121984 H24020 Hs.12787 F62842 Hs.11085 M73406 Hs.94844 AA463458 Hs.82327	AA609122 Hs.112645 AA883788 Hs.68665 AA449813 Hs.27407 AA405559 Hs.94887 AA459652 Hs.99487 W44411 Hs.7143
W45330 R07142	R28423 AA490162 N94372 R28660 N24910 AA400186	W62676 N62263 R61780 AA626364	H92556 AA630120 N47003 N49962	AA777910 H24020 T62842 W73406 AA463458	AA883788 AA883788 AA449813 AA405558 AA459653 W44411
328689 126763	133178 839986 309493 133864 269997 742763	416071 290201 42636 745101	221632 855061 280131 282717	449328 51585 86035 344091 811792	1031362 1461604 788620 772447 795540 323623
GF202 GF201	GF200 GF202 GF201 GF201 GF201 GF201	GF202 GF203 GF204 GF204	GF203 GF201 GF202 GF201	GF203 GF201 GF201 GF201 GF200	GF202 GF204 GF203 GF202 GF202 GF202

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	1.1966563 1.05639596	1.10774435	-1.0570444 1.92116778 1.24520513	1.08228267	1.04627252 2.11798111 1.14646431	-1.2030408	-1.0942768	1.81353786
4701.612	4693.146 4693.146 4685.873 4678.412	466.105 4666.105 4662.766	4659.657 4659.029 4659.029	4657.137 4657.137 4646.248	4645.778 4643.376 4639.31	4638.121 4637.5	4637.011 4634.362	4632.366
EDG4	FOXG1B SPAG6	KIAA0980 DUSP12	JUNB	YDD 19 GCMB FLJ20323	PBX3 DKFZP564O123 CD68	MAFF	QP-C	
endothelial differentiation, lysophosphatidic acid G- protein-coupled receptor, 4 ESTs, Weakly similar to proline-rich protein M14	precursor [M.musculus] forkhead box G1B sperm associated antigen 6 ESTs	ESTS KIAA0980 protein dual specificity phosphatase 12	jun B proto-oncogene ESTs ESTs	YDD19 protein glial cells missing (Drosophila) homolog b hypothetical protein pro-B-call leukemia	transcription factor 3 DKFZP564O123 protein CD68 antigen	v-maf musculoaponeurotic fibrosarcoma (avian)oncogene family, protein F ESTs ow molecular mass	ubidunone-anding protein (9.5kD) ESTS Home sapiens mRNA; cDNA	DKFZp56400122)
Hs.122575	Hs.3743 Hs.2714 Hs.158213 Hs.44071	Hs.117048 Hs.227743 Hs.44229	Hs.198951 Hs.269062 Hs.177469	Hs.25615 Hs.227098 Hs.83937	Hs.171680 Hs.11449 Hs.246381	Hs.51305 Hs.8207	Hs.3709 Hs.54607	Hs.22370
AA419092 Hs.100160	W46985 Hs.3743 R19033 Hs.2714 N62418 Hs.30938 N29682 Hs.44071	AA887547 Hs.117048 AA205072 Hs.34151 AA485951 Hs.44229	N94468 RG.37 H80519 Hs.53495 AA101173 Hs.67496	AA055768 Hs.122576 W16423 Hs.55313 AA883729 Hs.125310	W48726 Hs.117921 AA433891 Hs.71218 AA421296 Hs.25856	T47418 Hs.51305 AA452813 Hs.8207	AA133191 Hs.3709 N90218 Hs.54607	AA504609 Hs.22370
755526	325088 33051 288705 257919	1500894 647842 843328	309864 239712 563860	510576 322441 1466771	325014 773656 739183	71087 788533	490778 305556	825582
GF201	GF203 GF200 GF203 GF201	GF204 GF203 GF202	GF200 GF200 GF202	GF202 GF202 GF204	GF203 GF202 GF200	GF201 GF202	GF201 GF202	GF203

Atty Docket No. 21726/92	1.28404857				1.41585514		1.07336458		1.49837983										-1.0956029	1.26828573	1.09281147			1.25958443	1.25414327		2.1226682				1.03261372		
Atty	4630.5 4626.188		4623.412	4622.575	4622.229		4620.388	4619.609	4619.529	4619.366			4618.832		4617.514			4614.859	4612.518	4610.445	4608.934		4598.752	4597.298	4595.771	4587.121	4584.612			4584.202	4582.085	4579.583	
	PGM1									LYZ					TFE3			DYRK1A		KIAA0478			PI9		VRK2	KIAA0061	RPS23				POLRMT		
APPENDIX A	phosphoglucomutase 1 ESTs	Homo sapiens cDNA FLJ20360 fis, clone	HEP16677	ESTs	ESTs	ESTs, Moderately similar to	cadherin 12 [H.sapiens]	ESTs	ESTs	lysozyme (renal amyloidosis)	Homo sapiens mRNA; cDNA	DKFZp586L1121 (from clone	DKFZp586L1121)	transcription factor binding to	IGHM enhancer 3	dual-specificity tyrosine-(Y)-	phosphorylation regulated	kinase 1A	EST	KIAA0478 gene product	ESTs	protease inhibitor 9 (ovalbumin	type)	ESTs	vaccinia related kinase 2	KIAA0061 protein	ribosomal protein S23	ESTs, Highly similar to	hepatocyte nuclear factor 4	gamma [H.sapiens] polymerase (RNA)	thondrial (DNA directed)	ESTS	
	Hs.1869 Hs.177482		Hs.26434	Hs.91202	Hs.129368		Hs.44898	Hs.238964	Hs.260899	Hs.234734			Hs.81376		Hs.274184			Hs.75842	Hs.55476	Hs.4236	Hs.23531		Hs.104879	Hs.99718	Hs.82771	Hs.170114	Hs.3463			Hs.102867	Hs.153880	HS.120011 Hs.35096	
	AA488504 Hs.1869 AA406069 Hs.33636		N23185 Hs.78753	AA151480 Hs.91202	T41032 Hs.8369		AA418564 Hs.47075	Ξ	_	N63943 Hs.76360			R44327 Hs.22970		AA403035 Hs.75503			AA676749 Hs.75842	W31685 Hs.55476	AA033948 Hs.4236	R26094 Hs.23531		AA430512 Hs.104879	AA419390 Hs.99718	AA282292 Hs.89007	N33237 Hs.80500	AA634008 Hs.3463			H18950 Hs.102867	R31115 Hs.30419	AA/0/450 HS.120011 AA284243 Hs 100289	
ok et al.	843174 743025		267691	503096	61638		767345	1055540	246652	293925			34597		741885			897006	320770	429864	132159		769948	746264	713058	270560	868308			51406	134269	325583	
Westbrook et al.	GF200 GF202		GF201	GF201	GF202		GF200	GF204	GF200	GF201			GF201		GF201			GF201	GF202	GF202	GF200		GF201	GF203	GF203	GF201	GF203			GF201	GF200	GF204	3

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Ally Dockel No. 217			1.25931157			1.39691299		-1.1674891	-1.8545506	1.23852099	-1.1082712	1.9/1494/2				
H.	4579.195	4575.687	4574.919 4571.849	4559.19		4551.431	4551.178	4543.51	4538.342 4537.475	4537.474	4529.731	4521.979		4516.042 4515.58		4509.33 4507.37
		ELL2					CYP2J2			ATRX						
APPENDIX A	ESTS ELL-RELATED RNA POLYMERASE II,	ELONGATION FACTOR Homo sapiens mRNA; cDNA DKFZp434N2420 (from clone	DKFZp434N2420); partial cds ESTs	ESTs FSTs	Homo sapiens mRNA; cDNA OKFZp566D244 (from clone	OKFZp566D244); partial cds sytochrome P450, subfamily IJ (arachidonic acid	epoxygenase) polypeptide 2	EST ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	H.sapiens] ESTs	alpha thalassemia/mental etardation syndrome X-linked ATRX	ESTs	ESTS	Homo sapiens cDNA -LJ11130 fis, clone	PLACE1006246 FSTs	Homo sapiens mRNA; cDNA DKFZp586l0324 (from clone	OKFZp58610324) ESTs
	Hs.269852 E	Hs.173334 E	Hs.23794 E			Hs.8694 C	· ·	Hs.47442 E	Hs.206594 [Hs.96264		Hs.97808 E		Hs.237480		Hs.193700 Hs.260603
	Hs.43502	AA284232 Hs.55983	AA286905 Hs.23794 V36794 Hs.93816			AA047340 Hs.8694			Hs.29210 Hs.21782	AA410435 Hs.96264	Hs.31740	AA400475 Hs.97808		AA983410 Hs.41151		AA024832 Hs.47283 R97055 Hs.93022
	N35922	AA2842;	AA286905 N36794	AA115244		AA0473	H09076	N52137	R71738 H29052	AA4104	H20204	AA40047			70	AA0248′ R97055
∢etal.	272600	324672	701460	501407	25500	509516	46166	284357	155542 52710	753430	172957	742794		1598787	2000	365004 201559
Westbrook et al	GF201	GF201	GF203 GF201	GF201	5	GF202	GF201	GF202	GF203 GF201	GF200	GF203	GF202	3	GF204	5	GF201 GF201

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GF201 GF201	342500	W68262 N93715	Hs.539	Hs.106204 Hs.539	Homo sapiens mRNA for KIAA1827 protein, partial cds ribosomal protein S29 ESTs, Weakly similar to hyperpolarization-activated,	RPS29	4505.575 4499.929	
GF202 GF204	795243 745165	AA453999 AA626725	AA453999 Hs.99354 AA626725 Hs.119164	Hs.99354 Hs.119164	cyclic nucleotide-gated channel 2 [H.sapiens] ESTs T-cell lymphoma invasion and		4499.396 4499.38	1.97320856
GF202 GF204 GF204	742739 745318 113033	AA400155 AA625583 T87150	AA400155 Hs.62490 AA625583 Hs.125223 T87150 Hs.15367	Hs.12598 Hs.190719 Hs.189723	netastasis 2 ESTs	TIAM2	4499.274 4497.052 4496.066	1.11605551
GF202 GF203	591101 755409	AA161073 AA424706	AA161073 Hs.36672 AA424706 Hs.124214	Hs.36672 Hs.111680	ESTs endosulfine alpha ESTs, Weakly similar to SM22-	ENSA .	4495.842 4493.089	-1.1061829 1.25562326
GF200	325160	W48780	W48780 Hs.100242	Hs.169330	[H.sapiens]		4492.021	1.0591283
GF203	506658	AA708798	AA708798 Hs.8939	Hs.8939	yes-associated protein 65 kDa YAP65 putative serine-threonine	YAP65	4486.389	-1.0377259
GF201	796876	AA463188 Hs.9625	3 Hs.9625	Hs.9625	protein kinase ESTs, Weakly similar to CALPAIN 2. LARGE	SID6-1512	4484.425	
GF201	365665	AA02603C	AA026030 Hs.61311	Hs.61311	[H.sapiens] Homo sapiens mRNA; cDNA DKFZp434N1710 (from clone		4479.068	
GF203 GF201 GF201	277266 502690 884867	N34395 AA127100 AA669443	N34395 Hs.9095 AA127100 Hs.2280 AA669443 Hs.40502	Hs.9095 Hs.2280 Hs.184242	DKFZp434N1710); partial cds ribophorin I eukaryotic translation initiation factor 5	RPN1 EIF5	4476.321 4475.722 4473.319	-1.0884968
GF201 GF200 GF202	271683 197637 729972	N35086 R87194 AA416911	N35086 Hs.81956 R87194 Hs.34114 AA416911 Hs.104784	Hs.169370 Hs.271686 Hs.178062	FYN oncogene related to SRC, FGR, YES ESTs ESTs	FYN	4472.704 4449.601 4449.32	1.95891242 1.21698925
GF200	130280	R21172	Hs.149	Hs.149	cAMP response element- binding protein CRE-BPa	H_GS165L15.1	4449.077	1.01695757

1.33271562		1.12773826 1.94623519		1.56154297	1.07496869 1.53164587 -1.483197	11000
4445.141 4444.706 4443.57 4442.345	4439.938	4435.59 4434.882 4434.239	4433.26 4429.611 4421.595	4419.512 4416.056	4414.98 4413.383 4411.349 4403.972	1001001
	GPX1	CTNND2 PIM1		SSA1 ALF	KIAA0564 IQGAP2	
Homo sapiens mRNA; cDNA DKFZp654M113 (from clone DKFZp664M113) ESTs ESTs	ESTs, Highly similar to KIAA0886 protein [H.sapiens] glutathione peroxidase 1 catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat	protein) pim-1 oncogene ESTs	EST Homo sapiens mRNA for KIAA1232 protein, partial cds ESTs, Moderately similar to PNG gene [H.sapiens]	Siggren syndrome antigen A1 (St&D, rhonucleoprotein autoantigen SS-ARe) TFIIA-alpha/beta-like factor Human DNA sequence from PAC 15448 on chromosome Xp11.3-Xp114. Contains	protein smillar to protein prosphatase inhibitor 2 (IPP-2) ESTs and STS KIAA0564 protein IQ modif containing GTPase activating protein 2 ESTs	200
Hs.205678 Hs.29088 Hs.127679 Hs.113574	Hs.125019 Hs.76686	Hs.80220 Hs.81170 Hs.26088	Hs.209757 Hs.11101 Hs.192822	Hs.1042 Hs.44385	Hs.127689 Hs.151385 Hs.78993 Hs.48382	US.Z.I.Z.S.D
H05769 Hs.29310 N62936 Hs.29088 AA865737 Hs.127679 AA628865 Hs.113574	H17143 Hs.56909 AA485362 Hs.76686	H17139 Hs.75077 W49487 Hs.56040 R54061 Hs.26088	AA702407 Hs.114117 H99215 Hs.77079 AA670373 Hs.121738	N45131 Hs.1042 N32789 Hs.44385	AA864288 Hs.127689 AA171735 Hs.86013 W32272 Hs.78993 N59432 Hs.48382	AA599107 HS.Z1Z55
43828 278729 1469233 1033989	51185 810999	51083 324983 40021	447540 261851 878447	282956 259637	1470424 594871 321386 246297	950461
GF203 GF201 GF204 GF204	GF201 GF201	GF201 GF202 GF202	GF204 GF201 GF204	GF201 GF202	GF204 GF202 GF200 GF200 GF202	GF202

1.16315113 1.06099643 1.08352689 2.080643101 1.43804553 1.0006361	1,57697572 1,34080892 1,78012279 -1,7735572 1,15760197 -1,3804362 1,4524115 1,7410305 1,2099903 1,41517368	1.10901362 1.10901362 1.32877836
4397.055 4395.513 4394.499 4392.473 4390.888 4385.519 4385.081	4382.876 4376.099 4370.887 4369.79 4366.824 4365.34 4361.891 4361.891	4358.947 4358.947 4356.651 4348.188 4346.666
SLC31A1 EXTL1 TFCP2	LOC51678 C8ORF1 KIAA0381	MGAT2 MGAT2 LEU2
solute carrier family 31 (copper transporters), member — exostoses (multiple)-like 1 ESTs ESTs ESTs EST transcription factor CP2 ESTs	MAGUK protein p55T; Protein Associated with Lins 2 ESTs chromosome 8 open reading frame 1 Frame 1 ESTs chromosome 8 cone ESTs chromosome 8 cone HEMBS1001289 EST ESTS ESTS	mannosyl (alpha-1.6-)- glycoprotein beta-1.2-N- acelyglucosaminyltransferase MGAT2 mannosyl (alpha-1.6-)- glycoprotein beta-1.2-N- acelyglucosaminyltransferase MGAT2 ESTs leukemia associated gene 2 LEU2
Hs. 73614 Hs. 150956 Hs. 173065 Hs. 172084 Hs. 50212 Hs. 105309 Hs. 154970 Hs. 39546	Hs. 108931 Hs.191361 Hs.40539 Hs.100113 Hs.112873 Hs.142613 Hs.269387 Hs.269387 Hs.182817	Hs.172195 Hs.172195 Hs.127268 Hs.123679 Hs.43628
AA191488 Hs.73614 H19522 Hs.101128 AA001648 Hs.13065 N63646 Hs.94147 N72288 Hs.50212 AA49015 Hs.105309 AA498618 Hs.77370 AA461499 Hs.99546	AA609421 Hs.108931 N6377 Hs.109416 H25042 Hs.4411 AA406231 Hs.100113 AA427885 Hs.29170 AA427482 Hs.99170 AA434482 Hs.98812 N48913 Hs.29363 AA609965 Hs.104794 AA400076 Hs.97772	AA485653 Hs.94246 AA485653 Hs.36573 N71157 Hs.102801 R45627 Hs.123679 AA867999 Hs.120777
627251 172765 427838 292770 291385 839978 843067	743532 293056 160672 753248 1048722 773465 838003 279613 743445 742573	840404 840404 298966 35612 1461120
GF202 GF200 GF200 GF200 GF202 GF202 GF202	GF202 GF203 GF203 GF202 GF202 GF202 GF202 GF202 GF202	GF200 GF200 GF201 GF203 GF203

1.17541702 2.38756321 1.80053805 -1.0241415	1.20053759 -1.0118755 1.23506016		1.36364485	1.67582779	1.34351707	1.19187222 1.07292196
4346.349 4344.363 4343.877 4343.646 4343.32 4343.102	4340.878 4339.215 4329.06	4328.203 4324.531	4324.216	4320.797 4319.545	4317.642 4316.881 4315.798	4312.559 4311.487
FBL CTPS	SCNN1A LOC51135 KlAA0406	CRABP1 KIAA1029	SLC21 A3	AQP4	KIAA0868 KIAA0370	
in mrthase sapiens cDNA 777 fis, clone 22000097		-	Human DNA from overlapping chromosome 19 cosmids R31076 R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence solute carrier family 21 (organic annon transporter), member 3 Cox R310 R310 R310 R310 R310 R310 R310 R310		370 protein	Runal clolle 23303 limits sequence ESTs
Hs.100425 ESTS Hs.99833 fibrillar Hs.251871 CTP s; Hs.271930 ESTS Homo FLJ100 Hs.7432 NT2RF Hs.24944 ESTS	sodi Hs.2794 gate puta Hs.142295 REN	cellu Hs.7678 prot Hs.5307 synd	Hurn chro R31 R31 R31 R48.5086 gen gen H8.46440 men Horn Der	Hs.27552 DKF Hs.171963 aqui	Hs.106552 Caspr2 Hs.181551 ESTS Hs.70500 KIAA03	Hs.11506 seque Hs.44238 ESTs
154474 Hs.100425 AA663986 Hs.99653 109614 Hs.35112 175490 Hs.35138 AAZ78401 Hs.88707 735253 Hs.24944	AA459197 Hs.2794 R77079 Hs.96831 R85537 Hs.18414	AA421218 Hs.7678 H49443 Hs.117778	Hs.106281 Hs.46440	Hs.27552 Hs.6183	R40031 Hs.106552 AA490341 Hs.109870 AA027230 Hs.70500	AA234889 Hs.11506 AA460260 Hs.44238
T54474 AA66398 H09614 H75490 AA27840 R35253	AA45919 R77079 R85537	AA42121 H49443	R37738 N62948	N29454 H09087	R40031 AA49034 AA02723	AA23488 AA46026
70384 855755 46182 230637 712525 136775	810873 144029 180179	739193 178792	26806	259267 46376	27404 824487 469229	669471 796531
GF201 GF200 GF200 GF200 GF203 GF203	GF200 GF200 GF203	GF201 GF201	GF203 GF201	GF201 GF202	GF202 GF204 GF201	GF200 GF203

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1.05251042	-1.3268688	1.17652737	1.77414354	1.13670042	2.09370696	-1.2051827 -2.1054783 1.01690838	
4311.33 4302.834	4299.206 4295.367 4293.333 4289.935	4287.574 4285.006	4283.808	4280.591	4279.723 4279.723 4276.79	4269.57 4265.02	4263.325
JUN DKFZP564M182	RPS24	SNT2B2		ST14			SGNE1
v-jun avian sarcoma virus 17 oncogene homolog DKFZP564M182 protein ESTs, Weakly similar to !!!! A I I I CA SS. R WARNING	ENTRY !!!! [H.sapiens] ESTs ESTs ribosomal protein S24	syntrophin, beta 2 (dystrophin- associated protein A1, 59kD, basic component 2) ESTs	ESTS ESTS suppression of tumorigenicity 14 (colon carcinoma,	matriptase, epithin) Homo sapiens mRNA; cDNA DKFZp566C034 (from clone	DKFZp566C034) ESTs ESTs ESTs, Weakly similar to similar to ERG-3 like protein	[C.elegans] ESTs ESTs secretory granule,	neuroendocrine protein 1 (7B2 protein)
Hs.78465 Hs.20760	Hs.271660 Hs.184389 Hs.122058 Hs.180450	Hs.172278 Hs.271640	Hs.55179	Hs.56937	Hs.29464 Hs.191869 Hs.269109	Hs.17783 Hs.121064 Hs.14165	Hs.2265
W96155 RG.47 Al024780 Hs.30251	AA700664 Hs.117809 W52355 Hs.122754 AA778717 Hs.122058 AI005519 Hs.23623	AA489861 Hs.53593 R91375 Hs.117733	AA/U1163 HS.114042 N95835 Hs.55179	AA489246 Hs.56937	N93236 Hs. 54922 AA778212 Hs. 116042 N63034 Hs. 48671	AA406354 Hs.17783 AA705219 Hs.121064 R12267 Hs.14165	AA670429 Hs.2265
358531 1631472	432509 325526 1049079 1637296	839516 195925	308579	825085	308726 448728 278875	753195 461436 129331	878836
GF200	GF204 GF202 GF204 GF204	GF200 GF204	GF202	GF200	GF202 GF204 GF201	GF202 GF203 GF200	GF201

nydroxyacyl-Coenzyme A

dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-

Coenzyme A hydratase

1.23615642 1.12467712 2.26608548 2.61143719 1.15150558 07571882 2,14964481 1.00837935 1.66015587 2.18455521 -1.1179354 .3759419 4263.119 4247.436 4242.443 4231.361 1229.803 225,105 1220.458 4217.156 4216.342 4216.175 1260.883 1260.682 1258.825 4251.123 4246.047 4236.891 1226.422 1225.602 1218.311 4216.087 1218.53 1255.67 DKFZP58611023 RANGAP1 DNAH17L MMSDH CAPN7 CDKL1 HADHA cyclin-dependent kinase-like 1 methylmalonate-semialdehyde Ran GTPase activating protein finger protein ZFY [H.sapiens] ESTs, Weakly similar to zinc (trifunctional protein), alpha dynein, axonemal, heavy OKFZP58611023 protein CDC2-related kinase) calpain like protease oolypeptide 17-like dehydrogenase subunit ESTS STS **ESTs** ESTS STS ESTS ESTs ESTS STS STS STS STS ST TS: 4s.111515 4s.169148 4s.170008 4s.183800 Hs.110640 4s.105684 4s.192724 4s.193957 4s.122366 4s.152699 4s.116532 ls.166551 4s.119997 4s.71957 4s.96910 4s.37282 4s.75860 4s.22879 4s.54976 -ls.44089 4s.22928 4s.7145 4s.110640 4A496542 Hs.116532 Hs.105684 AA279083 Hs.111406 AA707185 Hs.119997 AA131016 Hs.131909 AA788788 Hs.122366 AA620612 Hs.129821 1473300 AA916323 Hs.75860 AA255876 Hs.86919 Hs.24437 Hs.54976 AA151413 Hs.71957 Hs.96910 Hs.44089 4s.13055 4s.22928 AA447742 Hs.73184 AA460298 Hs.99524 Hs.37282 Hs.7145 AA485734 Hs.5923 AA885344 193615 N77514 N37372 331426 N29796 W32751 113257 110641 58615 460306 048681 240411 795744 135094 755893 504742 270766 148297 246541 451936 321859 321523 885609 308926 587005 703976 813637 311150 59301 16328 GF203 GF202 GF202 GF204 GF204 GF203 3F200 GF203 GF202 GF204 GF204 GF204 3F200 **GF203** GF203 3F201 3F201 3F201 3F202 3F201 3F201

1.24948196	1.14086962	1.26304991	1.47672343	1.1185936	1.1150379
4215.726 4213.588 4207.477 4205.82 4201.703 4199.767 4198.452	4192.037 4183.147	4179.13	4178.089 4174.833 4174.723 4172.534	4155.099	4154.075 4153.513 4151.819 4148.529 4146.813
RPL24 ZNF162	BMP5	TIP47 WIF-1		GNPI	POLHZA
Homo sapiens cDNA FL/20195 fis, clone COLF0930 ESTs ribosomal protein 162 ESTs ESTs	bone morphogenetic protein 5 BMP5 ESTs cargo selection protein (mannose 6 phosohate	receptor binding protein) Wnt inhibitory factor-1 Homo sapiens mRNA; cDNA DKFZp434E0211 (from clone	DKFZp434E0211) EST ESTs ESTs ESTs	deaminase ESTs polymerase (RNA) II (DNA directed) polypeptide A	(\$20kD) ESTs ESTs ESTs ESTs
Hs.104036 Hs.4916 Hs.184582 Hs.180677 Hs.61461 Hs.103005 Hs.32148	Hs.1104 Hs.22226	Hs.140452 Hs.26471	Hs.34516 Hs.47021 Hs.268656 Hs.47650	Hs.278500 Hs.269391	Hs.171880 Hs.139615 Hs.174312 Hs.30868 Hs.268947 Hs.268628
146447 HS.82476 R39897 HS.47105 R66885 HS.106678 A445472 HS.64749 A4135722 HS.61481 W31389 HS.103005 W89584 HS.32148	AA779457 Hs.1104 H09322 Hs.22226	N52178 Hs.29230 R55809 Hs.26471	AA894457 Hs.34516 N50108 Hs.47021 R00130 Hs.116894 N53436 Hs.47650	H48661 Hs.3090 AA490077 Hs.104194	AA010216 Hs.59337 V24157 Hs.43523 AA425128 Hs.31926 AA427404 Hs.30868 H55897 Hs.37222 R06874 Hs.15664
GF201 279496 1 GF204 24097 1 GF204 41411 GF200 809648 0 GF201 501602 2 GF201 320602 1 GF201 343607 1	GF203 1032405 GF201 46105	GF203 284247 GF201 40908	GF204 1417886 GF202 282780 GF202 122872 GF204 284115	207082	GF201 430236 GF201 289567 GF203 768606 GF201 770989 GF200 204098
222222	P P	9.9	P P P P	<u> </u>	88888

					2.03361968		1.47430628			-1.4486261		1.02709574		1.24746966		1.22580511	1.23458317			1.12334343	1.17062791		1.4053636		1.22440466	1.50454481
	4141.77	4141.739	4140.876	4137.172	4136.356		4136.296	4136.292		4134.9	4134.873	4131.867		4130.402		4128.207	4127.314		4123.862	4116.187	4116.012	4115.305	4110.6	4110.545	4108.649	4108.043
	ADAMTS1	BMPR1A								B3GAT1		AKAP12		MGAT3					DSCR1		PXN					PNT5
a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin	type 1 motif, 1 bone morphogenetic protein	receptor, type IA	ESTs	ESTs	ESTs	ESTs, Weakly similar to hook1	protein [H.sapiens]	ESTs	beta-1,3-glucuronyltransferase	uronosyltransferase P)	ESTs A kinase (PRKA) anchor	protein (gravin) 12	mannosyl(beta-1,4-)- glycoprotein beta-1,4-N-	acetylglucosaminyltransferase MGAT3 Homo sapiens mRNA; cDNA	DKFZp434D0428 (from clone	DKFZp434D0428); partial cds	ESTs	Down syndrome candidate	region 1	EST	paxillin	ESTs	ESTs	ESTs	EST	purine 5' nucleotidase
	Hs.8230	Hs.2534	Hs.176626	Hs.271536	Hs.61341		Hs.130707	Hs.33461		Hs.3353	Hs.193348	Hs.788		Hs.112		Hs.236547	Hs.44404		Hs.184222	Hs.88754	Hs.102497	Hs.222819	Hs.26942	Hs.108213	Hs.86322	Hs.138593
	T41173 Hs.90484	AA927193 Hs.2534	AA431795 Hs.56561	AA022679 Hs.55257	AA026333 Hs.61341		N67300 Hs.50147	AA022935 Hs.33461			T62969 Hs.51509	AA478542 Hs.788		AA421473 Hs.31644		AA489662 Hs.5726	AA707999 Hs.44404		4A629707 Hs.82803	AA280426 Hs.88754	4A430573 Hs.102497	4A705102 Hs.121061	4A463206 Hs.26942	472612 Hs.108213	AA206914 Hs.86322	4A404619 Hs.2382
	62263 T	1540433 A	782545 A	364468 A	366407 A		286545 N	364568 A		_	80729 T	784772 A		731060 A			392440 A		`	712257 A	_	`	796916 ▶	_	_	725076 4
	GF201	GF204	GF201	GF201	GF202		GF202	GF201		GF203	GF201	GF200		GF202		GF203	GF203		GF201	GF203	GF200	GF204	GF202	GF204	GF203	GF203

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	-1.1383725 1.70173836	-1.0806153 1.01597075 1.17033594	2.02481088	1.94835244 1.11209978	1.20889735	1,74507302 1,10987116 1,10987116	1.00240013
4108.037	4106.1 4105.657 4100.262	4098.963 4096.359 4093.349 4092.601	4091.588	4090.753 4089.574	4084.662 4083.218 4081.394	4079.616 4078.953 4078.953 4068.705 4067.826 4067.826 4066.947	4064.505 4063.747
CRY2	SLC22A3		LIMK2	KIAA0356	LOC51231	MGAT1 CTBP1 CTBP1 DKFZP586B2420 PRKX	STK25
cryptochrome 2 (photolyase- like) solute carrier family 22 (extraneuronal monoamine	transporter), member 3 ESTs EST EST	protein (H.sapiers) hypothetical 43.2 Kd protein ESTs	LIM domain kinase 2 ESTs, Weakly similar to transglutaminase X	[H.sapiens] KIAA0356 gene product VRK3 for vaccinia related	kinase 3 ESTs EST	mannosyl (alpha-1,3-)- glycoprotein beta-1,2-N- acetylglucosaminyltransferase C-terminal binding protein 1 ESTs ESTS ESTS DKFZP588B2420 protein protein Kinase 25 setfinethroonine kinase 25	(Ste20, yeast homolog) ESTs
Hs.7278	Hs.81086 Hs.98603 Hs.98340	Hs.19513 Hs.169992 Hs.256375 Hs.44216	Hs.278027	Hs.164661 Hs.32312	Hs.98289 Hs.46756 Hs.168055	Hs.151513 Hs.239737 Hs.239737 Hs.177313 Hs.6774 Hs.7949 Hs.147996	Hs.155206 Hs.30891
AA461181 Hs.7278	AA428628 Hs.98603 AA4281271 Hs.98340	W47099 Hs.19513 AA457092 Hs.1335 W46986 Hs.12780 N30728 Hs.44216	AA877845 Hs.75338	AA027266 Hs.61328 AA810039 Hs.32312	AA775422 Hs.98289 N47713 Hs.46756 AA186335 Hs.85572	AA775378 Hs.117946 AA478268 Hs.10986 AA478268 Hs.110761 AA011833 Hs.108715 AA115248 Hs.5774 W58343 Hs.22857 AA778448 Hs.122021	AA664007 Hs.119585 H09029 Hs.30891
796809	795603 781420 731040	324651 810408 325090 257436	1160723	375619 1367678	878127 281035 625684	878689 740914 740914 429505 501430 341641 1032170	855391 45929
GF201	GF201 GF202 GF202	GF203 GF200 GF201 GF202	GF203	GF202 GF203	GF204 GF201 GF202	GF203 GF200 GF200 GF201 GF201 GF201 GF201	GF203 GF201

	1.57624284	1.23659847	1.11111193	-1.0502659	1.23800525	0000	1.14002430 1.01911212 -1.3429751 1.67060437 -1.0102608
4063.35	4062.349	4062.017 4059.444	4057.713 4055.541	4049.934 4048.997	4041.855	4035.79	4035.782 4032.324 4030.881 4028.898 4023.994
ITGAV	PEX11B	COX6B	SMARCA2				PSMD4 HSPC220
inlegrin, alpha V (vitronectin receptor, alpha polypeptide, argian (DS1) ESTs, weakly sinilar to BUTYROPHILIN PRECURSOR HIL sapiens)	11B cytochrome c oxidase subunit	SWI/SNF related, matrix associated, actin dependent reculator of chromatin.	subfamily a, member 2 ESTs	ESTS, Highly similar to cacicum-regulated heat stable protein CRHSP-24 [H.sapiens] ESTS ESTS, Weekly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII	[H.sapiens] ESTs Homo sapiens cDNA FLJ10323 fis, done	NT2RM2000540 proteasome (prosome, macropain) 26S subunit, non-	A l Pase, 4 ESTs hypothetical protein EST
Hs.118512 Hs.61958	Hs.83023	Hs.174031 Hs.269528	Hs.198296 Hs.46990	Hs.92198 Hs.22247	Hs.192732 Hs.102915	Hs.7049	Hs.148495 Hs.38038 Hs.278345 Hs.104820 Hs.26255
AA029934 Hs.118512 AA046498 Hs.61958	R42195 Hs.83023	N71160 Hs.83379 AA678176 Hs.10522	AA481026 Hs.77590 N51291 Hs.46990	W77951 Hs.92198 AA455087 Hs.22247	4	N94612 Hs.7049	AA45027 Hs.11709 H62267 Hs.38038 W69639 Hs.11524 AA469954 Hs.104820 R42714 Hs.26255
469969 <i>P</i>	30793 F	298965 N 430830 A	814636 A 283058 N	346134 V 812294 A		_	789232 / 207665 H 343628 V 730363 / 32310 F
GF201 GF201	GF203	GF202 GF203	GF200 GF201	GF200 GF203	GF204 GF202	GF201	GF200 GF200 GF203 GF202 GF202

					neurexin 4 (contactin			
GF202	171916	H18963	Hs.107544	Hs.31622	associated protein)	NRXN4	3965.627	1.25884349
					Homo sapiens cDNA			
					FLJ20845 fis, clone			
GF200	325370	W52208	Hs.29748	Hs.29748	ADKA01901		3965.196	1.12444543
					ESTs, Weakly similar to !!!!			
					ALU CLASS B WARNING			
GF202	271082	N34441	Hs.93780	Hs.93780	ENTRY !!!! [H.sapiens]		3959.666	-1.0950588
					membrane protein,			
					palmitoylated 3 (MAGUK p55			
GF201	323777	W44685	Hs.83044	Hs.37144	subfamily member 3)	MPP3	3958.209	
GF204	29989	R40123	Hs.100868	Hs.170141	ESTs		3958.01	
GF201	611443	AA176581	AA176581 Hs.118836	Hs.118836	myoglobin	MB	3957.218	
					guanine nucleotide binding			
					protein (G protein), alpha z			
GF201	40773	R56046	Hs.92002	Hs.92002	polypeptide	GNAZ	3954.967	
					SRY (sex determining region			
GF201	366815	AA029415	AA029415 Hs.100328	Hs.83484	Y)-box 4	SOX4	3952.777	
GF204	1460130	AA864496 Hs.8583	: Hs.8583	Hs.8583	similar to APOBEC1	APOBEC1L	3951.366	
GF202	730834	AA417011	4A417011 Hs.98175	Hs.98175	EST		3949.822	1.27593994
GF201	342082	W60310	Hs.108662	Hs.6979	ESTs		3943.332	
GF202	320588	W31566	Hs.55459	Hs.55459	EST		3943.287	1.04325917
GF200	197933	R96358	Hs.35552	Hs.35552	ESTs		3942.74	1.17880352
GF203	1404841	AA838730	AA838730 Hs.119014	Hs.119014	zinc finger protein 175	ZNF175	3941.839	-1.0043154
					Not56 (D. melanogaster)-like			
GF201	131091	R23251	Hs.23487	Hs.153591	protein	NOT56L	3939.692	
GF204	144012	R76896	Hs.29590	Hs.29590	ESTs		3939.577	
GF203	1468722	AA885210	AA885210 Hs.125765	Hs.194061	ets variant gene 2	ETV2	3938.526	1.84951261
GF204	1519013	AA910981	AA910981 Hs.13580	Hs.13580	ESTs		3938.195	
					Wolf-Hirschhorn syndrome			
GF204	1587178	AA977080	AA977080 Hs.21771	Hs.21771	candidate 2	WHSC2	3937.886	
					retinoblastoma-binding protein			
GF201	324703	AA284235	AA284235 Hs.109905	Hs.16003	4	RBBP4	3937.486	

	-1.3912647	1.31209972		1.23098089	-1.0596541	1.85688444		2.09330193		1.15489532 -1.0276271		
	3937.085	3935.3 1 3933.113	3930.142	3927.026		3909.878 3909.465	3909.258	3908.291	3905.155	3901.047 1 3900.892 -	3898.491	
		UGT2B10		STAM	D5S346 RPS19 KIAA0770		TNRC1		ID3	RPS6KA1	CDH11	
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ	WARNING ENTRY !!!! [H.sapiens] IIDD glycosuffransforase 2	amily, polypeptide B10	Homo sapiens mRNA for KIAA1183 protein, partial cds	signa narsouching adaptor molecule (SH3 domain and ITAM motif) 1 DNA segment, single copy	deleted in polyposis ribosomal protein S19 KIAA0770 protein	ESTs ESTs rinuclantida rangat containing	1 ESTs, Weakly similar to	ribosomal protein S6 kinase 3 [H.sapiens] nhibitor of DNA binding 3, dominant negative helix-loop-	nelix protein diposomal protein S6 kinase	90kD, polypeptide 1 ESTs	cacterin 1 (Or-cauterin, osteoblast) by Human DNA from chromosome 19-specific cosmid F25965, genomic sequence	
ES.	WA Hs.182391 [H.s	Hs.76800 family,		Hs.153487 ITA	Hs.178112 (del Hs.126701 ribo Hs.9452 KIA	Hs.29019 ESTs Hs.53810 ESTs	Hs.103315 1 ES ⁻	ribo Hs.205244 [H.s inhi	Hs.76884 heli	Hs.149957 90k Hs.114202 ES	Hs.75929 ost Hur Chr cos Hs.42514 seq	
	Hs.108456	Hs.76800 Hs 53113	Hs.7193	Hs.82899	Hs.74648 Hs.113908 Hs.61998	Hs.107360 Hs.53810	AA147043 Hs.103315	Hs.38654	Hs.76884	Hs.2079 Hs.114202	Hs.77142 Hs.42514	
	H79007	H68509		AA485996 Hs.82899	H99681 H41165 AA156801	W47552 N26011	AA147043	H67666	AA482119 Hs.76884	AA452753 Hs.2079 H67883 Hs.11420	AA136983 Hs.77142 AA626310 Hs.42514	
	233645	212021	277044	843076	263727 192242 502464	324323 268850	588559	211202	756405	788511 229809	491113	
	GF200	GF200	GF201	GF200	GF201 GF202 GF201	GF201 GF202	GF201	GF200	GF201	GF200 GF203	GF201 GF201	

A second	1						Attv	Atty Docket No. 2172
Westbrook et al.	k et al.				APPENDIX A			
GF201	293110	N63848	Hs.108285	Hs.269116	ESTs prepared plasma		3832.064	
GF203 GF203	137704 48181	R37986 H12277	Hs.114964 Hs.30509	Hs.75874 Hs.30509	programs according protein A ESTs ESTs, Weakly similar to	РАРРА	3823.043 3822.019	-1.2512081 1.22791018
GF203	685185	AA252651	AA252651 Hs.43897	Hs.43897	PROTEIN PHOSPHALASE 2C ALPHA ISOFORM [H.sapiens]		3821.139	1.58833322
GF200 GF204	813460 366525	AA455427 AA026771	AA455427 Hs.32978 AA026771 Hs.49169	Hs.32978 Hs.49169	proprotein conventase subtilisin/kexin type 7 ESTs	PCSK7	3819.464 3815.08	-1.2578751
GF200 GF201	767769 429927	AA418224 AA034058	AA418224 Hs.10315 AA034058 Hs.61709	Hs.10315 Hs.61709	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6 ESTs	SLC7A6	3814.077 3813.27	1.08258227
GF200	143519	R75819	Hs.1034	Hs.227729	FK506-binding protein 2 (13kD) ESTs, Moderately similar to !!!!	FKBP2	3811.308	-1.5737323
GF201 GF203	81589 272140	T65857 N35469	Hs.11785 Hs.42532	Hs.271498 Hs.42532 Hs. 97980	ALC SUDFAMILE 19 WARNING ENTRY !!!! [H.sapiens] ESTS Halingseundi	K1AA0928	3810.48 3807.657 3806.044	1.57330861
GF201 GF203	292015 413109	N73278 AA707814		Hs.52792 Hs.7396	Homo sapiens mRNA; cDNA DKFZp58611823 (from clone DKFZp58611823)		3802.239 3792.689	1.40532552
GF201 GF201	758356 298662	AA404288 N74313	4A404288 Hs.110700 N74313 Hs.93999	Hs.18442 Hs.42746	Homo sapiens mRNA; cDNA DKFZp586M0524 (from clone DKFZp586M0524) ESTs		3790.901 3790.07	
GF201 GF202	62114 758371	T41078 AA404360	T41078 Hs.8383 AA404360 Hs.27067	Hs.8383 Hs.103283	bromodomain adjacent to zinc finger domain, 2B KIAA0594 protein	BAZ2B KIAA0594	3789.368 3788.695	-1.3944583

-1.1766791	1.17621258	1.06106641	-1.217603	1.7281624			1.03161964			1.02950249		1 17983746			1.21844219	1.81299612		1.61869923	1.20532654		
3787.42	3784.898	3782.619	3781.905	3780.662 3778.138		3777.396	3776.205	3775.251	3//4./4	3773.122		3769 422	17.00.00	3768.992	3768.345	3767.861		3767.482	3765.78		3765.274
	RAB36 RPS11	KIAA0188						KIAA1350		CFL2				PER3	PNUTL2	ONON		SSR3			M11S1
Homo sapiens mRNA; cDNA DKFZp586E2023 (from clone DKFZp586E2023) RAB36, member RAS	oncogene family	KIAA0188 protein	ESTs	ESTs ESTs	ESTs, Weakly similar to WDNM1 PROTEIN	PRECURSOR [R.norvegicus] ESTs. Weakly similar to	W05H7.3 [C.elegans]	KIAA1350 protein	ESIS	cofilin 2 (muscle)	Homo sapiens cDNA	FLJ109/6 fis, clone	ברוסווסס	period (Drosophila) homolog 3 PER3	peanut (Drosophila)-like 2 non-Pou domain-containing octamer (ATGCAAAT) binding	protein signal seguence receptor.	gamma (translocon-	associated protein gamma)	ESTs	membrane component, chromosome 11, surface	marker 1
Hs.59384	Hs.38772 Hs 182740	Hs.81412	Hs.53687	Hs.54960 Hs 28096		Hs.56105	Hs.27445	Hs.101799	HS.216726	Hs.180141 Hs.125691		He 94469	118.24402	Hs.12592	Hs.155524	Hs.172207		Hs.28707	Hs.269778		Hs.278672
AA775270 Hs.29005	H69004 Hs.38772	AA446822 Hs.81412	H99640 Hs.53687	AA435940 Hs.54960		AA284262 Hs.56105				W47364 Hs.106879	200000000000000000000000000000000000000	D97711 Hs 94469	N2// 11 NS.24402	AA521459 Hs.112290	T64878 Hs.12609	AA056465 Hs.76335		AA424586 Hs.28691	AA179510 Hs.124040		AA670155 Hs.119283
878605	234080	783698	262823	730554		325247	200900	321886	291706	324717	00702	194405	134493	826218	66714	509887		767206	612685		845663
GF203	GF200	GF200	GF202	GF202	5	GF201	GF203	GF201	GF201	GF203	5	0000	GFZ00	GF204	GF200	GF202		GF202	GF202		GF201

		1.04404555		1.07703405		-2.6445815		1.23030463	1.1010052			1.78637361	1.14560259			1.25864103		1.0077776		-1.1778754
3764.028	3763.24	3762.12	3757.086	3755.246 3753.755	3750.592 3750.192	3748.615		3748.291	3746.397	3744.311		3741.589	3740.566		3732.739	3727.079		3726.019		3720.459
MAP2K7	IFRD1		CDH16	D6S52E GPM6A				ICMT	LCN2				PRL					TEK		
mitogen-activated protein kinase kinase 7	interferon-related developmental regulator 1 ESTs, Weakly similar to finger protein HZE10 Kingonal.	related [H.sapiens]	cadherin 16; KSP-CADHERIN CDH16	HLA-B associated transcript-3 D6S52E glycoprotein M6A	ESTs	ESTs	soprenylcysteine carboxyl	nethyltransferase	ipocalin 2 (oncogene 24p3)	ESTs	Homo sapiens mRNA for	KIAA1140 protein, partial cds	prolactin	ESTs, Highly similar to DYNEIN HEAVY CHAIN,	CYTOSOLIC [R.norvegicus]	ESTs	TEK tyrosine kinase, endothelial (venous malformations, multiple	cutaneous and mucosal)	ESTS, Moderately similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	H.sapiens]
HS.110299 k	Hs.7879	Hs.20369 r	Hs.115418	Hs.274348 H Hs.75819 g	Hs.60455 E	4		Hs.183212 r	_	Hs.178443 E	_	Hs.131728 P	Hs.1905		Hs.169115 (Hs.173961 E	,	Hs.89640		Hs.193876
Hs.14476	Hs.7879	Hs.20369	AA886340 Hs.115418	R39334 Hs.113402 AA448033 Hs.75819	4A010870 Hs.60455	AA704908 Hs.120848		Hs.98457	AA401137 Hs.82238	AA707499 Hs.104819		AA504156 Hs.59574	Hs.1905		Hs.102362	Hs.100640		Hs.89640	18.102971	Hs.52988
1456602 AA864681 Hs.14476	AA676598 Hs.7879	R09497	AA886340	R39334 AA448033	AA010870	AA704908		H77506	AA401137	AA707499		AA504156	AA133920 Hs.1905		H97017	R06642		H02848	ccccom	H86589
1456602	882483	127708	1493060	24392 784910	359647	461363		233299	741497	1292011		825261	504236		251618	126438		151501	320380	223231
GF204	GF201	GF203	GF204	GF204 GF200	GF201	GF203		GF200	GF200	GF204		GF203	GF200		GF204	GF200		GF201	GF-202	GF203

	1.63585714	1.15958754	1.66809016	-1.0061792	1.05347416	-1.6886815	2.59781002		1.9534474			1.21923194			-1.4924215		1.15677452							1.09079469		1.09079469	1.13383798					1.35444038
3719.904	3714.787	3714.345	3712.152	3710.579	3706.327	3705.766	3705.65	3704.936	3701.482	3701.373	3701.27	3701.248			3699.407		3697.141				3696.74	3695.576		3695,319		3695.319	3692.264		3689.262			3688.024
EIF4B		SNW1	CAV3		KRTHB5			KIAA0211			HBZ				SGCA		MAPK6				KIAA0001			E2F4		E2F4	CA1		ABCA5			
eukaryotic translation initiation factor 4B	ESTs	SKI-INTERACTING PROTEIN	caveolin 3	ESTs	keratin, hair, basic, 5	ESTs	ESTs	KIAA0211 gene product	ESTs	ESTs	hemoglobin, zeta	ESTs	sarcoglycan, alpha (50kD	dystrophin-associated	glycoprotein)	mitogen-activated protein	kinase 6	KIAA0001 gene product;	putative G-protein-coupled	receptor; G protein coupled	receptor for UDP-glucose	ESTs	E2F transcription factor 4,	p107/p130-binding	E2F transcription factor 4,	p107/p130-binding	carbonic anhydrase I	ATP-binding cassette, sub-	family A (ABC1), member 5	Homo sapiens mRNA; cDNA	DKFZp761M222 (from clone	DKFZp761M222)
Hs.93379	Hs.25968	Hs.79008	Hs.98303	Hs.129692	Hs.182507	Hs.190399	Hs.59085	Hs.79347	Hs.71023	Hs.91789	Hs.272003	Hs.45209			Hs.99931		Hs.271980				Hs.2465	Hs.12315		Hs.108371		Hs.108371	Hs.23118		Hs.180513			Hs.273186
4A115266 Hs.34267	Hs.25968	Hs.79008	4A425319 Hs.98303	Hs.63788		Hs.55475	Hs.59085	Hs.79347	Hs.71023	Hs.91789	Hs.117808	AA609511 Hs.45209			Hs.99931		Hs.75465				Hs.2465	Hs.12315		AA448641 Hs.108371		4A448641 Hs.79397	Hs.23118		Hs.26035			Hs.111599
AA115266	R67259	H17512	AA425319	R46700	AA022951	W31683	W87781	H23198	AA127743	R43158	H60173	AA609511			AA461125 Hs.99931		H17504				AA027011 Hs.2465	R56055		AA448641		AA448641	R93176		R53428			H73777
491733	41558	50614	773276	36491	364569	320764	417263	51975	490333	32537	207558	1031640			796258		20506				469358	40881		786048		786048	275738		39821			214980
GF204	GF203	GF200	GF202	GF202	GF202	GF202	GF202	GF201	GF202	GF204	GF204	GF202			GF200		GF200				GF201	GF201		GF200		GF200	GF200		GF201			GF203

-1.0921698		1.6253424	.06675617 .0072904 .06766597	-1,8967032 1.14976974	1.34821948		-1.0813787
3687.292 3683.859	3679.224 3679.002	3678.826 3678.813 3676.052	3675.774 3669.155 3669.127	3668.875	3667.672	3664.696	3663.861 3660.399 3660.05
LAPTM5			SFI				PPP3CA
al-associated ining membrane eakly similar to !!!! FFAMILY SX G ENTRY !!!!	[H.sapiens] ESTs Homo sapiens mRNA; cDNA DKFZp434C0926 (from clone	DKFZp434C0926); partial cds EST ESTs colony stimulating factor 1	ONA one	DKFZp761H221) ESTs	ES 1 S, Highly similar to 45kUa splicing factor [H.sapiens] ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	[H.sapiens] protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A	ä
Lysosom multispar protein-5 EST ESTs, WA ALU SUE WARNIN	[H.sapiens] ESTs Homo sapie DKFZp434(DKFZp4 EST ESTs colony s	(macrophage) ESTs ESTs Homo sapiens DKFZp761H2:	DKFZp7 ESTs	Splicing splicing and splicing	[H.sapiens] protein phos (formerly 2E alpha isofor	alpha) ESTs EST
Hs.79356 Hs.117212	Hs.6986 Hs.238936	Hs.177956 Hs.69306 Hs.42424	Hs.173894 Hs.49299 Hs.50770	Hs.10702 Hs.112954	Hs.107001	Hs.271495	Hs.272458 Hs.125398 Hs.72062
AA410265 Hs.79356 AA682183 Hs.117212	AA137260 Hs.6986 AA058709 Hs.49625	AA682223 Hs.96763 AA101876 Hs.69306 H97701 Hs.42424	T5558 Hs.82813 N66985 Hs.49299 N78889 Hs.50770	AA670330 Hs.10702 AA621224 Hs.112954	AA458853 Hs.107001	H82867 Hs.20190	AA682631 Hs.92 AA878772 Hs.125398 AA150260 Hs.72062
753313 AA 1293093 AA	502818 AA 488145 AA	1293118 AA 489633 AA 251569 H9	73527 T58 287258 N6I 300000 N7I	878373 AA 744436 AA	814386 AA	198854 H8	431296 AA 1417972 AA 491627 AA
GF200	GF201 GF201	GF204 GF202 GF203	GF202 GF202 GF202	GF203 GF202	GF203	GF204	GF201 GF204 GF202

	1.1593962	1.60722275		-1.4127207	1.10990596 1.40035398 1.1356847 -1.0019471
3659.85 3659.824 3658.107	3657.062 3656.115	3654.483 3654.361 3654.316	3653.169	3649.135 3647.893 3647.572	3645.192 3640.335 3639.874 3639.783
SLC11A2	GS3686 KIAA0391		PSMC6 VATI	TIE PPIC	SFRS10
solute carrier family 11 (proton- coupled divalent metal ion transporters), member 2 ESTs ESTs ESTs hunching protein	expressed in osteoblast KIAA0391 gene product ESTs, Moderately similar to !!!! ALU SUBFAMILY SIB ENTEY !!!	H.sapiens] ESTs ESTs Proteasome (prosome, macronain) 368 euhinit	The state of the s	grown rackor normology domains peptidyprolyl isomerase C (cyclophilin C) ESTs	splicing factor, arginine/serine- rich (transformer 2 Drosophila homolog) 10 ESTs ESTs Homo sapiers cDNA FLJ10088 fis, clone HEMBA1002460
Hs.57435 Hs.40249 Hs.107795	Hs.75470 Hs.154668	Hs.132207 Hs.40421 Hs.34789	Hs.79357 Hs.157236	Hs.78824 Hs.110364 Hs.15536	Hs.30035 Hs.48520 Hs.46669 Hs.217489
N72116 Hs.25103 AA017225 Hs.40249 R83004 Hs.107795	AA410567 Hs.75470 AA426039 Hs.5917	N90774 Hs.54656 N36853 Hs.40421 AA115535 Hs.34789	R94943 Hs.107963 AA669603 Hs.75130	AA432062 Hs.78824 AA043412 Hs.82863 W74565 Hs.15536	Hs.30035 Hs.48520 Hs.46669 Hs.108782
N72116 AA017225 R83004	AA410567 AA426036	N90774 N36853 AA115538	R94943 AA669603	AA432062 AA043412 W74565	H11792 N62346 N47090 H94745
291059 361091 194381	754479 773426	303110 273394 491392	198614	784124 487437 344672	47681 290423 280329 256477
GF201 GF204 GF201	GF200 GF201	GF202 GF201 GF201	GF201	GF200 GF201 GF200	GF200 GF202 GF202 GF202

		1.03691547	1.22167951	-1,453634			1.05453805		-1.0603053 1.38796145		-1.2775435	1.1450937		1.1472971	1.39213623	
3637.288	3635.282	3633.849	3632.562	3631.891		3621.934	3620.227 3619.503		3618.224 3618.115		3617.573	3617.43	3616.293	3616.199	3615.835 3611.571	3610.151 3606.027
	NTMR4		TIF1			FCN3	NOD		NRBP			TARBP2	ASL	DRG2		ACO2
ESTs, Weakly similar to Nod1 [H.sapiens]	myotubularin related protein 4 MTMR4 ESTs, Weakly similar to coded for by C, elegans cDNA	/k44f2.5 [C.elegans] ranscriptional intermediary	ar to	hypothetical protein [H.sapiens] FSTs	ficolin (collagen/fibrinogen domain-containing) 3 (Hakata			nuclear receptor binding	protein	Homo sapiens mRNA; cDNA DKFZp434K1815 (from clone	OKFZp434K1815); partial cds TAR (HIV) RNA-binding	protein 2	argininosuccinate lyase	GTP-binding protein 2	ESTs EST	Homo sapiens mRNA; cDNA DKFZp564E193 (from clone DKFZp564E193) aconitase 2, mitochondrial
E Hs.189183 (F	Hs.141727 m E	Hs.26110 ył	Hs.183858 fa E	h) Hs.58428 [F Hs.189004 F		Hs.272576 au	Hs.78465 or Hs.50742 E	_	Hs.272736 pi Hs.179520 E		Hs.274135 D	Hs.326 pl	Hs.61258 au	Hs.78582 G	Hs.83071 E Hs.112509 E	
1049135 AA620975 Hs.116281	AA699784 Hs.124734	AA405543 Hs.26110	0 Hs.25299	W90748 Hs.58428		AA666363 Hs.9225	W96134 Hs.78465 AA451742 Hs.50742		W45701 Hs.109892 AA456018 Hs.47673		7 Hs.93342	AA436409 Hs.326	AA486741 Hs.61258	AA456688 Hs.78582	H17055 Hs.7167 AA599142 Hs.112509	3 Hs.101016 40 Hs.31702
35 AA620			35 R39430						-		39 H73947				_ `	
	04 462506)2 772416	00 137535	71 418297		94 858877	358531		323522		00 232789	00 756488)1 841221	00 813158	50132	
GF204	GF204	GF202	GF200	GF201	i 5	GF204	GF200	i S	GF202	i i	GF200	GF200	GF201	GF200	GF201 GF202	GF204 GF201

1.24857832	-1.2920883	1.02820109	-1.1158982	1.61265287	1.7878078	1.13301811	1,10439588 -1.0390399	1.13048285 2.36243333 1.38931706	1.06718389
3604.969	3600.992	3598.856	3596.938 3596.492 3595.989	3592,431	3590.146	3586.417	3586.207 3584.169 3583.791	3582.109 3580.941 3580.475	3578.473 3578.304
A HEQ			PROZ	PABPC1	SMARCC1	FUT8	PI YAF2 RBM9		DKFZP564G1964 TSN
requiem, apoptosis responsee zinc finger gene ESTs ESTs. Moderately similar to IIII ALU SUBFAMILY SB2 MARNING ENTRY IIII Handarel	ESTS, Weakly similar to hypothetical protein [H.sapiers] [H.sapiers] [ESTS, Weakly similar to transposon LREZ reverse transcriptase homolog	[H.sapiens] protein Z, vitamin K-dependent	plasma glycoprotein ESTs ESTs	poly(A)-binding protein, cytoplasmic 1 SWI/SNF related, matrix associated, actin dependent	regulator of chromatin, subfamily c, member 1 fucosyltransferase 8 (alpha	(1,6) fucosyltransferase) protease inhibitor 1 (anti-	elastase), alpha-1-antitrypsin YY1-associated factor 2 RNA binding motif protein 9	ESTs EST	DKFZP564G1964 protein translin
Hs.13495 Hs.55445 Hs. 270572	Hs.184341	Hs.269113	Hs.1011 Hs.136227 Hs.50382	Hs.172182	Hs.172280	Hs.118722	Hs.75621 Hs.180324 Hs.5011	Hs.30563 Hs.143992 Hs.44001	Hs.5801 Hs.75066
AA609415 Hs.109285 W31352 Hs.55445	AA434300 NS.6/430	N63727 Hs.48852	AA680349 Hs.1011 AA007619 Hs.103294 W00794 Hs.50382	AA486626 Hs.66311	AA872122 Hs.85813	7	R93723 Hs.107938 AA758082 Hs.115369 W90660 Hs.26127	AA235286 Hs.30563 R53900 Hs.26075 N20801 Hs.44081	31
743519 320568	267736	293539	430471 429446 296568	840940	1475797	627541	197794 1320746 417976	138165	754312 795936
GF202 GF202	GF203	GF200	GF201 GF201 GF200	GF200	GF203	GF200	GF203 GF203 GF201	GF203 GF200	GF203 GF200

1.09032108 1.8972804 -1.0162908 1.64834659	1.80394905	1.13825659 1.17965905 1.03099999	1.03957603 2.51166121 1.51093698	1.20075928 -1.1533058 1.17025664 2.27472246	1.01605384
3575.01 3575.769 3570.972 3570.731 3569.994	3564.275	3564.01 3563.152 3561.291 3559.628 3559.324	3559.282 3559.25 3556.427 3555.895	3550.641 3546.323 3546.052 3545.011 3544.526 3544.526	3542.568 3542.236 3541.878
CHN2	G9A	ASAHL PKM2	KIAA0376 CHN2	rceal: Madh2	ATP2A2
rin (chimaerin) 2 n reneal-containing	phingosine ydrolase (acid	idase)-like ite kinase, muscle	376 protein rin (chimaerin) 2	ription elongation factor like 1 sapiens clone 25116 sequence requence muthers against matabegic, Drosophila) og 2 sapiens mRNA; cDNA sapiens mRNA; cDNA	se, Ca++ transporting, c muscle, slow twitch 2
Hs.7149 EST Hs.131003 ESTs Hs.15202 chimel Hs.275254 EST Hs.111991 ESTs	Hs.75196 protein N-acyls amidoh	Hs.264330 ceram Hs.198281 pyrruva Hs.31028 ESTs Hs.27463 ESTs Hs.268981 ESTs			
AA131794 Hs.71449 Hs. H14078 Hs.131003 Hs. H79888 Hs.78041 Hs. AA102035 Hs.44106 Hs. AA418984 Hs.111991 Hs.	_	747576 Hs.78264 Hs.78272 Hs.42814 Hs. 742572 Hs.42814 Hs. 74453014 Hs.31028 Hs. 747625 Hs.27463 Hs. 7473628 Hs.108382 Hs.			AA865355 Hs.127068 Hs H85355 Hs.1526 Hs N64746 Hs.1526 Hs
AA131794 H14078 H79888 AA102035 AA418984	AA434117 Hs.75196	W47576 N72272 AA453014 H16725 H73628			10
503966 163807 233365 510760 768096	770216	324342 291370 788332 48955 234955	() () W ()		233399 1469945 222181 284524
GF202 GF204 GF200 GF200 GF203	GF200	GF200 GF204 GF203 GF203 GF201	GF201 GF200 GF203 GF202	GF200 GF200 GF200 GF200 GF200	GF204 GF204 GF200 GF201

Westbrook et al	k et al.				By Made State State State State State Spirit State	Anal Bart Stan Area Land Wall Said Start	Atty	Atty Docket No. 2172
					APPENDIX A			
					capping protein (actin filament)			
GF201	322961	W45165	Hs.55198	Hs.76368	muscle Z-line, beta	CAPZB	3538.693	
GF202	286490	N67355	Hs.50162	Hs.50162	ESTs		3531.069	1.7339987
GF202	731275	AA420998	AA420998 Hs.46600	Hs.178095	ESTs		3527.069	-1.2401281
GF203	42070	R60343	Hs.76856	Hs.153952	5' nucleotidase (CD73)	NT5	3526.334	1.15418704
GF202	743321	AA400595	AA400595 Hs.97817	Hs.97817	ESTs		3523.857	-1.8056678
GF201	51052	H18657	Hs.6498	Hs.6498	ESTs		3522.384	
					Homo sapiens cDNA			
					FLJ20203 fis, clone			
GF203	195817	R92186	Hs.20594	Hs.20594	COLF1334		3521.435	-1.00403
GF202	744447	AA621236	4A621236 Hs.112955	Hs.112955	EST		3520.294	1.92698803
GF200	666377	AA232647	4A232647 Hs.6557	Hs.167558	zinc finger protein 161	ZNF161	3520.093	1.02381068
GF200	666377	AA232647	AA232647 Hs.83611	Hs.167558	zinc finger protein 161	ZNF161	3520.093	1.02381068
					SMT3 (suppressor of mif two			
GF203	1472719	AA872379	AA872379 Hs.85119	Hs.85119	3, yeast) homolog 1	SMT3H1	3518.163	1.32705707
GF203	785342	AA476494	AA476494 Hs.47246	Hs.172788	ALEX3 protein	ALEX3	3517.986	1.41806872
GF200	134525	R27581	Hs.18283	Hs.78946	cullin 3	CUL3	3517.622	1.09737864
GF202	344550	W73597	Hs.58317	Hs.229128	EST		3513.438	-1.179242
GF200	239708	H79640	Hs.46158	Hs.262198	ESTs		3512.326	1.25271456
GF203	306513	N91811	Hs.35092	Hs.35092	ESTs		3511.446	1.09234051
GF203	269612	N24163	Hs.45033	Hs.222579	ESTs		3509.851	-1.9317933
GF200	196148	R92352	Hs.14478	Hs.14478	ESTs		3508.348	2.22158562
GF200	132373	R26526	Hs.64025	Hs.64025	basonuclin	BNC	3507.649	1.0971792
GF204	859654	AA666418	3 Hs.9728	Hs.9728	ALEX1 protein	LOC51309	3505.818	
GF202	773083	AA425307	4A425307 Hs.22581	Hs.22581	ESTs		3505.452	1.32940795
GF202	241241	H81083	Hs.114247	Hs.205893	ESTs		3505.146	-1.0379971
					lymphocyte cytosolic protein 1			
GF201	344589	W73144	Hs.76506	Hs.76506	(L-plastin)	LCP1	3500.37	
GF204	1420810	AA826251	AA826251 Hs.130862	Hs.192040	ESTs		3499.785	
GF201	51743	H23081	Hs.26396	Hs.117077	zinc finger protein 264	ZNF264	3499.615	
					upidniin specilic protease /	1	007 1070	4 000004
GF200	525518	AA064681	4A064681 Hs./8683	HS./8683	(nerpes virus-associated)	USF/	3496 224	1.36716618
20210	220360	HARATE	He 40528	He 40528	ESTS		3496.114	1.13733323
200	322286	W39600	Hs 22003	Hs 22003	ESTS		3488.025	1.24727897
GF201	70027	T48767	Hs.76061	Hs.173936	interleukin 10 receptor, beta	IL10RB	3484.596	

1.63837717

1.27903317

1.4170316

1.30995018

1.0716561

1.24180805 1,14900336 .22246668 1.07712162

-1.0015371	1.52610628 1.26370039		1.19959808	1.05650805		1.05488314	-1.2370698	1.49219873
3458.192	3457.612 3456.594	3454.987	3450.894	3448.493 3447.458	3446.921	3445.54	3445.344	3442.113 3441.274 3440.066 3437.66
CITED1	DKFZP434F2021		CG005		CEACAM5	ATP50	YG81	LRRFIP1 MBNL
Cbp/p300-interacting transactivator, with Glu/Asprich carboxy-terminal domain, 1 ESTs, Highly similar to transcription elonoation factor	TEIIS.h [H.sapiens] DKFZP434F2021 protein Homo sapiens mRNA; cDNA DKFZp761C1712 (from clone	DKFZp761C1712) Homo sapiens mRNA; cDNA DKFZp564D1462 (from clone DKFZp54D1462)	hypothetical protein from BCRA2 region	ESTs ESTs	cardinoening yonic anugenrelated cell adhesion molecule 5 ATP synthase, H+ transporting, mitochondrial F1	complex, O subunit (oligomycin sensitivity conferring protein) ESTs, Weakly similar to transformation-related protein	[H.sapiens] chromosome 21 open reading frame 7	leucine rich repeat (in FLII) interacting protein 1 muscleblind (Drosophila)-like EST ESTs
Hs.40403	Hs.94952 Hs.78277	Hs.4774 Hs 85335	Hs.23518	Hs.101191 Hs.117582	Hs.220529	Hs.76572	Hs.24529 Hs.49391	Hs.239894 Hs.28578 Hs.116807 Hs.138660
AA432143 Hs.40403	R09980 Hs.62527 AA426041 Hs.111666	R15441 Hs.4774 M15339 Hs.55331		Hs.101191 Hs.29569	AA130584 Hs.84960	1472150 AA873577 Hs.76572	R06599 Hs.106193 AA400378 Hs.49391	AA085597 Hs.61771 AA777913 Hs.121985 AA634132 Hs.116807 N24880 Hs.43486
AA4321	R09980 AA4260	R15441	N59893	R45367 N90608	AA1305	AA8735	R06599 AA4003	AA085597 AA777913 AA634132 N24880
781510	128738 773430	52990	289677	35769 306300	586706	1472150	126447	562927 449340 858363 269878
GF200	GF200 GF202	GF201	GF203	GF203 GF201	GF201	GF203	GF201 GF202	GF200 GF204 GF204 GF201

Ally DOCKEL NO. 21720	3435.258 3430.896	2 3430.712	3429.853 2.55320877 3427.092	3426.471 3425.787 1.13487706		•		3421.352 1.3430687	3420.457 1.12071888 3419.915	3412.886 1.45762496 3411.658		3411.508 144 3409.948 1.10549322 3408.086 1.16810963	3406.005 1.18400202 3404.599 -1.1981551
		UBE2D2	E	TLE3				СОСН		RNF6	i i	KIAA0944 RIAA0944 PLAB	FACL3
APPENDIX A	ESTs, Weakly similar to /prediction ESTs ubiquitin-conjugating enzyme EST /propertyme ubiquitin-conjugating enzyme	UBC4/5)	thromboplastin antecedent) ESTs	transducin-like ennancer of split 3, homolog of Drosophila E(sp1)	ESTS ESTs	ESTS	coagulation factor C (Limulus polyphemus) homology	(cochlin) Homo sapiens cDNA FI.110972 fis. clone	PLACE1001000 ESTs	type) 6 ESTs	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein	(liprin), alpha 2 KIAA0944 protein prostate differentiation factor fattv-acid-Coenzyme A ligase.	long-chain 3 ESTs
	Hs.6667 Hs.55118	Hs.108332	Hs.1430 Hs.274231	Hs.31305	Hs.113759	Hs.12891		Hs.21016	Hs.3542 Hs.7404	Hs.32597 Hs.16603		Hs.30881 Hs.97403 Hs.116577	Hs.268012 Hs.4811
	Hs.6667 Hs.55118	AA431869 Hs.108332	R89539 Hs.34226 AA452151 Hs.99266	AA136692 Hs.103850	Hs.19227	Hs.12891		Hs.21016	AA504164 Hs.3542 AA931102 Hs.7404	N57005 Hs.32597 AA129974 Hs.16603		H08850 Hs.30881 AA620890 Hs.97403 AA450062 Hs.64037	W31074 Hs.24550 AA193405 Hs 4811
	H17038 N95187	AA431869	R89539 AA452151	AA136692	R01706	W96189		R60995	AA504164 AA931102	N57005 AA129974		H08850 AA620890 AA450062	W31074
k et al.	50582 307244	773617	195358 787867	490971	123700	361659		42627	825176 1554167	277589 503682		46055 1055588 788832	310493
Westbrook et al.	GF201 GF201	GF201	GF200 GF204	GF201	GF200 GF200	GF203		GF202	GF203 GF204	GF203 GF201		GF201 GF202 GF200	GF200

	17 17 1				the later dies. July later was a series of the later of t	tons franch Bard Shadl Street	Attv	Atty Docket No. 21726
Westbrook et al.	۲ وا ما				APPENDIX A			
GF204	392096	AI003694	Al003694 Hs.130344	Hs.130344	EST		3400.814	
					ESTs, Weakly simitar to BE I A- GALACTOSIDASE			
GF204	1502466	AA894618 Hs.32764	Hs.32764	Hs.181173	PRECURSOR [H.sapiens] DEAD/H (Asp-Glu-Ala-		3400.713	
GF200	814119	AA465460	AA465460 Hs.115286	Hs.171872	Asprins) box polypeptide o (RNA helicase) chemokine (G-C motif)	DDX8	3400.659	1.02195101
GF200	247281	N57964	Hs.46468	Hs.46468	receptor 6	CCR6	3400.433	1.52215789
GF202	742737	AA400154 Hs.97785	Hs.97785 Hs 38/7	Hs.157526 Hs 3847	ESTS	PNUTL1	3396.976	1.09045355
8					ESTs, Weakly similar to transposon LRE2 reverse transcriptase homolog			
GF201	325172	W48580	Hs.39972	Hs.39972	[H.sapiens]		3393.915	
GF201	233277		Hs.108429	Hs.270149	ESTs		3392.741	
GF202	841471	AA487241	AA487241 Hs.124837	Hs.269414	ESTs		3392.515	-1.5641141
GF200	208699	H61003	Hs.101150	Hs.244452	EST		3389.606	-1.14/49/5
GF204	1474670	AA857001	AA857001 Hs.125108	Hs.189090	ESTs		3388.622	
GF204	1048678	AA608847 Hs.97514	Hs.97514	Hs.97514	ESTs		3386.832	
					Homo Sapiens minima for		2000 400	1 10001017
GF203	726661	AA398246 Hs.97594	Hs.97594	Hs.97594	KIAA1210 protein, partial cos Human DNA seguence from		3303.403	1.10291917
					clone RP1-12G14 on			
					chromosome 6q24.1-25.2.			
					Contains the 5' end of the			
					gene for a novel cyclophilin			
					type peptidyl-prolyl cis-trans			
					isomerase, a novel gene, an			
					RPS18 (40S Ribosomal			
GF203	257155	N26840	Hs.43863	Hs.240767	3' end of the KATNA1 ge		3385.258	-1.8580921
GF202	285581	N66454	Hs.49203	Hs.49203	ESTs		3382.421	1.70551035
GF201	126713	R07115	Hs.19890	Hs.271224	ESTs		3381.605	

1.35655103	1.03959216 1.16656233 1.11995877	-2.2237235 1.29759072 1.23845072	1.52514509	1.41436934 2.91526598	1.2475073	1.34715028
3381.453 3378.747 3377.14 3376.016	3372.438 3371.893 3366.997	3366.55 3366.55 3365.495 3364.935	3364,679	3364.057 3359.543 3358.753	3358.115 3357.559 3352.94	3352.888 3350.713
KIAA1240	CYP2E THBD	TRN2		HSPG2	ATP5B TUBA2 HSPC219	
ESTS, Weakly similar to rab- related GTP-binding protein [H sapiens] ESTs ESTs KIAA1240 protein	cytochrome P450, subfamily IIE (ethanol-inducible) ESTs thrombomodulin	karyophenin beta 2b, transportin EST ESTs	ESTs, Weakly similar to IIII ESTs, Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens] heparan sulfate proteoglycan 2	(perlecan) ESTs ESTs ATP synthase, H+	iransporting, mitochonornal F1 complex, beta polypeptide tubulin, alpha 2 hypothetical protein ESTs, Weakly similar to similar to zinc metalloprotease family of peptidases	[C.elegans] ESTs
Hs.24970 Hs.269181 Hs.44367 Hs.62576		Hs.278378 Hs.26457 Hs.14763 Hs.72087		Hs.211573 Hs.39474 Hs.103262	Hs.25 Hs.98102 Hs.9196	Hs.13056 Hs.268841
AA705288 Hs.104461 M92798 Hs.20260 M15500 Hs.44367 H51886 Hs.62576	4	9 93	AA448484 Hs.8154 AA088430 Hs.63037	AA427561 Hs.75578 473304 Hs.39474 AA598635 Hs.103262	AA708298 Hs.25 AA626698 Hs.7616 Al004187 Hs.9196	AA404341 Hs.13056 R95916 Hs.34431
462807 AA70528 418400 W92798 322896 W15500 39574 R51886			•	770059 AA42 235026 H733 897874 AA59	392622 AA70 745138 AA62 1631829 Al00v	758301 AA40434 199327 R95916
GF204 GF201 GF201 GF201	GF200 GF203 GF200	GF203 GF202 GF201 GF203	GF201	GF201 GF200 GF203	GF203 GF201 GF204	GF201 GF200

	1.11395833	1.04748415	1.42575494	1.59845765		1.01133361			-1.142895	1.24180972		1.41090429		-1.110606	1.51541072			1.32652664	-1.1334599			1.06874864			-1.0348114				-1.1518146	1.0072099	1.30956286
3348.385	3347.491	3346.737	3344.645	3343.159		3342.449	3341.053		3339.92	3335.355		3332.345		3332.004	3330.725			3329.231	3328.394			3325.615			3325.031	100	3323.861	3323.172	3322.388	3320.908	3339.091
HSPA10	s ARVCF				_	EIF4G2						ALDOA		EPHX1						ity		SLC1A1									
heat shock 70kD protein 10 (HSC71)	armadillo repeat gene deletes in velocardiofacial syndrome	ESTs	ESTs	EST	eukaryotic translation initiation	factor 4 gamma, 2	ESTs	ESTs, Weakly similar to	F31D4.2 [C.elegans]	EST	aldolase A, fructose-	bisphosphate	epoxide hydrolase 1,	microsomal (xenobiotic)	ESTs	Homo sapiens cDNA	FLJ20360 fis, clone	HEP16677	ESTs	solute carrier family 1 (neuronal/epithelial high affinity	glutamate transporter, system	Xag), member 1 Himan DNA from	chromosome 19-specific	cosmid R30923, genomic	sednence	ESTs, Moderately similar to	mBOCT [M.musculus]	ESIS	ESTs	EST	ESTs
Hs.180414	Hs.171900	Hs.46670	Hs.47193	Hs.98142		Hs.183684	Hs.120749		Hs.15929	Hs.50284		Hs.273415		Hs.89649	Hs.59529			Hs.26434	Hs.108790			Hs.91139			Hs.77876		Hs.21974	Hs.154/01	Hs.126639	Hs.230568	Hs.268651
AA629567 Hs.103424	H17975 Hs.14636	4	N51079 Hs.47193	AA412477 Hs.98142			AI004349 Hs.120749		AA449754 Hs.15929	N73510 Hs.50284		AA775241 Hs.75181		AA838691 Hs.89649	W94363 Hs.59529			N27933 Hs.109024				AA504845 Hs.91139			AA705966 Hs.119943		AA862473 Hs.21974	Q			T98458 Hs.18394
01 884719	50413		.,	02 730146		02 357190	04 1624497		03 785795	00 295873		03 878578		03 1387760	02 358800			02 270134				03 825742			03 1239840			•	_	-	00 122161
GF201	GE200	GF203	GF202	GF202		GF202	GF204		GF203	GF200		GF203		GF203	GF202			GF202	GF200			GF203			GF203		GF204	GF201	GF203	GF202	GF200

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GF200	795827	AA461506 Hs.79358	Hs.79358	Hs.79358	testis-specific kinase 1 cyclin-dependent kinase inhibitor 2A (melanoma, p16,	TESK1	3319.075	1.07029354
GF203 GF201	1161155 344975	AA877595 Hs.1174 W73010 Hs.32219	Hs.1174 Hs.32219	Hs.1174 Hs.179779	inhibits CDK4) ribosomal protein L37 ESTs, Weakly similar to IIII ALU SUBFAMILY SB2 WARNING FNTRY IIII	CDKN2A RPL37	3317.71	1.781059
GF203	289653	N59885	Hs.113660	Hs.113660	[H.sapiens] a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin		3316.609	-1.3212281
GF200 GF201	727026 322860	AA402760 Hs.27916 W44933 Hs.10642	Hs.27916 Hs.106423	Hs.27916 Hs.42676	type 1 motif, 3 KIAA0781 protein	ADAMTS3 KIAA0781	3316.462 3315.68	1.34873864
GF203 GF200	754002 262932	AA479972 Hs.85591 H99699 Hs.75900	Hs.85591 Hs.75900	Hs.85591 Hs.75900	ESTs aconitase 2, mitochondrial nuclear receptor subfamily 4.	ACO2	3315.559 3315.13	-1.2967679 1.11012697
GF201	309893	N94487	Hs.1119	Hs.1119	group A, member 1 karyopherin beta 2b,	NR4A1	3313.153	
GF201 GF202	127860 282327	R08897 N51964	Hs.20180 Hs.47382	Hs.278378 Hs.47382	transportin EST autocrine motility factor	TRN2	3311.187 3310.132	-1.0181254
GF200	753897	AA479243 Hs.80731	Hs.80731	Hs.80731	receptor periodontal ligament fibroblast	AMFR	3306.698	1.12242738
GF203	823954 273425	AA490843 Hs.7101 N33195 Hs.4272	Hs.7101 Hs.42722	Hs.7101 Hs.42722	protein ESTs	PDL-108	3305.951 3305.285	-1.0851944 1.22327101
GF200 GF204	124824 757255	75	Hs.76067 Hs.98453	Hs.252574 Hs.98453	ribosomal protein L10a ESTs	RPL10A	3304.749 3303.961	1.27867328
GF200	840404	AA485653 Hs.94246	Hs.94246	Hs.172195	mannosyl (alpha-1,6-)- glycoprotein beta-1,2-N- acetyglucosaminyltransferase MGAT2	9 MGAT2	3303.711	1.0856298
GF200	840404	AA485653 Hs.36573	Hs.36573	Hs.172195	mannosyl (alpha-1,6-)- glycoprotein beta-1,2-N- acetylglucosaminyltransferase MGAT2	• MGAT2	3303.711	1.0856298

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GF202 GF203 GF202 GF201	593780 796643 594633 810008	AA159729 Hs.72350 AA461473 Hs.10977 AA171613 Hs.5338 AA454867 Hs.15869	Hs.72350 Hs.10977 Hs.5338 Hs.15869	Hs.252124 Hs.5025 Hs.5338 Hs.165662	ESTs nebuleite carbonic anhydrase XII KIAA0675 gene product natural killer cell receptor,	NEBL CA12 KIAA0675	3303.325 3303.318 3303.121 3303.114	2.06258644 1.34015178 -1.1063293
GF202	797055	AA463248 Hs.81743	Hs.81743	Hs.81743	immunoglobulin superfamily member ESTs, Moderately similar to !!!! ALU SUBFAMILY SX	BY55 !!	3302.986	-1.2287644
GF203 GF202	413120 290251	AA707819 N62275	AA707819 Hs.124885 N62275 Hs.48503	Hs.241160 Hs.48503	WAHNING EN INY !!!! [H.sapiens] EST EST	.	3302.217 3302.069	-1.8312836 1.18691253
GF201	757144	AA496097 Hs.83267 H16801 Hs.5354	Hs.83267 Hs.5354	Hs.249247 Hs.5354	Similar to far hells destabilishing protein to protein Homo sapiens mRNA; cDNA DKFZp434N0317 (from clone DKFZp434N0317)	FBRNP	3300.75	
GF200	795330	AA453202 Hs.724	Hs.724	Hs.276916	nuclear receptor subfamily 1, group D, member 1 Homo sapiens cDNA	NR1D1	3298.534	1.08378115
GF200 GF201	244202 308747	N52973 N93255	Hs.100069 Hs.101451	Hs.278619 Hs.128754	FLJ10099 fis, clone HEMBA1002462 ESTS Homo sapiens mRNA; cDNA NFZP554A186 ffrom clone		3296.982 3293.175	-1.9432978
GF201 GF203	810795 134168	AA458876 R30956	AA458876 Hs.104916 R30956 Hs.52308	Hs.104916 Hs.268689	DKFZp564A186) ESTs nolymerase (DNA directed).		3289.429 3289.199	1.15689486
GF202 GF201	786078 196070	AA448664 R89374	AA448664 Hs.99185 R89374 Hs.17842	Hs.99185 Hs.275040	epsilon 2 ESTs Homo sapiens hepatic anglopoletin-related protein	POLE2	3289.048 3289.048	1.57871738
GF200 GF201	310356 322695	W30988 W15386	Hs.9613 Hs.13278	Hs.9613 Hs.26750	cds ESTs		3287.528 3283.619	1.12487167

GF203 GF203	150058 701778	H00982 Hs.96513 AA292659 Hs.93667	Hs.96513 Hs.93667	Hs.96513 Hs.93667	ESTs ESTs		3248.502 3247.142	1.04602844 -1.0327286
GF200	357046	W93472	Hs.1323	Hs.1323	-	CNGA1	3246.669	1.14331569
GF201	325024	AA284236 Hs.89318	Hs.89318	Hs.93379	eukaryotic translation initiation factor 4B	EIF4B	3245.952	
GF200 GF202 GF201	210548 731319 195547	H65052 Hs.37926 AA416770 Hs.98255 R89225 Hs.10782	Hs.37926 Hs.98255 Hs.107827	Hs.76530 Hs.98255 Hs.177291	coagulation factor II (thrombin) F2 EST ESTs Homo sapiens mRNA, chromosome 1 specific	F2	3244.669 3241.063 3236.24	-1.0794437
GF204	1460375	AA883597 Hs.15019	Hs.15019	Hs.92381	transcript KIAA0487		3235.804	
GF202 GF201 GF201	744647 343867 129766	AA621315 Hs.58488 W69954 Hs.76364 R12785 Hs.21160	Hs.58488 Hs.76364 Hs.21160	Hs.58488 Hs.76364 Hs.21160	_	CTNNAL1 AIF1	3235.541 3235.241 3232.104	1.29050619
GF203 GF201	753034 285344	AA436459 Hs.35841 N66336 Hs.7360	Hs.35841 Hs.7360	Hs.35841 Hs.7360	ā	NFIX	3231.83 3227.837	1.14417931
GF203 GF203	37665	R61374 R50775	Hs.26878 Hs.21992	Hs.234434 Hs.21992	with YRPW motif 1 KIAA0689 protein Homo sapiens clone 24758	HEY1 KIAA0689	3226.394	1.03945775
GF202 GF201 GF201 GF204	40010 324345 429353 234985	H54036 HS.10602 W47585 HS.4074 A400752 HS.15726 H79123 HS.53454 A700500 LS.1449	H54036 Hs.10602/ W47585 Hs.44074 AA007522 Hs.15726 H79123 Hs.53454	HS.18580/ HS.44074 HS.138777 HS.53454	mrivA sequence ESTs, Highly similar to KIAA0810 protein [H.sapiens] ESTs ESTs		3225.08 3221.849 3221.535	-1.103613
GF201 GF201	53092 501981	R15785 Hs.110 AA128561 Hs.4107	Hs.110 Hs.41071	Hs.110 Hs.117938	putative L-type neutral amino acid transporter collagen, type XVII, alpha 1	KIAA0436 COL17A1	3217.687 3217.324	
GF201	284479	N52350	Hs.3843	Hs.3843	dual specificity phosphatase 7 DUSP7	DUSP7	3215.064	

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GF201	120678	T95650	Hs.17646	Hs.17646	ESTs		3213.34	
GF202	754008	AA478965	AA478965 Hs.64084	Hs.173043	metastasis-associated 1-like 1 MTA1L1	MTA1L1	3212.543	1.59685286
GF201	810621	AA464/44 TEG056	4A464/44 Hs.105061 F66956 Hs 64946	Hs.105061 Hs 5807	KIAA1111 protein hynothetical protein	NIAATTIT DKFZnZ62K0911	3208.65	1.13019892
GF201	52191	H24355	Hs.28255	Hs.28255	ESTs		3206.931	
					Fn14 for type I			
GF200	135791	R33355	Hs.100507	Hs.10086	transmenmbrane protein	LOC51330	3206.702	-1.1823054
GF204	1505893	AA907721	AA907721 Hs.128610	Hs.128610	ESTs		3205.978	
					translocase of inner			
					' Illinocitoridi al Ille Illoria le o	-	10000	4 00447400
GF202	359836	AA011211	4A011211 Hs.110250	Hs.268561	(yeast) nomolog B	LIMIMSB	3202.167	1.0941/402
GF202	772470	AA40558E	AA405588 Hs.110352	Hs.174038	ESTs		3201.875	-1.1296217
GF202	757190	AA443958	AA443958 Hs.90960	Hs.90960	ESTs		3201.11	1.11041426
GF201	82869	T69270	Hs.11805	Hs.11805	ESTs		3199.97	
					lymphotoxin alpha (TNF			
GF201	345232	W72329	Hs.36	Hs.36	superfamily, member 1)	LTA	3197.229	
					Homo sapiens cDNA			
GF201	841624	AA487462	AA487462 Hs 7537	Hs.179669	FLJ20637 fis. clone KAT03212		3195.079	
GESON	47043	H10721	Hs 9973	Hs 154138	chitinase 3-like 2	CHI3L2	3193.553	1,20504545
GE200	322447	W16425	Hs 55315	Hs 55315	EST		3193,365	1.20747772
Grzuz	355441	V 10423	19:00:01	0.000	Homo saniens CDNA			
					FLJ20061 fis, clone			
GF202	648047	AA207083	4A207083 Hs.7576	Hs.7576	COL01383		3190.91	1.71862406
GF200	142733	B71414	Hs.29160	Hs.271736	ESTs		3190.83	1.05784983
GF204	1055737	AA628146	"	Hs.118747	ESTs		3190.12	
GF201	289107	N63623	Hs.44291	Hs.242271	KIAA0471 gene product	KIAA0471	3189.76	
GF203	294591	N71061	Hs.109507	Hs.30376	hypothetical protein	HSPC194	3189.432	1.04125491
GF204	502791	AA126914	4A126914 Hs.16930	Hs.16930	ESTs		3184.943	
					interferon, alpha-inducible			
GF200	782513	AA43203(AA432030 Hs.118288	Hs.265827	protein (clone IFI-6-16) Homo saniens clone 24466	G1P3	3182.51	1.25240519
CE201	467.40	H10068	He 05024	He 25924	mBNA segrence		3182.506	
GF200	321189	W53016	RG.38	Hs.156764	DKFZP586H0723 protein	DKFZP586H0723	3180.743	1.25216613

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-1.1715679 1.10175609	1.21366747		1.15583322	1.27753771 1.07353678	-1.1402243	1.06965021	1.26957349 1.0301339	1.81988242	1.10554197	1.15397043		-1.2707422 1.04932761
3178.36 3178.054	3178.035	3176.395	3176.284	3169.824 3167.773	3167.738	3166 086	3164.49 3164.149	3158.788 3157.688	3156.603 3155.172	3154.568	3154.432	3153.177 3150.284
	PIK3C2B	PRRG2	EIF3S2	STAT5B						ΓΟΧ	HAB36	CXORF1
ESTS, Moderately similar to COLLAGEN ALPHA 1(XII) CHAIN [R.norvegicus] ESTS	prosprintositude-5-rintase, class 2, beta polypeptide proline-rich Gla (G-	polypeptide 2 eukaryotic translation initiation factor 3. subunit 2 (beta,	36kD) signal transducer and activator	of transcription 5B ESTs ESTs, Moderately similar to	pIL2 hypothetical protein [R.norvegicus]	ESTs, Weakly similar to weakly similar to gastrula zinc	ESTs ESTs	ESTs, Weakly similar to T09A5.6 [C.elegans] ESTs ESTs, Moderately similar to	K02E10.2 [C.elegans] EST	lysyl oxidase RAB36, member RAS	oncogene family chromosome X open reading	frame 1 ESTs
Hs.16869 Hs.24895	Hs.132463	Hs.35101	Hs.192023	Hs.244613 Hs.148504	Hs.5243	78851	Hs.47026 Hs.96125	Hs.13885 Hs.93338	Hs.11067 Hs.121963	Hs.102267	Hs.38772	Hs.106688 Hs.86489
AA478481 Hs.16869 AA495952 Hs.24895	AA699876 Hs.101238	AA430552 Hs.35101	AA936783 Hs.89996	AA282023 Hs.2287 N59474 Hs.54118	AA437236 Hs.5243	79991 NU 9967794 N	4A487846 Hs.47026 A22252 Hs.96125	AA460004 Hs.13885 H73013 Hs.93338	T62552 Hs.11067 AA777700 Hs.121963	16	N47972 Hs.46778	R59087 Hs.106688 W52273 Hs.54485
786609 ,	461327	770074	1486109	712840 284681	757462	47.47.00	840726 130835	795606	79726	789069	281489	41940 325365
GF202 GF203	GF203	GF201	GF203	GF200 GF202	GF203	C	GF202 GF200 GF200	GF201 GF200	GF201 GF203	GF200	GF201	GF202 GF200

1.04932761 2.21255805	1.34216864	1.37614388	1.73891745 -1.7015876 2.06181916	1.07277256	1.08275696	-2.2199454 2.09865497 -1.1616457 1.9394552
3150.284 3148.875	3148.48 3147.721 3147.347 3145.879	3141.188 3140.422 3140.114	3139.099 3136.657 3134.128 3134.087	3132.649 3132.078 3131.23 3127.109	3126.964 3124.03 3120.387	3118:045 3118:574 3118:574 3118:408 3117:636 3115:311
	KIAA0220 CPD MYO5B	GRM3		PMAIP1 YDD19 HLA-DRB1	LOC51663 SAM68	KIAA0663 KIAA0404
ESTs ESTs	Homo sapiens cDNA FL20688 is, clone KAIA2890 KIAA0220 protein carboxypeptidase D myosin VB Homo sapiens clone DT171A10 mRNA, CAG	repeat region glutamate receptor, metabotropic 3 EST	ESTS ESTS ESTS ESTS	protoute Trynstae To- protoute Trynstae To- YDD19 protein ESTs major histocompatibility complex, class II, DR Beta 1 M-phase phosphoprotein	homolog GAP-associated tyrosine phosphoprotein p62 (Sam68) ESTs, Weakly similar to B0495.6 [C.elegans]	ESTs ESTs KIAA0663 gene product ESTs KIAA0404 protein ESTs
Hs.86489 Hs.170310	Hs.99115 Hs.110613 Hs.5057 Hs.172506	Hs.178207 Hs.3786 Hs.102935	Hs.6591 Hs.48926 Hs.119945 Hs.180187	Hs.96 Hs.25615 Hs.53126 Hs.180255	Hs.173518 Hs.119537 Hs.110695	Hs. 183767 Hs. 129871 Hs. 17969 Hs. 30484 Hs. 105850 Hs. 29390
W52273 Hs.86489 R98295 Hs.8520	AA447553 Hs.99115 R84893 Hs.77479 T56021 Hs.85101 AA460302 Hs.26941	AA464965 Hs.61810 AA670430 Hs.3786 N95073 Hs.102935	440	AA458838 Hs.96 AA45827 Hs.62707 AA432081 Hs.53126 AA664195 Hs.114210	AA045458 Hs.37946 AA995783 Hs.119537 R78514 Hs.110695	AA025662 Hs. 103001 R64103 Hs. 129871 AA486288 Hs. 17969 H23137 Hs. 30484 AA875955 Hs. 105850 AA458827 Hs. 29390
325365 206816	782622 275180 73268 795754	810093 878838 305408	35758 435056 395409 428952	814353 809960 784142 855547	487850 1606780 144926	365877 139586 842847 52303 1492258 814350
GF200 GF200	GF201 GF200 GF200 GF201	GF201 GF201 GF202	GF202 GF203 GF203 GF201	GF201 GF201 GF202 GF201	GF204 GF204 GF200	GF201 GF203 GF202 GF201 GF203

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Atty Docket No. 21726/92526

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Atty Docket No. 21 /26/92	-1.0211104 1.15619853	2.10720247	1.29807106			-1.0339105				1.50811414	1.21273046		-1.3328249	-1.1686022			1.77891622		1.19714427	-1.5465553	1.38263634			1.32925173			1.03291783	-1.0946235		-2.1186654		-1.2698188	
Atty	3113.649	3113.025	3107.562		3106.253	3103.157	3102.468	3101.337	3100.738	3100.674	3099.143		3098.76	3096.946		3096.505	3093.755		3086.041	3086.028	3085.344			3084.627	3083.58		3081.652	3080.757	3078.96	3071.94		3071.899	
	CLCN4	CD34	YDD19			HARP				KIAA0676	MLANA		2	KIAA0685		SHB			IGFBP3	KIAA1029				DDX5	FGL1							MAZ	
APPENDIX A	chloride channel 4	CD34 antigen	YDD19 protein	ESTS, Weakly similar to unknown protein	[R.norvegicus]	HepA-related protein	ESTs	ESTs	ESTs	KIAA0676 protein	melan-A	Lutheran blood group	(Auberger b antigen included)	KIAA0685 gene product	SHB adaptor protein (a Src	homology 2 protein)	ESTs	insulin-like growth factor	binding protein 3	synaptopodin	EST	DEAD/H (Asp-Glu-Ala-	Asp/His) box polypeptide 5	(RNA helicase, 68kD)	fibrinogen-like 1	Homo sapiens cDNA	FLJ20484 fis, clone KAT07770	EST	ESTs	ESTs	MYC-associated zinc finger protein (purine-binding	transcription factor)	
	Hs.199250 He 66450	Hs.85289	Hs.25615		Hs.192265	Hs.16933	Hs.43894	Hs.191223	Hs.153800	Hs.155829	Hs.154069		Hs.155048	Hs.153121		Hs.244542	Hs.205260		Hs.77326	Hs.5307	Hs.98534			Hs.76053	Hs.107		Hs.5080	Hs.121999	Hs.55256	Hs.270231		Hs.7647	
	AA019316 Hs.32790	H72113 Hs.108360	T86027 Hs.7900		N27758 Hs.43993	유	N27154 Hs.43894	AA777372 Hs.122499	_	_	N26562 Hs.67555		H24954 Hs.119481	AA490924 Hs.71846			N69574 Hs.93012		AA449821 Hs.104571	AA664237 Hs.5307	AA427858 Hs.98534			AA460957 Hs.50131	AA677287 Hs.107		AA489022 Hs.5080	요	W02227 Hs.55256	R66923 Hs.101489		AA704613 Hs.7647	
κetal.	363058	213635	112576		255777	450131	269820	448667	220608	127549	266361		160656	824557		323950	293510		788617	855610	773464			796126	454771		824911	449513	327425	140299		450777	
Westbrook et al.	GF200	GF202	GF200		GF204	GF203	GF201	GF204	GF201	GF203	GF200		GF200	GF203		GF201	GF200		GF203	GF203	GF202			GF202	GF201		GF203	GF203	GF201	GF203		GF203	

-1.0415365 1.3729304	1.1000696	1.69902677	1.57712814	1.11412746	1.88870383
3070.792 3070.541	3068.548 3067.785 3067.409 3067.098 3066.428 3062.931	3062.009	3060.916 3060.511 3059.634 3059.076	3055.079 3054.011 3052.898 3051.481 3050.936 3044.06	3042.267 3040.609 3039.031 3036.286 3035.109
DKFZP434B168	BCL7B		NDUFB7 GYPC	IDUA NXPH3 OCLN	
DKFZP434B168 protein ESTs Homo sapiens mRNA for	KIAA1228 protein, partial ods ESTs B-oell CLL/lymphoma 7B ESTs EST EST	ESTs, Highly similar to F1954_1 [H.sapiens] ESTs NADH dehydrogenase (ubiquinone) 1 beta	subcomplex, 7 (18KD, B18) glycophorin C (Gerbich blood group) ESTs ESTs	EST ESTs, Moderately similar to MLN 62 protein [H-saptens] utoronidase, alpha-L- ESTs neurexophilin 3 neurexophilin 3 cocididin Homo saaiens cDNA	FLJ11271 fis, clone PLACE100319, moderately similar to Ratus 10, rovegicus outer membrane protein mRNA ESTs ESTs ESTS
Hs.48604 Hs.42721	Hs.22151 Hs.7459 Hs.16269 Hs.25068 Hs.121308 Hs.269436	Hs.166357 Hs.87327	Hs.661 Hs.81994 Hs.45057 Hs.239052	Hs.35437 Hs.89560 Hs.138517 Hs.55069 Hs.71952	Hs. 109654 Hs. 66960 Hs. 16617 Hs. 260657 Hs. 182585
H69691 Hs.38900 H99722 Hs.42721	AA885126 Hs.125738 N56925 Hs.7459 AA291513 Hs.16269 R49117 Hs.25068 AA758268 Hs.121308 T90446 Hs.51732	AA977282 Hs.128834 AA460369 Hs.87327	AA428058 Hs.112342 W74668 Hs.81994 AA452140 Hs.45057 N29465 Hs.43720	AA777428 Hs.121919 H95689 Hs.35437 AA988345 Hs.89560 N70411 Hs.81010 W52190 Hs.55069 H94471 Hs.93518	AAB88224 Hs.109654 AA702195 Hs.69960 M69170 Hs.83475 H60317 Hs.37832 W68753 Hs.57688
212784 H64 262968 H99	1466529 AA 280039 N57 724831 AA 3804 R4 396880 AA 110903 T90	m	344720 W7 787860 AA 270376 N2		1492285 AA 384140 AA 343695 WE 207881 H6
GF202 GF202	GF204 GF204 GF201 GF203 GF203	GF204 GF202	GF201 GF203 GF203 GF201	GF203 GF204 GF201 GF201 GF201	GF204 GF203 GF201 GF201 GF200

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	3033.01	3031.968	07000	3027.340	3023.152		3020.778	3019.102	3017.686	3014.78		į	3014.778	3014.596	3011.508	3011.287			3011.208	3009.023		3008.939	3004.434	3002.7		3002.323		97,000	90.1006
	CCT2	KIAA0092	č	KAF			PKD2						CRSP8	DKFZP547E1010		KIAA0855			ATP1B2	YDD19						TGFB2		College	IAF3C
chaperonin containing TCP1,	subunit 2 (beta)	KIAA0092 gene product	I RFZ-Interacting teromenc	HAP1 protein	ESTs	polycystic kidney disease 2	(autosomal dominant)	ESTs	ESTs	ESTs	cofactor required for Sp1	transcriptional activation,	subunit 8 (34kD)	DKFZP547E1010 protein	EST	golgin-67		ATPase, Na+/K+ transporting,	beta 2 polypeptide	YDD19 protein	ESTs, Weakly similar to	CAGH4 [H.sapiens]	ESTs	ESTs	transforming growth factor,	beta 2	TATA box binding protein	(TDP)-associated factor, nive	polymerase III, C, 90kD
	Hs.6456	Hs.151791		Hs.274428	Hs.221979		Hs.82001	Hs.137260	Hs.189866	Hs.47501			Hs.28166	Hs.227391	Hs.57653	Hs.182982			Hs.78854	Hs.25615		Hs.41641	Hs.58714	Hs.30853		Hs.169300			Hs.32935
	N38959 Hs.6456	C)		W43028 Hs.109875	AA680379 Hs.125121		R48232 Hs.82001	AA284259 Hs.100632	AA679306 Hs.117881	N66852 Hs.47501			AA490614 Hs.28166	AA628232 Hs.106575	AA037399 Hs.57653	AA099819 Hs.110733			H14841 Hs.78854	W32409 Hs.42304		AA669357 Hs.114944	AA465354 Hs.58714	H08428 Hs.30853		N45138 Hs.82468			AA453787 Hs.32935
	243343	489662		329059	431668		153473	325150	432097	295630			824132	1055764	321253	489798			48799	321376		884838	814084	45728		282978			813738
	GF200	GF201		GF202	GF203		GF200	GF201	GF203	GF200			GF203	GF203	GF202	GF202	5		GF200	GF201		GF204	GF203	GF201		GF201			GF202

Homo sapiens cDNA FLJ10752 fis, clone NT2RP3004480, weakly

	1.20924336	1.30070635					1.38703697	1.1472803			-1.5488996			-1.2715238	1.28041518	-1.9418067			-1.0067581	-1.1197844		1.15400308	-1.6159197	-1.1050706	
	3001.524	3000.831				2998.355	2995.995	2995.768			2995.445			2994.968	2993.418	2992.173	2987.828	2986.651	2986.041	2985.906		2985.586	2985.449	2984.674	2984.648
						YWHAE									KIAA0626								HRIHFB2122		
similar to VACUOLAR PROTEIN SORTING- ASSOCIATED PROTEIN	VPS35	ESTs	tyrosine 3-	monooxygenase/tryptophan 5-	monooxygenase activation	protein, epsilon polypeptide	EST	ESTs	Homo sapiens mRNA; cDNA	DKFZp564H203 (from clone	DKFZp564H203)	Homo sapiens cDNA	FLJ10749 fis, clone	NT2RP3001915	KIAA0626 gene product	ESTs	EST	ESTs	ESTs	ESTs	ESTs, Weakly similar to	centaurin beta2 [H.sapiens]	putative nuclear protein	ESTs	ESTs
	Hs.264190	Hs.13845				Hs.79474	Hs.230664	Hs.55561			Hs.8736			Hs.24641	Hs.178121	Hs.58429	Hs.121954	Hs.22906	Hs.49576	Hs.190129		Hs.4273	Hs.40342	Hs.125830	Hs.12348
	AA620415 Hs.76294	AA521247 Hs.13845				N21624 Hs.79474	AA489826 Hs.105301	W37694 Hs.55561			R27327 Hs.23828			AA504130 Hs.24641	R02095 Hs.17555		AA777607 Hs.121954	R44949 Hs.22906	W30810 Hs.49576	AA456651 Hs.88249		AA469961 Hs.4273	AA046650 Hs.40342	N24155 Hs.125830	N48096 Hs.12348
	951010	827152				266106	839837	322021			132354			825228	124320	346897	449187	34321	309685	811975		730385	488390	269563	281829
	GF203	GF203				GF201	GF202	GF202			GF203			GF203	GF200	GF202	GF204	GF201	GF200	GF203		GF202	GF202	GF203	GF204

KIAA0968 protein;

			-1.1605851			1.17435585			1.02757066			-1.2967931	-1.6130307	1.0046564					1.1469549											1.15847504	-1.0122046			
			2984.605			2983.471			2982.194			2981.978	2981.676	2981.346				2976.083	2972.399			2966.767			2965.217			2962.172		2961.185	2959.741	2958.151	2957.175	
			KIAA0968																											STAT5B		DKFZP586I1023		
osloji m/oslmodi ilin-dependent	protein kinase II alpha-B	subunit; calmodulin-dependent	protein kinase II alpha	Homo sapiens mRNA; cDNA	DKFZp564H1664 (from clone	DKFZp564H1664)	Homo sapiens mRNA; cDNA	DKFZp58610523 (from clone	DKFZp586l0523)	Homo sapiens cDNA	FLJ10058 fis, clone	HEMBA1001398	ESTs	ESTs	ESTs, Weakly similar to IIII	ALU SUBFAMILY SC	WARNING ENTRY !!!!	[H.sapiens]	EST	Homo sapiens cDNA	FLJ10439 fis, clone	NT2RP1000688	Homo sapiens cDNA	FLJ11189 fis, clone	PLACE1007547	ESTs, Moderately similar to	neuronal-STOP protein	[M.musculus]	signal transducer and activator	of transcription 5B	ESTs	DKFZP586I1023 protein	ESTs	
			Hs.143535			Hs.109201			Hs.93127			Hs.179615	Hs.185029	Hs.199362				Hs.268801	Hs.10477			Hs.3487			Hs.168095			Hs.48756		Hs.244613	Hs.50373	Hs.111515	Hs.121735	
			Hs.13385			Hs.109201			Hs.93127			AA609149 Hs.112653	AA195420 Hs.58229	AA400133 Hs.97777				Hs.31775	Hs.10477			Hs.3487			AA779722 Hs.122507			AA129861 Hs.48756		AA280647 Hs.15112	Hs.50373	Hs.46497	AA718915 Hs.121735	
			R37590			H87144			H52299			AA609149	AA195420	AA400133				H49517	T59014			AA425420 Hs.3487			AA779722			AA129861		AA280647	N73807	N80593	AA718915	
			24907			252453			202213			1031377	665542	743236				178856	74512			773324			1034480			490730		712840	289402	300899	1292444	
			GF202			GF202			GF200			GF202	GF203	GF202				GF201	GF202			GF201			GF204			GF201		GF200	GF202	GF201	GF204	

DOBGYYSB DYDEDI

APPENDIX A

Westbrook et al.

-1.0486631	1.91354777		1.06945204			2.35485113								-1.1725771	1.61969882		1.15042989	-1.277283
2955.795	2952.454	2950.353	2949.938	2949 848	2949.012	2948.681		2944.304	2943.321	2942.938		2941.038	2939.755	2939.628	2938.605		2938.294	2938.089
NUDT3		KCNA1		APACD	KIAA0375	FUT2						NDUFAB1					VDR	
nudix (nucleoside diphosphate linked moiety X)-type motif 3 I	unknown [M.musculus]	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	ESTs, Highly similar to CGI- 112 protein [H.sapiens]	ATP binding protein associated with cell	ne product	fucosyltransferase 2 (secretor status included)	hromosome	19, cosmid F22329	ESTs	ESTs	NADH dehydrogenase (ubiquinone) 1, alpha/beta	nplex, 1 (8kD, SDAP)	ESTs	ESTs	ESTs, Highly simitar to KIAA0612 protein [H.sapiens]	vitamin D (1,25-	dihydroxyvitamin D3) receptor VDR ESTs. Weakly similar to	M03F8.2 [C.elegans]
Hs.4815	Hs.110341	Hs.60843	Hs.271614	He 153884	Hs.26951	Hs.46328		Hs.180570	Hs.23862	Hs.106525		Hs.5556	Hs.7956	Hs.22246	Hs.6382		Hs.2062	Hs.182885
N33851 Hs.109088	AA481435 Hs.21186	AA018214 Hs.60843	AA495982 Hs.32319	A A D 8 5749 He 110890	W49494 Hs.26951	AA250771 Hs.46328			N90051 Hs.108612	AA872348 Hs.106525		AA447569 Hs.5556	AA933888 Hs.7956	AA279467 Hs.22246	N62979 Hs.6382		AA485226 Hs.2062	H95989 Hs.11644
272468	752903	362718	768491	488303	324927	724378		121731	305809	1472664		782635	1536991	704320	289760		815816	250699
GF202	GF203	GF201	GF202	CE201	GF201	GF200		GF201	GF201	GF204		GF201	GF204	GF203	GF203		GF200	GF202

1.04292094 1.14983685 1.03891464	1.06441796	1.01291146 1.60290103 -1.3551502	-1.0121797	-1.1694781	1.23682021	-1.0070269		1.9900943	1.25057218 1.4023985
2935.152 2932.932 2929.337 2929.024	2926.934 2926.73 2926.388	2922.638 2922.099 2921.106	2920.354	2915.321	2911.959	2910.323 2910.323	2909.66	2909.49	2909.363 2907.353
	LOC51340 LOC51306		OS4		TNFAIP2	RSN	SLC22A1L	ITGAL	EIF2S2
ESTs, Moderately similar to dJ1163J1.1 [H.sapiens] ESTs ESTs	CGI-201 protein EST GAP-like protein	ESTs ESTs ESTs Conserved gene amplified in	osteosarcoma Homo sapiens cDNA FLJ11296 fis, clone PLACE1009731, weakly	similar to AIG1 PROTEÍN Homo sapiens clone 24468 mRNA sequence	induced protein 2 restin (Reed-Steinberg cell- expressed intermediate	filament-associated protein) ESTs solute carrier family 22 (organic cation transporter),	member 1-like integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1;	alpha polypeptide) eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD) ESTs
Hs.164973 Hs.21745 Hs.21031 Hs.177983	Hs.268281 Hs.98750 Hs.82035	Hs.36190 Hs.268919 Hs.185771	Hs.180669	Hs.26194 Hs.13423	Hs.101382	Hs.31638 Hs.245257	Hs.50868	Hs.174103	Hs.12163 Hs.54681
AA827400 Hs.31621 R15880 Hs.21745 R39926 Hs.21031 AA400389 Hs.97802	Al018501 Hs.26089 AA431738 Hs.98750 W49785 Hs.42741	ŕΟ	AA401267 Hs.8558	AA150443 Hs.26194 H14949 Hs.13423	AA457114 Hs.75522	W60326 Hs.103136 AA454177 Hs.99252	AA406180 Hs.50868	R48796 Hs.51116	AA027240 Hs.12163 N91109 Hs.54681
1422447 53022 25355 742607	1630942 782276	246792 202704 814485	758365	491460	810444	342108 795325	742862	154015	469151 302956
GF204 GF203 GF202 GF202	GF204 GF202	GF200 GF200 GF203	GF200	GF201 GF202	GF200	GF201 GF202	GF201	GF200	GF203 GF202

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-1.1709265 1.20468674 1.20468674 -1.3648875 -1.0486688	-1.2737663	1.40523292	2.58196829 -1.7937118 -1.2661166 1.23908907
2889.826 2888.888 2888.765 2885.238 2885.238 2884.277 2880.908 2880.158	2877.454 2877.454 2877.259	2875.923 2875.16 2874.642 2874.47	2870.712 2866.545 2866.409 2862.424
KIAA0729 CTBP1 CTBP1	НРЯР3Р	CYP19	TID1 E2F4
ESTs KIAA0729 protein ESTS C-terminal binding protein 1 C-terminal binding protein 1 ESTS ESTS ESTS ESTS ESTS ESTS ESTS EST	[H.sepiens] ESTs UA/U6-associated RNA splicing factor Homo sapiens mRNA full	EUROIMAGE 381867 yorkohoma PA50, subfamily XIX (aromatization of androgens) Humo sapiens CDNA FLL20065 fis, clone KANA713, highly similar to AF151848 Humo sapiens CGI-90 protein mRNA ESTS	ESTs, Weakly similar to KIAA0765 protein IH sapiens] tumorous imaginal discs (Clossophila) homolog EST E2F transcription factor 4, p107/p130-binding
Hs.30715 Hs.180948 Hs.186815 Hs.239737 Hs.121932 Hs.122016 Hs.192016 Hs.192016	Hs.217942 Hs.2177942 Hs.11776	Hs.124154 Hs.78946 Hs.44222 Hs.122953	Hs.33540 Hs.6216 Hs.121987 Hs.108371
AI017405 Hs.30715 N73705 Hs.46726 AA/701300 Hs.119741 AA/78268 Hs.10986 AA/70857 Hs.121932 AA/70857 Hs.121932 AA/70857 Hs.11990 HS.2535 Hs.47507	N90667 Hs.49760 AA151945 Hs.72015 AA427927 Hs.11776	N64009 Hs.48909 R27767 Hs.91321 AA468483 Hs.4222 H26413 Hs.122953	N94814 Hs.109848 AA169872 Hs.6216 AA777915 Hs.121987 AA448641 Hs.108371
1635315 289287 435663 740914 740914 449409 451902 27916 244722	306318 566498 773500	278373 133717 809603 161362	306568 594079 449346 786048
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2862.424 2861.816 2860.875	2860.27 2859.91 2858.884	2858.03 2857.463 2856.524	2851.95	2845.671	2845.22 2844.962	2841.682	2840.989 2839.872 2838.067 2834.819 2834.425
E2F4	DCTN1 HRY	SULT1C1 GOLGA1	RLF	UAP1	PIK3R1	НЕСН	BST1
E2F transcription factor 4, p107/p130-binding ESTs ESTs character 1 (n150 Glued	opriesin (Processor) (Drosophila)-homolog ESTs (Hortzansferase family 10)	period autoantigen, golgin subfamily a, 1	rearianged Chilyo Lason sequence EST, Highly similar to PHENYLETHANOLAMINE N- METHYI TRANSFERASE	H. sapiensi UDP-N-actey/glucosamine pyrophosphorylase 1; Sperm associated antigen 2 phosphoinostitide-3-kinase,	regulatory subunit, polypeptide 1 (p85 alpha) ESTs	heterochromatin-like protein 1 hone marrow stromal cell	antigen 1 EST ESTs ESTs paraoxonase 2
Hs.108371 Hs.144014 Hs.97523	Hs.74617 Hs.250666 Hs.119280	Hs.38084 Hs.89143 Hs.172647	Hs.13321	Hs.229120 Hs.21293	Hs.6241 Hs.9965	Hs.278554	Hs.169998 Hs.48472 Hs.131908 Hs.269043 Hs.169857
AA448641 Hs.79397 R62773 Hs.28357 AA628207 Hs.97523	AA488221 Hs.74617 AA459983 Hs.78060 AA626063 Hs.119280	R86242 Hs.15640 AA455304 Hs.89143 R44140 Hs.79100	R58985 Hs.79303	N63192 Hs.1892 AA040861 Hs.21293	R54050 Hs.6241 AA029098 Hs.9965	AA132226 Hs.8123	N52293 Hs.32980 N62178 Hs.48472 AA421477 Hs.131908 T50995 Hs.51357 AA446301 Hs.75221
786048 138837 1055853	877613 796448 1055427	194515 810065 34102	41345	289857	39808 470249	566887	245970 289816 731061 76647 781019
GF200 GF200 GF204	GF200 GF202 GF204	GF201 GF201 GF201	GF201	GF201	GF200 GF204	GF200	GF200 GF202 GF204 GF202 GF202

-1.1407032

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2831.978	2827.482 2825.561 2825.401 2824.485	2822.888 2821.415 2821.104	2820.888	2819.751 2818.902 2818.789	2818.314 2818.183 2815.965 2815.941 2815.877
		_			2 9 -
ABCB7	SSR3 RPL26	PIM1 HNF3G	DDC		HMOX2 GS3686 TRD@ MSE55
ATP-binding cassette, sub- family B (MDR/TAP), member 7 signal sequence receptor, gamma (translocon-	associated protein gamma) ESTs ribosomal protein L26 ESTs ESTs ESTs, Weakly similar to IIII A I I CA ASS B WARNING	ENTRY III [H.sapiens] pim-1 oncogene hepatocyte nuclear factor 3, gamma	dopa decaboxylase (aromatic L-amino acid decarboxylase) emoparni-binding protein (sterol isomerase) Homo sapiens cDNA E-110937 fis, clone OVARC1001034, highly similar to Mus musculus Fn54	mRNA ESTs, Moderately similar to KIAA0664 protein [H.sapiens] EST	heme oxygenase (decycling) 2 HMOX2 hypothetical protein, expressed in osteoblast GS3886 T cell receptor delta locus TRD@ ESTs serum constituent protein MSE55
Hs.125856	Hs.28707 Hs.22509 Hs.91379 Hs.44035	Hs.173734 Hs.81170 Hs.36137	Hs.150403 Hs.75105	Hs.168640 Hs.69428 Hs.141075	Hs.63908 Hs.75470 Hs.2014 Hs.11259 Hs.148101
Hs.105781	Hs.47106 Hs.22509 Hs.118227 Hs.44035	Hs.79655 Hs.51655 Hs.36137	Hs.475 Hs.75105	Hs.111974 Hs.69428 Hs.101726	AA620546 Hs.63908 N67034 Hs.102765 AA670107 Hs.2014 AA443153 Hs.21259 H73234 Hs.1053
AA705237	N73309 H18645 N89671 AA424883	N55563 AA191318 R99562	AA702640 N67038	AA418007 AA192435 H16098	AA620546 N67034 AA670107 AA443153 H73234
461522	292082 51254 307029 768214	246073 626765 201288	384015 295986	767469 627555 48687	295939 844680 796774 214982
GF203	GF201 GF201 GF204 GF203	GF200 GF202 GF200	GF201	GF202 GF202 GF203	GF202 GF200 GF201 GF202 GF202
	ATP-binding cassette, sub- family B (MDR/TAP), member 461522 AA705237 Hs.105781 Hs.126856 7 ABCB7 signal sequence receptor, camma fignal sequence receptor,	ATP-binding cassette, sub- family B (MDR/TAP), member ABCB7 signal sequence receptor, gamma (translocon- gamma (translocon-gamma (translocon- gamma (translocon-gamma (translocon-	ATP-binding cassette, sub-family B (MDR/TAP), member family B (MDR/TAP), me	461522 AA705237 Hs.105781 Hs.126856 7 isignal sequence receptor, associated protein gamma (Harantsoon-associated protein gamma) SSR3 51254 H18645 Hs.22509 Hs.22509 ESTS 768214 AA424883 Hs.44035 Hs.44035 ESTS Walkling ESTS Walkling ESTS Hs.44035 Hs.137374 Hs.24035 ESTS Walkling Hyll (Haspiens) Hs.173734 Hs.36137 Hs.36137 Hs.36137 Hs.36137 Hs.36137 Hs.36137 Hs.36137 Hs.36137 Hs.36137 Hs.150403 Hs.75105 Hs.75105 Hardioxylase (aromatic empeantly-inding protein empeantly-inding empeantly-inding empeantly-inding empeantly-i	461522 AA705237 Hs.105781 Hs.125856 ramily B (MDR/TAP), member 7 ramily B (MDR/TAP), member 8 raminol rami

2.23655994 1.27025061 1.96262104

1.25704104

1.6694487

1.13161686

1.34750393

1.34727552

1.25814239

	-1.0500086	1.75058655	1.54662093	-1.2720713	1.41143804	-1.2970412	1.18276769		-1.2318796	1.03044791			-1.6265258
	2815.313 2807.479	2806.985 2805.892	2805.268	2803.42	2803.406	2803.113	2802.529	2801.551 2798.948 2796.212	2795.662 2795.464	2793.907	2792.393	2786.844	2783.134 2781.82
	ALDOC CTSB		RPS25	C110RF4			PDE4B	KIAA0955		ے	NRBF-2		LPP
aldolase C, fructose-	bisphosphate cathepsin B ESTs, Weakly similar to ZINC FINGER PROTEIN 132	[H.sapiens]	ribosomal protein S25 chromosome 11 open reading	frame 4 Homo sapiens mRNA; cDNA DKFZp434A2417 (from clone	DKFZp434A2417); partial cds ESTs, Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!	[H.sapiens] phosphodiesterase 4B, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase	ESTs, Weakly similar to Shc	binding protein [M.musculus] KIAA0955 protein ESTs	ESTs ESTs	ESTs nuclear receptor binding factor-	2 ESTs, Highly similar to CGI-91	protein [H.sapiens] LIM domain-containing preferred translocation partner	in lipoma ESTs
	Hs.155247 Hs.249982	Hs.129691 Hs 55213	Hs.113029	Hs.75859	Hs.14051	Hs.41640	Hs.188	Hs.164481 Hs.10031 Hs.204970	Hs.33417 Hs.40098	Hs.180136	Hs.27181	Hs.20776	Hs.180398 Hs.44792
	T77281 Hs.74618 AA775047 Hs.90313	Hs.76592		1 Hs.75859	AA398282 Hs.14051	Hs.41640	AA453293 Hs.188	AA404276 Hs.38687 AA027168 Hs.10031 R01448 Hs.108195	AA598828 Hs.33417 W47325 Hs.55864	AA708280 Hs.67009	3 Hs.27181	AA459419 Hs.20776	AA047443 Hs.83289 N36130 Hs.44792
	T77281 AA77504	T66930	T98662	W48701	AA3982	H92639	AA4532	AA4042 AA0271 R01448	AA5986 W4732	AA7082	N30573	AA4594	AA04744; N36130
	23831 868548	909406	122239	324885	726725	221694	788136	758332 366571 123811	898318	397660	257197	810979	488435 272616
	GF200 GF203	GF200	GF202	GF203	GF203	GF203	GF200	GF201 GF204 GF201	GF203 GF201	GF203	GF201	GF201	GF201 GF202

Westbrook et al.	ok et al.				APPENDIX A		Afty	Atty Docket No. 21 /2
GF201 GF202 GF200	281145 241343 293178	N50959 H81188 N63864	Hs.94003 Hs.114248 Hs.38502	Hs.143102 Hs.269571 Hs.205554	amine oxidase, copper containing 2 (retina-specific) ESTs ESTs ESTs. Weakly similar to	AOC2	2781.383 2779.705 2778.375	-1.1003043
GF201 GF203 GF201	306216 399387 320355	N90564 AA732842 W04525	N90564 Hs.24598 NA732842 Hs.117838 N04525 Hs.14627	Hs.24598 Hs.18827 Hs.14627	ubiquitous TPR motif, Y isoform [H.sapiens] KIAA0849 protein ESTs	KIAA0849	2776.906 2776.193 2774.567	1.10640475
GF201 GF200	771327 545189	AA476245 AA076063	AA476245 Hs.21090 AA076063 Hs.77497	Hs.194692 Hs.182183	cysteine desulfurase caldesmon 1	NIFS CALD1	2774.389 2772.426	1.04932409
GF200 GF201 GF204	144880 235104 810534	R78580 H79319 AA464550	378580 Hs.107203 479319 Hs.108461 44464550 Hs.98269	Hs.107203 Hs.268997 Hs.98269	ESTs ESTs ESTs		2771.442 2770.208 2767.199	-1.2869937
GF202	786194	AA448685	4A448685 Hs.127477	Hs.709	deoxycytidine kinase member of MYST family histone acetyl transferases,	DCK	2767.077	-1.0613245
GF201 GF201 GF201	810118 309499 782677	AA464974 N99256 AA447587	AA464974 Hs.42343 N99256 Hs.44850 AA447587 Hs.32112	Hs.42343 Hs.114611 Hs.32112	homolog of Drosophila MOF ESTs ESTs	MOF	2766.672 2765.338 2764.893	
GF202	69893	T48649	Hs.8856	Hs.209465	ESTs solute carrier family 2 (facilitated glucose		2764.663	-1.3398215
GF203	704085	AA279201	AA279201 Hs.86633	Hs.33084	transporter), member 5 corticotropin releasing	SLC2A5	2761.9	1.06286075
GF202	266336	N26546	Hs.114363	Hs.115617	hormone-binding protein heterogeneous nuclear	СВНВР	2761.707	-1.0805815
GF200 GF202 GF202	511586 280266 33294	AA127116 N47952 R43957	AA127116 Hs.75071 N47952 Hs.102624 R43957 Hs.101186	Hs.249495 Hs.102624 Hs.101186	ribonucleoprotein A1 EST ESTs	HNRPA1	2760.784 2760.384 2759.021	2.01009421 1.75898116 1.42594166
GF202 GF200 GF200	784010 824044 824044	AA443695 AA491206 AA491206	AA443695 Hs.98769 AA491206 Hs.78851 AA491206 Hs.119441	Hs.234734 Hs.78851 Hs.78851	lysozyme (renal amyloidosis) KIAA0217 protein KIAA0217 protein	LYZ KIAA0217 KIAA0217	2754.671 2754.665 2754.665	-1.0681288 1.2299278 1.2299278
GF201	300044	N91539	Hs.109659	Hs.172085	protein [H.sapiens]		2754.141	

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1.11468273	-1.0216975 -1.6229713		1.02819442 -2.5577593 1.98475204	1.30378619 -1.6909574		1.58878058 1.00720006 1.17941948		1.07073197	2.04163868	1.25031374	1.48796722
2749.725	2749.412 2748.211	2748.003	2747.354 2744.425 2744.4	2741.363 2740.695	2739.426 2739.416	2739.166 2737.743 2733.8	2731.222 2730.818	2730.563 2730.389	2729.724 2728.995	2722.345	2722.024 2719.892
EYA3	ARPC2	MPB1	SSR3	RPL27A	СУР		BAZ1B	DKFZP434H018	YDD19	DNC11	KEO4
eyes absent (Drosophila) homolog 3 actin related protein 2/3	complex, subunit 2 (34 kD) ESTs MYC promoter-binding protein	1 signal sequence receptor,	gamma (translocon- associated protein gamma) ESTs ESTs	ribosomal protein L27a EST	Clk-associating RS-cyclophilin CYP ESTs Homo saplens cDNA FLJ20037 ffs, clone	COL00314 ESTs ESTs	Diomocentain adjacent to zinc finger domain, 1B ESTs Homo sapiens mRNA; cDNA DKFZp761A1623 (from clone	DKFZp761A1623); partial cds DKFZP434H018 protein	YDD19 protein ESTs dynein, cytoplasmic,	intermediate polypeptide 1 similar to Caenorhabditis	elegans protein C42C1.9 EST
Hs.46925	Hs.83583 Hs.171088	Hs.273241	Hs.28707 Hs.9212 Hs.58201	Hs.76064 Hs.112789	Hs.77965 Hs.56276	Hs.10784 Hs.112993 Hs.187823	Hs.194688 Hs.221543	Hs.26849 Hs.24557	Hs.25615 Hs.49889	Hs.65248	Hs.15194 Hs.121953
AA262504 Hs.46925	H25917 Hs.83583 H05777 Hs.30569	AA708342 Hs.120109	AA405190 Hs.119191 T50661 Hs.9212 W72098 Hs.58201	AA599178 Hs.76064 AA609935 Hs.112789	AA426019 Hs.83591 Al003724 Hs.130345	R28669 Hs.121578 AA621480 Hs.112993 AA676340 Hs.116982	AA074596 Hs.67665 AA278387 Hs.88703	R61847 Hs.26849 AA142980 Hs.24557	H78365 Hs.81407 N70553 Hs.49889	R54443 Hs.100222	N74700 Hs.15194 AA777605 Hs.121953
685912	162208 43936	392678	742061 72745 346055	949940 1031158	773437 392022	133895 1055261 430527	366041 712512		233550 299182	39189	298769 449198
GF200	GF200 GF203	GF204	GF203 GF202 GF202	GF200 GF202	GF201 GF204	GF202 GF202 GF203	GF201 GF204	GF203 GF201	GF200 GF201	GF202	GF203 GF204

1.06210753	1.06164135	1.12623506	1.15707747	-1.0715245	1.40729703				1.46391242		-2.1868306	2.4208232			1.71067647	1.69204278			-1.336592	-1.7418516	1.18764829			1.34544265	-1.2221206			1 00000000	200000
2716.93	2713.955	2712.112	2711.073	2710.217	2708.759	2708.65	2/08.58		2708.257	2707.834	2706.626	2706.464		2705.869	2703.394	2701.282			2700.202	2699.891	2699.54			2699.075	2698.257		2696 213	2000.213	2030:025
					PIM1	LOC51059	grady				DKFZp547L134	KIAA0798		×		COL6A1											MOLIEAS	22.00	
ESTs Homo sapiens mRNA; cDNA DKFZo586F071 (from clone	DKFZp586F071)	ESTs	ESTs	EST	pim-1 oncogene	hypothetical protein	YDD19 protein	FLJ20079 fis, clone	COL03057	ESTs	hypothetical protein	KIAA0798 gene product	Kell blood group precursor	(McLeod phenotype)	ESTs	collagen, type VI, alpha 1	ESTs, Weakly similar to	INTERLEUKIN-17	PRECURSOR [H.sapiens]	EST	EST	ESTs, Weakly similar to !!!!	WARNING ENTRY !!!!	[H.sapiens]	ESTs	NADH dehydrogenase	(ubiquinone) 1 alpha	Subcomplex, 3 (and, bs)	ESIS
Hs.186486	Hs.22907	Hs.87586	Hs.34314	Hs.144174	Hs.81170	Hs.13497	Hs.25615		Hs.165948	Hs.118944	Hs.9877	Hs.178471		Hs.78919	Hs.203691	Hs.108885			Hs.110040	Hs.31771	Hs.15246			Hs.191207	Hs.64056		00000	HS. 198269	HS.102754
1048714 AAG20628 Hs.112358	R56916 Hs.22907	AA279431 Hs.87586	H97748 Hs.34314	H68380 Hs.57370	H84657 Hs.27264	_	H79308 Hs.129253		R99573 Hs.11248	æ	AA481531 Hs.9877	T90374 Hs.15162		H18932 Hs.78919	H78999 Hs.114242	H99676 Hs.108885			AA443286 Hs.110040	H20757 Hs.31771	T90794 Hs.15246			T77891 Hs.113141	AA487550 Hs.64056			_	N66393 Hs.102/54
1048714	41432	704300	209583	212441	219888	50329	235084		201301	745217	815276	111004		51599	233644	263716			783987	51542	111510			108797	841393			/43081	285443
GF202	GF202	GF203	GF200	GF202	GF203	GF201	GF204		GF200	GF204	GF203	GF200		GF201	GF202	GF203			GF202	GF202	GF200			GF200	GF202	i		GF201	GF202

DAMBANDO DESCRIPTION

	1.84318797	.33747893	-1.0295263	1.07228703	.44365194	.19664616	.06229432			.70517864	-1.5258242		1.27455333		-1.0546243		40.40700	-1.4642/36		.16575869	1.19918095		1.21873452		-1.1146842
		-			_	_	÷			_			÷		7										
2695.169	2693.716	2693.072	2687.515	2687.436	2687.405	2687.194	2685.59		2684.709	2684.519	2683.356	2682.641	2681.52	;	2678.88	2678.46	707	26/8.132		2677.908	2677.858	2677.718	2676.965		2675.835
α	0	2	2	Ø	2	2	0		α	2	7	N	2	•	N	0	c	N		2	8	67	N		N
22						_	KIAA1049		TNFRSF1B	C210RF45	KIAA1089						9	ARHGDIB				51757	KIAA0630		
VAMP2		HEC			HIS1	FGL1	KIAA			_	KIAA				RGN			AHH		NET-7		t Lock	KAA		
vesicle-associated membrane orotein 2 (synaptobrevin 2) ESTs, Weakly similar to stearoyl-CoA desaturase	cancer,	rich in leucine heptad repeats						tumor necrosis factor receptor	superfamily, member 1B chromosome 21 open reading	Į.				nce			Rho GDP dissociation inhibitor		transmembrane 4 superfamily	NET-7)		p36 TRAP/SMCC/PC2 subunit LOC51757		r to iefinder	
vesicle-associated membra protein 2 (synaptobrevin 2) ESTs, Weakly similar to stearoyl-CoA desaturase	[H.sapiens] highly expressed in cancer,	e hepta			iple	te 1	rotein	sis facto	superfamily, member 1B chromosome 21 open rec		rotein			regucalcin (senescence	ein-30)	-	ssociati		ane 4 sı	member (tetraspan NET-7)		MCC/P	rotein	EST, Weakly similar to oredicted using Genefinder	
ein 2 (sy s, Weal oyl-Co	H.sapiens]	n leucir	co.	s	HMBA-inducible	fibrinogen-like 1	KIAA1049 protein	r necro	rfamily, mosom	frame 45	KIAA1089 protein	s	ø	calcin (marker protein-30)	S	GDP of	(GUI) beta	membr	ıber (tel	s	TRAP/S	KIAA0630 protein	, Weakl icted us	C.elegans]
vesic prote EST; stear	H.s	흔	ESTs	ESTs	HWE	fibrin	ΚĮΑ	tumo	supe	fram	ΚĮΑ	ESTs	ESTs	regu	mar	ESTS	PP 6	(E)	trans	men	ESTs	p36	Κ¥	EST	Ce
4534	7474	169	2971	805	299	7	7835		6278	932	06	9040	198		854	0352		929		583	566	1112	259		1993
Hs.194534	Hs.247474	Hs.58169	Hs.112971	Hs.97805	Hs.15299	Hs.107	Hs.227835		Hs.256278	Hs.49932	Hs.4990	Hs.269040	Hs.34198		Hs.77854	Hs.120352	:	Hs.83656		Hs.95583	Hs.33266	Hs.181112	Hs.12259		Hs.121993
864	Hs.53800	Hs.58169	12971	7805	03582	Hs.100812	09594		9521	9932	066	Hs.108914	Hs.34198		Hs.77854	20352		3656		5583	Hs.33266	4203	Hs.12259		21993
2 Hs.6	Hs.5	Hs.5	3 Hs.1	0 Hs.9	3 Hs.1		9 Hs.1		6 Hs.8	2 Hs.4	5 Hs.4	Hs.1	Hs.3		Hs.7	4 Hs.1	:	4 Hs.8		8 Hs.9	Hs.3	5 Hs.1	Ŧ.		8 Hs.1
AA425682 Hs.6864	N25650	N72679	AA621323 Hs.112971	AA400470 Hs.97805	AA598983 Hs.103582	R10378	AA424509 Hs.109594		AA150416 Hs.89521	AA065042 Hs.49932	AA476305 Hs.4990	F84479	388748		H05140	AA890104 Hs.120352		AA487634 Hs.83656		AA161188 Hs.95583	N48982	AA454015 Hs.14203	R28649		AA777928 Hs.121993
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773183	267864	345787	1048792	742774	897722	129024	767078		491403	525478	770709	111406	194987		45099	1461006		841332		591157	279655	795282	133820		449504
GF201	GF202	GF203	GF202	GF202	GF202	GF202	GF203		GF201	GF202	GF202	GF204	GF203		GF200	GF204		GF200		GF202	GF203	GF201	GF200		GF203

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2673.61	2669.545 2667.753	2663.617	2662.702 2660.77		2659.032 2658 55	2655.524	2655.459		2655.435		2653.826		2652.299	2651.457		2649.375	2645.942	2645.62	2645.225		2643.336	2642.224
		1	I HOD		97007	2							MX1									
EST Human clone CE29 8.1 (CAC)n/(GTG)n repeat-	containing mRNA ESTs	ESTs	cortistatin EST	ESTs, Weakly similar to CLEAVAGE STIMULATION FACTOR, 64 KD SUBUNIT	[H.sapiens]	EST	ESTs	Homo sapiens mRNA; cDNA DKFZp434A1114 (from clone	DKFZp434A1114)	Homo sapiens mRNA; cDNA DKFZp434M0420 (from clone	DKFZp434M0420) mvxovirus (influenza)	resistance 1, homolog of murine (interferon-inducible	protein p78)	EST	ESTs, Moderately similar to hypothetical protein	[H.sapiens]	ESTs	ESTs	ESTs Homo sanions mRNA: CDNA	DKFZp564C0716 (from clone	DKFZp564C0716)	ESTs
Hs.117164	Hs.173421 Hs.193735	Hs.87530	Hs.44205 Hs 92511		Hs.142838	Hs 60242	Hs.14947		Hs.10175		Hs.273369		Hs.76391	Hs.47188		Hs.190421	Hs.267844	Hs.72092	Hs.55378		Hs.180477	Hs.44033
AA679487 Hs.117164	AA434112 Hs.83884 AA400152 Hs.97314	ဖ	N50745 Hs.44205 H11658 RG 58		AA456437 Hs.20386	W3/44/ HS.42220 AA007623 Hs 60242	AA193579 Hs.14947		T57834 Hs.10175		AA487899 Hs.10920		AA456886 Hs.76391	N51068 Hs.47188		AA777432 Hs.124910	W19461 Hs.102934	m	W16834 Hs.55378		AA843231 Hs.124132	AA412212 Hs.44033
828906	770199	712592	283751		788415	321900	666029		80692		840584		815542	281934		449376	305227	682052	320396		1405214	731438
GF204	GF201 GF202	GF203	GF201	3	GF202	GESOS	GF203		GF201		GF202		GF200	GF202		GF204	GF200	GF203	GF204		GF203	GF202

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1.62963253	-1.0070205	-1.2239853 -1.2606037 -1.1100175	1.04150777 1.48100325 -1.5858973	1.05474242	1.00656232
2641.341	2632.993 2632.809	2631.853 2630.273 2629.22 2628.04	2625,637 2624,861 2624,799 2623,578 2622,778	2621.052 2619.579 2619.523 2618.233	2616.215
ώ	YWHAZ	HNRPAB	e BAG4	MGST3	CHAF1A
ESTS. ESTS, Highly similar to DYNEIN LIGHT CHAIN 1, CYTOPLASMIC [H.sapiens] tyrosine 3. monooxyganase/typlophan 5- monooxydanase advitytion	protein, zeta polypeptide ESTs	Intercognitions increased information A/B ESTs ESTs ESTs ESTs ESTs Addressed in A/B ESTs vacuolar protein sorting homeloar -vars3th	[R.norvegicus] ESIs ESIs ACL2-associated athanogene 4 ESIs ESIs microsomal clutathione S-	transferase 3 transferase 3 ESTs ESTs ESTs	subunit A (150) ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]
Hs.118795 Hs.58044	Hs.75103 Hs.23783	Hs.81361 Hs.104834 Hs.98992 Hs.66072	Hs.26510 Hs.190785 Hs.194726 Hs.18845 Hs.47338	Hs.111811 Hs.103008 Hs.155512 Hs.112623	Hs.79018 Hs.269019
W80404 Hs.58439 AA401429 Hs.58044	H94670 Hs.114305 H09620 Hs.23783	W72693 Hs.81361 AA719128 Hs.104834 AA463632 Hs.98992 AA461490 Hs.66072	AA953644 Hs.26510 AA191322 Hs.68705 N25897 Hs.7300 H65569 Hs.18845 N31761 Hs.47338	R02085 Hs.113145 W32303 Hs.103008 AA663966 Hs.105398 AA608977 Hs.112623	AA704459 Hs.79018 R93412 Hs.35128
415417 7	243238 1 46287 1	345833 1292628 7811844 796671	1591222 626773 7 258454 1 209264 1 281786	124298 1 321470 7 855735 7	450711
GF202 GF201	GF203 GF201	GF202 GF204 GF202 GF202	GF204 GF202 GF201 GF200 GF202	GF204 GF201 GF204 GF202	GF203

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2613.631	2611.949	2610.939	2608.402				110 0000	2606.269			2605.542	2605.45	2604.548	2603.937				3603 605	2002.093		2601.709	2601.203	2600.58			210000	2599.044
NDUFB1		T1A-2									U2AF65																
NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL)	ESTs	lung type-I cell membrane- associated glycoprotein	ESTs Human DNA sequence from	clone RP5-1046G13 on chromosome 6q12-13	Contains part of a gene similar	to Rattus norvegicus rab3	effector (RIM), ESTS, STSS	and Goos FST	U2 small nuclear	ribonucleoprotein auxiliary	factor (65kD)	ESTs	ESTs	ESTs	Homo sapiens cDNA	FLJ10862 fis, clone	NIZAT 40013/4, IIIgiliy sililiigi	to homo sapieris coat protein	gamma-cop mena Homo saniens cDNA	FLJ10252 fis, clone	HEMBB1000807	ESTs	ESTs	ESTs, Weakly similar to !!!!	ALU SUBFAMILY SC	WARNING ENIT III	[H.sapiens]
Hs.183435	Hs.177331	Hs.135150	Hs.12250					HS.129190 Hs 229641			Hs.7655	Hs.39278	Hs.178569	Hs.269033				010007	Hs.102950		Hs.53913	Hs.94893	Hs.98127			:	Hs.271963
AA443099 Hs.102418	7 Hs.44192	AA046430 Hs.112172	W31675 Hs.12250					8 HS.48462 5 Hs 48086			4A405748 Hs.7655	.0 Hs.39278	4A702470 Hs.111899	l2 Hs.42512					0 Hs.102950		'6 Hs.42309	10 Hs.94893	AA412403 Hs.98127				AA705118 Hs.121020
AA443	N30557	AA046	W3167					N62128			AA405	N52340	AA702	N71792				000014	N26390		N32876	W81410	AA412				AA70E
809455	257170	488207	320712					28/581			742064	284463	448110	290748					258167		259344	347516	731422				462680
GF202	GF202	GF202	GF201					GF202	5		GF201	GF201	GF204	GF201					GF203		GF201	GF201	GF202				GF203

2588.795 275926 1.0 2.1 2.1 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.2 2.	2598.795 1.05810725	2596.56 1.12379727		2593.289 1.08881251	2592.931	2592.3 1.30687816	2590.163 1.14509471 2589.6 1.19752504	2588.798	2588.405 -1.3631617	2587.492 1.10505013 2586.756 1.5767826	2586.342		2584.076 -1.2515323
AA451861 Hs.12940 1 AA451861 Hs.12940 1 AA451861 Hs.115537 Hs.115537 Hs.24755 Hs.24775 Hs.24775 Hs.24775 Hs.24775 Hement mRhAL DIFETTIDASE Human transposon-like desmoplakin (DPI, DPII) N29456 Hs.125172 Hs.74316 Hement mRhAL DPII) AA60438 Hs.75118 Hs.7518 Hougulin carboxyl-terminal esterase. L1 (ubiquiin problemin (DPI, DPII) NS2182 Hs.26403 Hs.75209 alpha Horolen kinase (CAMP-Depondent Catalytic) inhibror alpha NA621381 Hs.111723 Hs.26439 HEP10273 fils, clone alpha H60460 Hs.2441 Hs.24639 HF.10273 fils, clone alpha H60460 Hs.2441 Hs.164 Horolosapica product advanced glyocosylation end W74538 Hs.115890 Hs.183384 Hernocapica product advanced glyocosylation end AA505116 Hs.115890 Hs.183384 Horon sapiens (clone p5-23-3) R37865 Hs.24177 Horon sapiens (clone p5-23-3) R37865 Hs.110706 Hs.2568B0223 Horon sapiens (clo		259	528	259					258	258			258
N50828 Hs.92942 Hs.12940 AA451861 Hs.115537 Hs.115537 AA496800 Hs.84775 Hs.84775 AA496800 Hs.8775 Hs.74316 AA670438 Hs.76118 Hs.76118 N52162 Hs.84403 Hs.75209 RA670438 Hs.111723 Hs.264636 H60460 Hs.2441 Hs.2441 W74536 Hs.115690 Hs.184 AA505116 Hs.107167 Hs.29417 AA50516 Hs.107365 Hs.129935 W58563 Hs.26585 Hs.12995 Hs.117026 W58563 Hs.43251 Hs.44228 Hs.44228 W74257 Hs.58984 Hs.58987 Hs.159990		Weakly similar to SSOMAL DIPEPTIDASE JRSOR [H.sapiens]		70			_	ကို	sapiens mRNA; cDNA	586B0323)			
N50828 AA451861 AA496800 N29455 AA670438 N52162 N74536 N68948 AA505116 AA50517							•						
		61 Hs.115537	00 Hs.84775	Hs.125172	38 Hs.76118		81 Hs.111723 Hs.2441			16 Hs.107167 55 Hs.5887			_
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1.04052346 1.24083991		1.11418807		1.87012076 1.12233661	1.88512026 -1.0627082 -2.0906001 1.71580618	1.18970911 -1.1400606 1.01090699 1.01396615	-1.0963321
2577.9 2577.343 2577.25	2576.089	2574,785 2574,482 2573,462	2572.472	2570.956 2569.267	2569.091 2568.97 2567.342 2565.506	2564.763 2563.066 2561.516 2560.48	2559.691
PDIR SNX1		MMP9 LAMA4		DIO2	KIAA1027	KIAA0303	INA
for protein disulfide isomerase- related sorting nexin 1 Sorting nexin 1 ESTs ESTs ESTs, Moderately similar to Lumon nerosisi fator-alpha- indired moriein B1?	[H.sapiens] matrix metalloproteinase 9 (gelatinase 8, 92kD	collagenase) laminin, alpha 4 ESTS Weakly similar to	using exon 13A [H.sapiens] ESTs, Highly similar to CALCIUM-BINDING PROTEIN P22 [H.sapiens] deirofinase indothuronine	type II ESTs ESTs, Weakly similar to IIII ALU CLASS B WARNING	ENTRY !!!! [H.sapiens] KIAA1027 protein ESTs ESTs	KIAA0303 protein EST ESTs ESTs	internexin neuronal intermediate filament protein, alpha
Hs.76901 Hs.75283 Hs.188935	Hs.271277	Hs.151738 Hs.78672 Hs.6195	Hs.262958 Hs.168069	Hs.154424 Hs.28974	Hs.193618 Hs.18420 Hs.16586 Hs.271628	Hs.54985 Hs.97964 Hs.44698 Hs.190266	Hs.76888
AA404394 Hs.76901 AA449430 Hs.75283 AA707582 Hs.124090	H16796 Hs.22756	772581 Hs.75557 N94616 Hs.91873 AA454745 Hs.6195	AA460304 Hs.21205 AA705060 Hs.85301	T67093 Hs.13035 AA446655 Hs.28974	AA676354 Hs.118343 AA678226 Hs.63580 R96478 Hs.16586 H47475 Hs.33946	33	AA448015 Hs.76888
772220 785574 1292094	50566	22040 309826 809788	795758	66582 784190	431573 430894 198023 193586	768031 742853 271743 236355	784876
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2.51111197	1.11743055	-1.0146819		1.18263265	1.22389503		1	1.33832134		1.53271056		-1.1963951	-1.2073902		1 40010060	1.42013002	1.01868673	1.11331302	1.30426.1	1.17486511	1.791474
2556.966 2556.785	2556.761	2554.731 2552.335	2550.422	2547.441	2546.764 2545.648		2545.052	204.1.402		2539.929		2538.46	7934.00/		0504 60	2331.00	2528.71	2527.694	2020.004	2526.427	2524.099
		TERF1 FUS2			DKFZP586H0723		CHD2					TRC8			1700	BPAL	CDC37			CASP7	
ESTs ESTs Homo sapiens mRNA; cDNA DKF2x58RD0923 ffrom clone	DKFZp586D0923) telomeric repeat binding factor	(NIMA-interacting) 1 putative tumor suppressor	Homo sapiens cDNA FLJ10300 fis, clone NT2RM2000030	ESTs	DKFZP586H0723 protein EST	chromodomain helicase DNA	binding protein 2	ESIS	ESTs, Moderately simitar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!	[H.sapiens]	patched related protein	translocated in renal cancer	ESIS	biphenylhydrolase-like (serine	Ilydiolase, Dieast epitiella	mucin-associated antigen) CDC37 (cell division cycle 37,	S. cerevisiae, homolog)	EOIS	caspase 7, apoptosis-related	cysteine protease	ESTs
Hs.68856 Hs.194368	Hs.62669	Hs.194562 Hs.22919	Hs.42233	Hs.7869	Hs.156764 Hs.40357		Hs.36787	HS.8/138		Hs.269176 Hs.46764		Hs.28285	Hs.30998		001101	HS.184552	Hs.160958	HS.14119	ns.1/0193	Hs.9216	Hs.44748
AA088761 Hs.68856 AA708240 Hs.120101	Hs.62669	Hs.117769 Hs.22919	_	10	Hs.11834 Hs.40357		AA461509 Hs.99548	AA6098/1 Hs.112/74		Hs.113183 Hs 46764	1000	AA455970 Hs.28285	AA425773 Hs.30998		00010	AA169798 Hs.95938	AA458870 Hs.83985	0	HS.Z 1064	Hs.9216	AA132185 Hs.44748
AA08876 AA70824	W69379	R99110 R44982	W04706	AA46351	W53015 H82212		AA46150	AA60987		R07268		AA45597	AA42577		0.000	AA16979	AA45887	AA20483	H497 14	T50828	AA13218
511844	343555	201443	320456	797038	321189		795833	1031048		126810	701.07	812050	773248		0000	/60019	810806	645565	38048	72778	588187
GF202 GF203	GF202	GF204 GF200	GE201	GF202	GF200 GF202		GF201	GF202		GF202	707	GF203	GF202		200	GF 202	GF203	GF203	GF 202	GF200	GF202

Westbrook et al. GF202 364885	AA024493	AA024493 Hs.61198	Hs.61198	APPENDIX A ESTs	And Walls field field And	Atty 2522.901	Atty Docket No. 2172
3 5	000000000000000000000000000000000000000		0 0 0	S-adenosylmethionine	Ž.	0500044	1 05640444
825842 246598	AA504772 N73264	AA504772 HS.100182 N73264 HS.5996	Hs.262476 Hs.5996	oecarboxylase i ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!	James -	2519.041	1.0527244 -1.0527244
291618		N67816 Hs.53263	Hs.53263	[H.sapiens]	CT2CA1 VI	2517.692	1.16898387
837891		AA434092 Hs.124217	Hs.271869	ESTs		2516.051	1.09089612
				sulfotransferase family 2A, dehydroepiandrosterone			
1342650		AA725397 Hs.81884 AA135868 Hs.95783	Hs.81884 Hs.95783	(DHEA) -preferring, member 1 SULT2A1 ESTs	SULT2A1	2514.197 2512.27	-1.2091344
781444	AA428604	4A428604 Hs.107231	Hs.241543	DKFZP586F1524 protein	DKFZP586F1524	2511.62	-1.3983527
384397	AA708676	AA708676 Hs.26690	Hs.26690	ESTs		2511.231	-1.2006926
795572	AA459677	AA459677 Hs.6621	Hs.259729	KIAA0596 protein	KIAA0596	2511.187	
269752	N24807	Hs.43573	Hs.115175	sterile-alpha motif and leucine zipper containing kinase AZK	LOC51784	2509.315	-1.2641757
214201	H77625	Hs.39785	Hs.39785	ESTs		2507.948	
878193	AA77575E	4A775755 Hs.122585	Hs.210645	ESTs		2507.808	
856585	AA669222	AA669222 Hs.23441	Hs.154057	matrix metalloproteinase 19	MMP19	2507.738	
40771	AA669446 R56045	756045 Hs.26488	Hs.268733	ESTs		2504.855	
241474	H90415	Hs.66746	Hs.194143	breast cancer 1, early onset hect (homologous to the E6- AP (UBE3A) carboxy	BRCA1	2501.839	1.77579973
322553	W15351	Hs.109395	Hs.76127	(CHC1)-like domain (RLD) 1	HERC1	2501.34	1.29025602

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chromosome 22q13.31-13.33 Contains the MAPK12 gene Human DNA sequence from for mitogen activated protein kinase 12 (SAPK3), the MAPK11 gene for mitogen activated protein kinase 11 (PRKM11), gene KIAA0315, clone RP3-402G11 on

	-1.1472501		-1.0280045	-1.0342385	1.06834141			2.49380165				1.56389579	-1.3154928			-1.1467069			-1.2666287		-1.1066718		1.2036242		-1.0339857		-1.2001919
	2501	2500.015	2497.762	2497.761	2497.474	2496.976	2496.055	2494.265	2493.456	2493.297		2492.559	2492.45	2492.156	2492.046	2490.162		2489.971	2484.884	2484.746	2484.466		2484.163	2483.975	2480.689	2480.595	2480.495
			LOC51704				ERO1L		EPHB1			EPB72			SECRET			UQCRB									뜐
LINNIII), gene Nivosio,	the gene for a novel protein s	ESTs	G protein-coupled receptor	ESTs	ESTs	ESTs	ERO1 (S. cerevisiae)-like	EST	EphB1	ESTs	erythrocyte membrane protein	band 7.2 (stomatin)	ESTs	ESTs	secretagogin	ESTs	ubiquinol-cytochrome c	reductase binding protein	ESTs	ESTs	ESTs	Homo sapiens mRNA for	KIAA1226 protein, partial cds	ESTs	ESTs	ESTs	H factor (complement)-like 1
	Hs.33026		Hs.242407		8		Hs.25740	Hs.55015	Hs.78436	Hs.41269		Hs.160483	Hs.180197	Hs.128689		Hs.188697		Hs.131255	Hs.98132	Hs.189114	Hs.187621		Hs.22151	Hs.171485	Hs.173949	Hs.117569	Hs.278568
	AA029368 Hs.33026	N26172 Hs.43760	W32884 Hs.21866		_	_	W81375 Hs.58546	_	_	AA126261 Hs.41269		R62868 Hs.74478	AA449105 Hs.41028	AA776828 Hs.128689	AA644563 Hs.116428	AA199733 Hs.115056		AA664284 Hs.118560	AA412443 Hs.98132	AA890146 Hs.126073	AA706627 Hs.87020		AA455999 Hs.22151	R56233 Hs.22139			AA703392 Hs.70541
	470368	269427	321580	295410	129570	306996	347546	309264	153541	502778		138936	785836	1291673	845521	647514		855843	731445	1461068	1239953		812088	40963	207427	146912	450060
	GF200	GF204	GF200	GF200	GF203	GF201	GF201	GF202	GF201	GF204		GF200	GF203	GF204	GF204	GF203		GF201	GF202	GF204	GF203		GF202	GF201	GF203	GF204	GF203

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-1,4430664 -1,0110048 1,49009771 1,02239916 1,5928439	1.19587517 1.03729102 1.80077833	1.49368115	1.05028133 1.18483684 1.16194669 -1.3688047 -1.200969 1.69009108
2480.147 2480.083 2478.349 2476.45 2475.98 2475.98 2475.924 2474.847	2474.156 2473.736 2471.578 2470.168 2469.591	2467.819 2466.408 2465.969 2465.606	2464.827 2464.04 2463.015 2462.824 2462.036 2460.277 2458.72
ACTN4 CHST5 DKFZP586A0522 PTD007 SPRR2C	LOCS1755 CLDN1 ATQ1 LCAT	SMT3H2 APBA2	TRA@ THBS4 KIAA0155
actinin, alpha 4 carbohydrate (N- carbohydrate (N- carbohydrates (N- carlotransferase 5 ESIs ESIs ESIs ESIs ESIs FTOO7 protein ESIS FTOO7 protein	CDC2-related protein kinase 7 LOC51755 claudin 1 antiquiin 1 ATO1 antiquiin 1 ATO1 electrin-cholesterol acyltransferase LCAT EST's Horn seniens mRNA: cDNA	DKFZp434A149 (from clone DKFZp434A149) ESTs SMT3 (suppressor of mif two sy axest) homolog 2 anyloid beta (A4) precursor protein-binding, family A, member 2 (71.1l/lee) ESTs Waskly Macket similar to	profine-rich protein [M.musculus] ESTs T cell receptor alpha locus ESTs T kitrombospondin 4 KIAAO155 gene product
Hs.1182485 Hs.31147 Hs.23359 Hs.108740 Hs.58919 Hs.112110 Hs.112110 Hs.12121	Hs.123073 Hs.7327 Hs.74294 Hs.242908 Hs.186648	Hs.22142 Hs.143942 Hs.180139 Hs.26468	Hs.25371 Hs.54542 Hs.74647 Hs.115426 Hs.98756 Hs.75774
113279 Hs.31147 722206 Hs.23359 770948 Hs.106232 AAC79309 Hs.58919 983740 Hs.14426 89861 Hs.54546 AA39964 Hs.54546 AA3964 Hs.2421	0 4	AA425316 Hs.22142 W52000 Hs.56127 AA775415 Hs.90182 R55789 Hs.26468	AA405740 Hs.25371 N98942 Hs.54542 AA427667 Hs.74647 AA868902 Hs.115426 AA431771 Hs.98756 AA437064 Hs.75774 AA133684 Hs.75932
H13279 H13279 H22206 HN70948 HN3740 HN83740 HN83740 HN83740 HN89861 HN99861 HN	R77955 H95362 AA10129 R06458 AA26235	AA42531 W52000 AA77541 R55789	AA405740 N89842 AA427667 AA868802 AA431771 AA437064
140951 148354 130858 294397 432105 307157 305538	145743 234490 563673 126390 666298	773106 324533 878130 40946	742979 305467 770014 1460696 782499 758266
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Attly	2458.527 2458.135	2456.77	2456.602 2454.099	2453.754 2451.56	2449.579		2445.915	2445.895 2445.836	2442.844 2442.467	2441.8 2440.514	2439.032	2437.073	2437.067 2436.522 2436.37
		AHCYL1			PCOLCE				HE1 LOC51253	COL8A1	SLC15A2	KCNK1	SIP
APPENDIX A	ESTs ESTs S-adenosylhomocysteine	hydrolase-like 1 Homo sapiens cDNA FLJ11223 fis, clone	PLACE1008209 ESTs	ESTs ESTs	procollagen C-endopeptidase enhancer	ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!	[H.sapiens] Homo sapiens mRNA; cDNA DKFZp762L137 (from clone	DKFZp762L137); partial cds ESTs epididymal secretory protein	(19.5kD) hypothetical protein	collagen, type VIII, alpha 1 ESTs solute carrier family 15 (H+/beotide transporter).	member 2	K, member 1 (TWIK-1) ESTs, Weakly similar to thioredoxin-like protein	[H.sapiens] SYT interacting protein ESTs
	Hs.142939 Hs.9343	Hs.4113	Hs.92308 Hs.173012	Hs.37308 Hs.127698	Hs.202097		Hs.91052	Hs.180780 Hs.6872	Hs.119529 Hs.4209	Hs.114599 Hs.9052	Hs.182575	Hs.79351	Hs.31819 Hs.11170 Hs.99595
	R67543 Hs.107124 AA994533 Hs.9343	AA176833 Hs.110089	AA156442 Hs.40584 V62996 Hs.48688	H56438 Hs.37308 AA864865 Hs.127698	AA670200 Hs.91299		781 Hs.119476	AA773358 Hs.68900 AA446361 Hs.6872	AA630449 Hs.119529 AA488652 Hs.4209	AA872420 Hs.114599 AA620598 Hs.9052	053 Hs.119715	520 Hs.79351	AA775431 Hs.31819 AA427767 Hs.98336 AA885132 Hs.99595
etal.	141931 R675 1631933 AA99	611373 AA13	505466 AA18 289790 N628	203850 H56 ^x 1456714 AA86	878652 AA67		293059 N63781	845723 AA7. 781311 AA4		1472775 AA8 951327 AA63	32509 R43053	288896 N62620	878152 AA7 770839 AA4 1466546 AA8
Westbrook et al.	GF200	GF202	GF201 GF202	GF200 GF204	GF203		GF203	GF203 GF201	GF203 GF202	GF203 GF202	GF204	GF200	GF204 GF203 GF204

					-1.0501104	-2.3235498				2.14266327			1.95188783	1.05496648				2.37867428				1.74930818	1.11956682	1.92260111	-1.451415		-1.0722399		1.07532947		1.07644843			1.55568997
	2436.162	2434.972	2434.899	2434.649	2433.894	2432.973				2432.968			2430.37	2429.985	2429.372	2428.181		2425.954			2424.262	2423.942	2422.971	2422.09	2421.591	2420.383	2417.672	2417.267	2417.11		2416.532	2415.585		2415.148
	EEF1A1		LOC54460	APM2	KIAA0220	VIM	==						ΓIW					SNAP23					ANKHZN	KIAA0623		KIAA0494			D1S155E		P2RX4			ATP6J
eukaryotic translation	elongation factor 1 alpha 1	ESTs	hypothetical protein	adipose specific 2	KIAA0220 protein	vimentin	ESTs, Moderately similar to !!!!	ALU SUBFAMILY SX	WARNING ENTRY !!!!	[H.sapiens]	LIM protein (similar to rat	protein kinase C-binding	enigma)	ESTs	ESTs	ESTs	synaptosomal-associated	protein, 23kD ·	Homo sapiens mRNA; cDNA	DKFZp434M245 (from clone	DKFZp434M245)	ESTs	ANKHZN protein	KIAA0623 gene product	ESTs	KIAA0494 gene product	ESTs	EST	NRAS-related gene	purinergic receptor P2X, ligand	gated ion channel, 4	ESTs	ATPase, H+ transporting, Ivsosomal (vacuolar proton	pump), member J
	Hs.181165	Hs.185889	Hs.81281	Hs.74120	Hs.110613	Hs.2064				Hs.240722			Hs.154103	Hs.21151	Hs.37386	Hs.105099		Hs.184376			Hs.5288	Hs.117887	Hs.6538	Hs.151406	Hs.87432	Hs.62515	Hs.42680	Hs.116612	Hs.69855		Hs.9610	Hs.165165		Hs.90336
	V95752 Hs.107259	4A620983 Hs.121568	720655 Hs.3405	4A478298 Hs.74120	4A448998 Hs.75813	4A487812 Hs.2064				N93967 Hs.55027			792455 Hs.34591	739804 Hs.21151	V20046 Hs.37386	AA291066 Hs.105099		R98877 Hs.15064			4A436008 Hs.5288	396198 Hs.117887	4A456130 Hs.99442	305458 Hs.106686	4A465714 Hs.87432	4A478158 Hs.62515	199398 Hs.42680	4A666341 Hs.116612	V76338 Hs.110641		R60722 Hs.9610	AA878648 Hs.122325		AA454616 Hs.99371
	308484 N	1049158 A	26307 R	740941 A	785605 A	`				309368 N			196345 R	26387 H	263049 N	700494 A		200863 R			730768 A	197838 R	796350 A	_	~	740707 A	262327 H	858852 A	245099 N		42118 H	1492881 A		811603 A
	GF201	GF204	GF204	GF201	GF200	GF200				GF202			GF200	GF202	GF201	GF204		GF200			GF201	GF202	GF202	GF202	GF203	GF204	GF202	GF204	GF200		GF200	GF204		GF202

	-1.0511975		-1.0975099			1.06755484				1.05589984		1.00746858	1.18196443	1.09066056							1.73593264	2.38438013				1,004,7004	1.391/2313		1.15245421			-1.0061858	1.09709807
2415.105	2414.97	2414.847	2413.673		2413.3	2412.746		2412.111		2412.039		2410.965	2410.607	2410.037						2408.971	2407.269	2406.712			2405.888	1000	2405.605	2405.792	2405.694	2405.047		2405.018	2404.585
	PTD010				LOC51279	ER3		HLA-C		CLTH		LIMS1	SS							TAC1					CD36L2			SCRG1	PLCB4			ICAM3	ABCF1
EST	PTD010 protein	ESTs	ESTs	complement C1r-like	proteinase precursor,	immediate early response 3	major histocompatibility	complex, class I, C	Clathrin assembly lymphoid-	myeloid leukemia gene	LIM and senescent cell	antigen-like domains 1	complement component 5	ESTs	tachykinin, precursor 1	(substance K, substance P,	neurokinin 1, neurokinin 2,	neuromedin L, neurokinin	alpha, neuropeptide	K,neuropeptide gamma)	ESTs	ESTs	CD36 antigen (collagen type I	receptor, thrombospondin	integral membrane protein (I)	-	melanoma adnesion molecule	scrapie responsive protein 1	phospholipase C, beta 4	ESTs	intercellular adhesion molecule	3 ATP-binding cassette, sub-	family F (GCN20), member 1 ABCF1
Hs.120367	Hs.182470	Hs.42245	Hs.28462		Hs.98571	Hs.76095		Hs.277477		Hs.7885		Hs.112378	Hs.1281	Hs.71721						Hs.2563	Hs.6658	Hs.209634			Hs.85963		HS:2115/9	Hs.7122	Hs.32539	Hs.40910		Hs.99995	Hs.9573
AA719160 Hs.120367	ဖွ	N26711 Hs.42245	R64008 Hs.28462		AA427778 Hs.98571	AA480815 Hs.76095		AA464246 Hs.85917		AA442040 Hs.7885		AA460330 Hs.89451	N73030 Hs.1281	AA142913 Hs.71721						AA446659 Hs.2563	AA490144 Hs.6658	N92136 Hs.48847			AA779835 Hs.122117		AA49/002 Hs.82914	AA460975 Hs.7122	W49563 RG.40	AA015782 Hs.40910		AA478647 Hs.99995	AA485752 Hs.9573
1292663	727278	266227	139689		771142	810724		810142		774071		795771	247816	504420						784179	839956	293421			1034625		897531	796148	324815	360674		754080	811161
GF204	GF203	GF201	GF200		GF201	GF200		GF201		GF200		GF200	GF200	GF202						GF201	GF202	GF200			GF204		GF200	GF201	GF200	GF201		GF200	GF203

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-1.0387338	-1.0715598	-1.5320077	1.50717808 1.29396322 1.1619703	-1.7826656 1.37481459 2.06000209	-1.0658873	1.47332903
2403.737 2402.708 2402.233 2401.995 2398.482	2398.441	2397.676 2396.473 2396.254 2394.706	2393.915 2392.876 2391.935 2391.221	2390.498 2390.441 2389.691	2388.626 2387.241 2386.574 2385.39	2384.751
TMSB4X PPOX SPIN		KIAA0607	SR-BP1	FLRT1 REV1		=
thymosin, beta 4, X chromosome ESTs protoporphyrinogen oxidase spindin ESTs ESTs Waakdy similar to !!!! ALU SUBFAMIL Y J MARNING FKTFY !!!	[H.sapiens] ESTs, Highly similar to DYNEIN HEAVY CHAIN.	CYTOSOLIC [R.norvegicus] ESTs ESTs neurochondrin	sigma receptor (SR31747 binding protein 1) ESTs ESTs	fibronectin leucine rich transmembrane protein 1 REV1 protein ESTs Homo sapiens clone 23582	Form Support Source ESTs ESTs ESTs	ESTs ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
Hs.75968 Hs.122110 Hs.100016 Hs.271871 Hs.124134	Hs.42656	Hs.169115 Hs.190117 Hs.177552 Hs.94653	Hs.2447 Hs.116290 Hs.23862 Hs.251792	Hs.12523 Hs.110347 Hs.120051	Hs.6421 Hs.54725 Hs.82213 Hs.22687	Hs.270559
AA634103 Hs.75968 AA779697 Hs.122110 AA157249 Hs.81311 AA417307 Hs.111980 R67886 Hs.28769	Hs.77085	W80389 Hs.42333 AA437107 Hs.98447 AA045175 Hs.61588 N66139 Hs.82757	W47484 Hs.24447 AA629014 Hs.116290 W58013 Hs.15253 R91060 Hs.34356	R42622 Hs.12523 AA481405 Hs.89373 AA707847 Hs.120051	Hs.6421 Hs.54725 Hs.82213 Hs.22687	
AA63410 AA77969 AA15124 AA41730 R67886	T80942	W80389 AA437107 AA045175 N66139	W47484 AA629014 W58013 R91060	R42622 AA481406 AA707847	R60014 N91566 N26407 B44707	N68966 N68966
868368 1034445 504452 731121 140240	109049	415406 757352 487766 278504	324210 743980 341336 194921	30963 746345 412967	42803 303023 258263	289145
GF201 GF204 GF201 GF202 GF201	GF200	GF201 GF202 GF204 GF201	GF200 GF204 GF200 GF200	GF202 GF203 GF203	GF202 GF202 GF201 GF201	GF202

	1.23833095	1 23833095	1.58536868		1.02743121				-1.3731953			1.01243153	-2.1233074	-1.1360725		-1.0181736	-1.3568157		-1.5374964		1.09413504		-1.1305724			1110050	1.15102563				1.47797361
2383.223	2382.402	9389 409	2381.679		2379.955				2377.168			2376.397	2376.33	2376.203		2376.165	2375.047	2374.819	2372.08		2369.449	2368.655	2367.84		000 2000	2307.003	2304.90			2364.555	2362.042
HUMRTVLH3	MAN1A2	MANIAS							PSMB9			CES1		DKFZP434C128		RY1	KRT7				MPV17		KIAA0628		COL V	10.01	FUXMI			NAPA	
endogenous retroviral protease	mannosidase, alpha, class 1A, member 2	mannosidase, alpha, class 1A,	EST EST	Homo sapiens (clone s153)	mRNA fragment	proteasome (prosome,	macropain) subunit, beta type,	 (large multifunctional 	protease 2)	carboxylesterase 1	(monocyte/macrophage serine	esterase 1)	ESTs	DKFZP434C128 protein	putative nucleic acid binding	protein RY-1	keratin 7	ESTs	ESTs	MpV17 transgene, murine	homolog, glomerulosclerosis	ESTs	KIAA0628 gene product	TATA box binding protein	(TDI)-associated lactor, Tilly	polyliletase II, G. 32AD	Torkhead box M1	N-ethylmaleimide-sensitive	tactor attachment protein,	alpha Homo sapiens mBNA for	KIAA1323 protein, partial cds
Hs.267319	Hs.239114	U. 220114	Hs.231499		Hs.6445				Hs.9280			Hs.76688	Hs.114438	Hs.222909		Hs.54649	Hs.23881	Hs.68490	Hs.10475		Hs.75659	Hs.271989	Hs.43133		0000	E/909'S	HS:239			Hs.75932	Hs.34892
N58401 Hs.118106	AA455062 Hs.101608	A A 4 E E O C 2 L 2 2 E 0 2 2	AA397918 Hs.97506		AA448690 Hs.6445				AA862434 Hs.9280			AA043436 Hs.76688	N54302 Hs.114438	AA062813 Hs.81499		AA293192 Hs.54649	AA489569 Hs.23881	AA778623 Hs.68490	R38613 Hs.106312		R55075 Hs.75659	H66670 Hs.108279	N56973 Hs.43133		01000	AAISU3UI HS.BUB/9	AA129552 HS.239			AA425754 Hs.75848	AA487510 Hs.35087
248098	812266	940066			786202				1456118			487458	244681	366154		714210	843321	1048969	22773		154707	211367	277536		001		564803			773381	839060
GF204	GF200	000	GF203		GF200				GF203			GF203	GF203	GF200		GF200	GF200	GF204	GF202		GF200	GF201	GF203			GFZOI	GF200			GF201	GF202

1,10142128	-1.8311278 -1.1355754	-1.9638651	1.18868715	1.44064619
2361.37 2361.349 2360.348 2359.321 2357.76	2356.245 2355.716 2355.617 2355.14	2354.979 2354.273 2352.11 2348.435	2347.054 2345.074 2345.074 2343.653	2342.15
AOP1 DTNA PIGR	0GT CYB561 DPEP1		MEIS2	DKFZP586I1023
antioxidant protein 1 ESTs dystrobrevin, alpha ESTs polymeric immunoglobulin receptor ESTs, Weakly similar to !!!! ALU SUBFAMILY SO WARNING ENTRY !!!!	O-linked N-acetylglucosamine (GicNAc) transferase (UDP-N-acetylglucosaminyl transferase) ESTs (Sydochrome b-561 dipeptidase 1 (renal) dipeptidase 1 (renal) estimation aminomenidase	[H.sapiens] ESTs ESTs ESTS Homo sapiens MEG3 mRNA, partial socionen imministration	gene ESTS ESTS, Moderately similar to hypothetical protein [H.sapiens] Meis (mouse) homolog 2 Homo sapiens clone 24583 mRNA sequence	DKFZP58611023 protein
Hs.75454 Hs.71052 Hs.54435 Hs.123468 Hs.205126 Hs.268904	Hs.100293 Hs.26622 Hs.153028 Hs.109	Hs.71746 Hs.48338 Hs.195822 Hs.114118	Hs.112844 Hs.27895 Hs.106642 Hs.104105 Hs.154336	Hs.111515
H19203 Hs.75454 AA127017 Hs.71052 H09172 Hs.54435 AA889055 Hs.123468 AA485303 Hs.108339 R00151 Hs.18860	AA425655 Hs.29483 R59116 Hs.26622 AA427768 Hs.119307 AA863424 Hs.109	AA778640 Hs.71746 AA056580 Hs.48338 AA485455 Hs.96602 AA702419 Hs.114118	H98695 Hs.26063 H15250 Hs.27895 H52543 Hs.22884 AA148641 Hs.6319 AA884648 Hs.126262	AA777488 Hs.26887
50888 502634 46518 1468764 840266	773220 41128 770845 1456900	1049006 489169 811071 447552	206907 49687 39885 503083 1502650	449112
GF201 GF201 GF200 GF204 GF204	GF201 GF202 GF204 GF203	GF203 GF201 GF201 GF204	GF200 GF201 GF201 GF201 GF204	GF203

No. 21726/92526

Deplet No. 9479	Atty Docket No. 2172	-1.2131518	1.50470872		1.45876506	1.08095366	1.36233039		1.24223396			1.43108178	1.98914913							-1.2298695		1.20365687	-1.4207532		-1.0281774		1.0/01/139		-2 5153236			1.30547177
· ++ V	Atty	2341.261	2340.281	2339.954	2339.493	2336.744	2336.289		2335.834	2334.523	2333.742	2330.702	2330.51				2329.525			2328.512		2327.548	2326.549	2325.959	2324.413		2323.722		2320 964	2320.671		2320.542
		DKFZP586B2420							DVL2				KIAA0264							ASNA1		RPC62							SMABCB1			
TO SECTION OF THE REPORT OF THE SECTION OF THE SECT	APPENDIX A	DKFZP586B2420 protein	EST	ESTs Human clone 23932 mRNA	sedneuce	ESTs	ESTs	dishevelled 2 (homologous to	Drosophila dsh)	ESTs	ESTs	ESTs	KIAA0264 protein	ESTs, Moderately similar to !!!!	ALU SUBFAMILY SQ	WARNING ENTRY !!!!	[H.sapiens]	arsA (bacterial) arsenite	transporter, ATP-binding,	homolog 1	polymerase (RNA) III (DNA	directed) (62kD)	ESTs	ESTs	EST	ESTs, Weakly similar to	unknown [H.sapiens] SWI/SNF related, matrix	associated, actin dependent	regulator of crifornatin,	ESTs	Homo sapiens mRNA; cDNA	DKFZp586J1717)
		Hs.7949	Hs.98341	Hs.20787	Hs.197766	Hs.269534	Hs.100912		Hs.118640	Hs.54544	Hs.99360	Hs.269135	Hs.122669				Hs.269589			Hs.165439		Hs.250745	Hs.32017	Hs.79013	Hs.112924		Hs.19002		He 150071	Hs.125406		Hs.56027
		N91382 Hs.54706	'n	R14869 Hs.108346	R39464 Hs.86921	_	_		AA448866 Hs.99146	N89857 Hs.54544	AA634472 Hs.99360	N69648 Hs.49724	AA486524 Hs.74588				AA705361 Hs.124879			AA504809 Hs.79354		AA282063 Hs.112003	AA398356 Hs.32017	AA152303 Hs.108684	AA620927 Hs.112924		R01499 Hs.19002		AAAA6000 He 76169	AA878939 Hs.125406		W48601 Hs.56027
	k et al.	306005	731048	129530	23932	126401	32683		786155	305515	743896	293654	843133				462079			825677		711959	726860	491237	1055636		123614		701010	1493217		325220
:	Westbrook et al.	GF202	GF202	GF201	GF200	GF200	GF202		GF200	GF201	GF204	GF203	GF200				GF204			GF200		GF200	GF202	GF201	GF202		GF200		000	GF204	ì	GF202

	2.38275862 1.01743406		1.41499658	-1.8794864	-1.2271097	-1.0621724		-1.862756	-2.6181909	-1.176217		1.05777125	1.06964451	1.50346539		-1.1550033	
	2319.189 2318.253	2318.052 2316.845	2316.792 2315.141	2314.963	2314.707	2313.496	2312.245	2311.354 2309.898	2309.886	2309.544	2307.787	2307.162	2306.068	2305.925	2305.865	2305.145	2304.516
		B3GAT1 MYF6					į	POP2			RHD			ACVR1		YDD19	GUCY1A3
APPENDIX A	ESTs, Highly similar to dJ1178H5.3 [H.sapiens] ESTs	beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) myogenic factor 6 (herculin) Homo sapiens mRNA for	KIAA1411 protein, partial cds ESTs Homo sapiens clone 23918	mRNA sequence Homo sapiens mRNA; cDNA DKFZp761K2312 (from clone	DKFZp761K2312) ESTs, Weakly similar to	MMSET type II [H.sapiens] ESTs, Weakly similar to DY3.6	[C.elegans]	POP2 (yeast homolog) ESTs	EST	ESTs Bhesus blood group, D	antigen	ESTs	ESTs	activin A receptor, type I ESTs, Weakly similar to HYPOTHETICAL PROTEIN	KIAA0063 [H.sapiens]	YDD19 protein	alpha 3
	Hs.43945 Hs.16570	Hs.3353 Hs.35937	Hs.107287 Hs.49059	Hs.108894	Hs.7159	Hs.203123	Hs.61661	Hs.26703 Hs.108358	Hs.105298	Hs.178331	Hs.108380	Hs.23630	Hs.18628	Hs.150402	Hs.116708	Hs.25615	Hs.75295
	AA418538 Hs.43945 V62763 Hs.16570	H11454 Hs.21391 AA176491 Hs.35937	33 Hs.6512 74 Hs.49059	AA421311 Hs.111923	AA704699 Hs.7159	9 Hs.35355	4A046700 Hs.61661	AA680279 Hs.26703 N66686 Hs.26934	AA489813 Hs.105298	AA465725 Hs.112162	9 Hs.108380		8 Hs.18628	4A136910 Hs.79127	2	6 Hs.101565	9 Hs.16711
			B55763 9 N64774			_	-	-	•	•	3 N53959	_	6 R07998	`	Ī	0 R78536	H24329
	767322 289562	47460 611255	40932 284569	739250	450926		487371	869182 279009	~	814992	247103	131563	127076	491066	~	144870	51749
	GF203 GF203	GF201 GF201	GF201 GF202	GF203	GF203	GF200	GF201	GF203 GF201	GF202	GF203	GF201	GF200	GF200	GF200	GF204	GF200	GF201

	1.13320151 -1.1065278 -1.1855031	1.28865117 -1.6770386 1.42285873		-1.0804289 2.56534212	1.19409082	-1.0218301 1.43649239 1.24518068	1.25727467
2302.666	2300.088 2298.399 2296.983	2296.676 2295.914 2295.318	2294.001 2291.675	2291.671 2289.25 2287.08	2282.91	2282.38 2282.047 2281.882 2280.368	2277.196 2276.978
	ЕТ	acr gcr	HMG1 CHN2	PME-1	NFAT5 .	PSPH STK9	EEF1G
ESTs, Weakly similar to faciogenital dysplasia protein 2 [M.musculus] fms-related tyrosine kinase 1 fms-related tyrosine kinas	factor receptor) EST EST lethal clant larvae (Drosophila)	Pentar gall ray var (2000) in the molog 1 ESTS grancatch high-mobility group (nonhistone chromosomal)	protein 1 chimerin (chimaerin) 2 protein phosphatase	methylesterase-1 ESTs ESTs ESTs transducin-like enhancer of spills, homolog of Drosophila	ESTS nuclear factor of activated T- cells 5 Homo sapiens mRNA; cDNA	UKF-Zp434U121) DKFZp434U121) phosphoserine phosphatase serine/threonine kinase 9 ESTs	EST eukaryotic translation elongation factor 1 gamma
Hs.58389	Hs.138671 Hs.98709 Hs.44753	Hs.95659 Hs.269513 Hs.79381	Hs.189509 Hs.15202	Hs.63304 Hs.170053 Hs.36574 He.31305	Hs.86998	Hs.98845 Hs.56407 Hs.50905 Hs.27946	Hs.54624 Hs.2186
AA443121 Hs.58389	AA058828 Hs.235 AA431187 Hs.98709 N35795 Hs.44753	AA026112 Hs.95659 AA680371 Hs.119282 R26792 Hs.91467	AA683085 Hs.74570 AA663933 Hs.105857	AA609009 Hs.63304 N48080 Hs.46815 AA029703 Hs.36574	AA478950 Hs.86998	AA435953 Hs.98845 AA488432 Hs.56407 N80713 Hs.50905 H18456 Hs.27946	4 Hs.54624 8 Hs.107159
809479 AA443	381931 AA05882 782158 AA43118 272458 N35795	469281 AA0261 430497 AA6803 132637 R26792	970591 AA683 855710 AA663	1030791 AA609 281757 N4808 366783 AA029		730564 AA4359: 843195 AA4884; 301018 N80713 50895 H18456	306121 N90514 141854 R70598
GF201 8	GF200 GF202 GF202	GF200 6 GF203 6 GF202 7	GF201 (GF204 (GF202 GF202 GF201		GF202 GF202 GF200 GF201	GF202 (

1.57124868 1.08765943 1.20692689	1.23336753 -1.99249 1.154271 1.70141979 -1.0897996 -1.250262 -1.215505 1.45710589 -1.0516614 2.19036795	-1.0579485	-1.2942575 -1.7826127 1.4236367 -1.1438603 -1.1089806
2276.974 2274.893 2274.015	2271.501 2271.36 2271.36 226.142 2265.303 2265.304 2265.304 2261.389 2261.389 2260.296	2257.958 2256.053 2254.071 2254.017 2253.915	2252.886 2252.714 2251.81 2251.401 2251.29 2260.124 2248.988
KIAA0860	FGFR3 KIAA0479	3C PKLR	DKFZP564M082 KIAA0397
Homo sapiens clone 643 unknown mRNA, complete sequence KIAAA0860 protein ESTs fibroblast growth factor receptor 3 achondroplasia.	thanatophoric dwarfism) KIAAQ479 protein ESTs ESTs ESTs ESTs ESTs ESTs ESTS ESTS	pyruvate kinase, liver and RBC PKLR ESTs ESTs, Weakly similar to unknown [H.sapiens] ESTs	DKFZP64M082 protein KIAA0937 protein EST EST's Homo sapiens mRNA; cDNA DKFZp434M196 (rom clone DKFZp434M196) EST's EST's
Hs.206501 Hs.26009 Hs.14855	Hs.1420 Hs.158244 Hs.19429 Hs.13012 Hs.86618 Hs.190151 Hs.26253 Hs.272024 Hs.272024 Hs.269106	Hs.35590 Hs.36565 Hs.15434 Hs.6553 Hs.250820	Hs.380.44 Hs.2255.60 Hs.12237.6 Hs.14398 Hs.125179 Hs.12700 Hs.58896
AA056375 Hs.110404 R61871 Hs.26009 R25980 Hs.14855	AA417654 Hs.1420 R98866 Hs.100227 AA468582 Hs.99429 AA287022 Hs.96618 AA448751 Hs.104279 N40186 Hs.45051 R42689 Hs.26255 R069890 Hs.26253 N76040 Hs.50678 N76040 Hs.50678	R08829 Hs.95990 W69160 Hs.36565 AA292721 Hs.96611 AA425382 Hs.6553 H97765 Hs.7729	AA47225 Hs.82904 AA47527 Hs.62284 AA788999 Hs.122376 H16581 Hs.52097 A4657705 Hs.125179 R42618 Hs.12700 W86791 Hs.58996
509458 43072 132630	752631 24938 809391 701579 683361 841697 276408 32095 128290 295359	127841 343688 701806 773157 209624	771317 841386 73787 1240243 49469 1435273 30959
GF202 GF203 GF200	GF200 GF201 GF202 GF203 GF203 GF202 GF202 GF200 GF200 GF200	GF200 GF204 GF203 GF201 GF201	GF201 GF202 GF202 GF203 GF201 GF204 GF202 GF202

Westbrook et al.	ok et al.				APPENDIXA		Atty	Atty Docket No. 2172
GF201 GF202	236034	H61243 N72300	Hs.80658 Hs.50214	Hs.80658 Hs.50214	uncoupling protein 2 (mitochondrial, proton carrier) UCP2 EST	UCP2	2248.362 2248.069	1.26567491
GF202	43729	H06195	Hs.7194	Hs.7194	Homo sapiens cDNA FLJ10614 fis, clone NTZRP2005436, weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 4 Homo sapiens mRNA; cDNA DKFZPS6RK1123 (fron clone	æ	2245.587	-1.0926023
GF204 GF204 GF201	856415 379796 321205	AA630768 AA706035 AA037352	AA630768 Hs.26837 AA706035 Hs.119946 AA037352 Hs.54567	Hs.26837 Hs.119946 Hs.54567	DKFZp586K1123) ESTs paired box gene 1	PAX1	2244.679 2244.621 2244.159	
GF202	731404	AA412247	4A412247 Hs.111970	Hs.111970	ESTs VRK3 for vaccinia related		2243.036	-1.5642168
GF203 GF202 GF203 GF204	1048698 52917 814816 450327	AA620609 H29231 AA455253 AA703619	AA620609 Hs.104841 H29231 Hs.32464 AA455253 Hs.99651 AA703619 Hs.119776	Hs.98289 Hs.27384 Hs.192837 Hs.188613	kinase 3 ESTs ESTs ESTs	LOC51231	2241.028 2240.331 2239.812 2238.475	-1.7154612 -1.1162536 1.50836658
GF204	432493	AA69950£	4A699505 Hs.17984	Hs.59255	DKFZP434N043 protein	DKFZP434N043	2238.178	
GF202 GF202 GF203	781404 727204 431263	AA430202 AA402484 AA682563	AA430202 Hs.125037 AA402484 Hs.8140 AA682563 Hs.17207	Hs.125037 Hs.8140 Hs.17207	Homo sapiens cDNA FLJ20548 fis, clone KAT11542 ESTs ESTs		2237.661 2237.221 2237.198	-1.7438511 -1.5619903 -1.8324234
GF200	949928	AA599173	AA599173 Hs.82210	Hs.82210	zinc finger protein 220 ESTs, Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII	ZNF220 !!	2236.38	1.20054208
GF202 GF200	511776 120173	AA088438 T95693	AA088438 Hs.68832 T95693 Hs.17614	Hs.129600 Hs.17614	[H.sapiens] ESTs ribonucleotide reductase M2		2235.375 2233.908	1.12331446
GF201 GF202 GF203	624627 841499 42389	AA187351 AA487264 R59992	AA187351 Hs.75319 AA487264 Hs.105712 359992 Hs.106675	Hs.75319 Hs.154974 Hs.271920	polypeptide ESTs ESTs	RRM2	2233.016 2231.03 2230.734	1.42783421

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-1.2982725	-1.1175949	-2.0454086	1.58810878	1.53039012	-1.0897371 -1.1026157	1.07248796	-1.0185702
2229.59 2229.537 2229.04	2227.639 2227.177	2226.463	2226.33	2226.296	2221.674 2220.957 2217.716	2217.223 2214.239	2213.922 2212.475
CTF1	H2AFY SPTI	CD36L2	FGFR1	GNAS1		FLOT2	PRKR KIAA0998
cardiotrophin 1 Homo sapiens clone 23645 mRNA sequence Homo sapiens mRNA; cDNA DKRZpA3410272 (from clone DKRZp434F0272)	HZA histone family, member Y HZAFY ESTs serine palmitoylfranslerase subunit CD36 antigen (collagen type I receptor, thrombospondin receptor, thrombospondin receptor Alface Spria.	integral membrane protein II) fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer	syndrome) guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide	1 ESTs, Moderately similar to IIII ALU SUBFAMILY SP WARNING ENTRY IIII	[H.sapiens] ESTs ESTs	flotillin 2 EST protein kinase, interferon- inducible double stranded	RNA dependent KIAA0998 protein
Hs.25537 Hs.6651 Hs.112594	Hs.75258 Hs.125024 Hs.90458	Hs.85963	Hs.748	Hs.273385	Hs.272122 Hs.233650 Hs.180115	Hs.184488 Hs.117009	Hs.274382 Hs.131525
AA708512 Hs.120129 AA455922 Hs.6651 AA599532 Hs.112443	AA488627 Hs.75258 N58473 Hs.47686 T49633 Hs.90545	AA776891 Hs.85963	AA281189 Hs.119017	W88587 Hs.59173	AA102223 Hs.125080 R53480 Hs.12375 AA707469 Hs.120018	R73545 Hs.22418 AA676866 Hs.117009	W42587 Hs.79121 R34225 Hs.24747
506583 813261 1090708	843075 248232 67735	858911	711857	417473	510906 40155 1291974	156386 460149	323185 13 6 026
GF204 GF203 GF204	GF202 GF201 GF202	GF203	GF200	GF202	GF202 GF203 GF204	GF200 GF204	GF201 GF203

-1.0427658	1.20879528	1.34488092	-1.1048462	1 70763256										-1.5811977		1.28024245			-1.0548818		1.41406991	1.04401566		-1.0169393	1.13579966			-1.0663935	1.09702899	
2211.616	2210.232	2209.638 2208.78	2208.674	2206 803		2206.619	2206.432		2203.324	2202.979		2202.731		2202.415	2202.004	2201.953			2201.166	2200.231	2200.034	2199.67	2199.609	2197.936	2197.552	2195.915		2194.952	2194.878	
HOFC1	NOTCH4	BZRP		9000	3	GRIA2	E2F3		PSG1			RBBP6		ATOX1		SIRT4						KIAA0990								
host cell factor C1 (VP16- accessory protein)	Notch (Drosophila) homolog 4 NOTCH4 benzodiazapine receptor	(peripheral)	EST	protein similar to E.coli yhdg	alutamate receptor, ionotropic,	AMPA 2	E2F transcription factor 3	pregnancy specific beta-1-	glycoprotein 1	ESTs	retinoblastoma-binding protein		ATX1 (antioxidant protein 1,	homolog 1	ESTs	sir2-like 4	ESTs, Weakly similar to	ACTIN, OT LOT LAGINIO 2	[H.sapiens]	ESTs	ESTs	KIAA0990 protein	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to !!!!	ALU CLASS B WARINING ENTRY !!!! [H.sapiens]	ESTs	
Hs.83634	Hs.11689	Hs.202 Hs.103840	Hs.48361	70020-11	13.37.027	Hs.89582	Hs.1189		Hs.173609	Hs.188750		Hs.85273		Hs.183373	Hs.264957	Hs.50861			Hs.23259	Hs.122161	Hs.93589	Hs.110488	Hs.109697	Hs.28631	Hs.267194	Hs.17674		Hs.28399	Hs.184183	
R69885 Hs.83634	AA419524 Hs.5205	AA455945 Hs.202 AA135933 Hs.103840	N59287 Hs,48361		77030457 115.37.057	H28734 Hs.89582	N92519 Hs.1189		N32768 Hs.119662	AA001950 Hs.14035		N26823 Hs.100117		R68360 Hs.28869	AA427396 Hs.108037	AA156947 Hs.50861			AA463453 Hs.23259	AA780365 Hs.122161	AA166703 Hs.93589	AA703453 Hs.110488	N75806 Hs.109697	N52591 Hs.28631	AA496666 Hs.13288	AA007370 Hs.17674		B63219 Hs 101460	_	
142395	752557	813444	289770	10000	1 20304	49987	304908		259591	427877		257106		137862	771050	502393			811775	1035664	593652	450160	300284	283878	755777	429299		138533	196544	
GF200	GF200	GF200 GF204	GF202	0	202 10	GF201	GF201		GF201	GF201		GF201		GF200	GF201	GF203			GF202	GF204	GF202	GF203	GF204	GF203	GF203	GF201		GE200	GF203	

	2.00601722	-2.2990282	-1.2270914		1.13986223	1.35036275				•	1.22688378	1.03803855			1.90413652		1.66908958	2.02220314						1 1349892	•	•				2.74872486			_		
2194.725	2193.304	2193.046	2192.179	2192.133	2190.785	2187.853		2187.046		2186.937	2186.467	2185.19		2185.005	2184.372	2183.338	2183.281	2183.279						9189 648	2182 234	2181 461				2180.607			2179.819	2179.651	
	RPS28				KIAA0372	HIRIP3		C220RF3		HSPA10														DAHR	<u> </u>			Θ		SLC25A6					
ESTs	ribosomal protein S28	ESTs	ESTs	ESTs	KIAA0372 gene product	HIRA-interacting protein 3	chromosome 22 open reading	frame 3	heat shock 70kD protein 10	(HSC71)	ESTs	ESTs	Homo sapiens mRNA for	KIAA1151 protein, partial cds	ESTs	ESTs	ESTs	ESTs	procollagen-proline, 2-	oxoglutarate 4-dioxygenase	(proline 4-hydroxylase), beta	polypeptide (protein disulfide	isomerase: thurnid hormone	hinding protein p55)	ESTs	ESTS	solute carrier family 25	(mitochondrial carrier; adenine	nucleotide translocator),	member 6	Homo sapiens mRNA full	length insert cDNA clone	EUROIMAGE 45912	ESTs	
Hs.16781	Hs.153177	Hs.101643	Hs.85885	Hs.31889	Hs.170098	Hs.26484		Hs.106730		Hs.180414	Hs.221988	Hs.217583		Hs.6298	Hs.99255	Hs.98006	Hs.182898	Hs.146278						He 75655	He 76611	Hs 268942	1			Hs.164280			Hs.27261	Hs.26216	
Hs.16781	AA287067 Hs.92402	Hs.101643	AA193569 Hs.85885	AA131664 Hs.31889	AA233339 Hs.18389	Hs.55862		Hs.19776		Hs.114004	AA400514 Hs.97816	AA485445 Hs.105666		AA411669 Hs.74947	4A451867 Hs.99255	Hs.48498	Hs.14385	Hs.108750						A A 408010 He 75655	AA420212 118.73033	Hs 51929				AA663439 Hs.74550			Hs.27261	Hs.26216	
T91039	AA28706	H05741	AA19356	AA13166	AA23333	H59788		H23229		H64147	AA400514	AA48544		AA411669	AA45186	N62248	N58198	H95956						A A A 10.501'	AA706738	H54659				AA66343			H09343	N93191	
112488	701677	43815	666028	503819	669999	208050		51991		209383	743377	811072		753271	786295	287762	247710	249953						760549	103005	203179				853570			45912	304854	
GF202	GF203	GF203	GF203	GF201	GF200	GF203		GF201		GF203	GF202	GF202		GF203	GF203	GF201	GF200	GF202						0000	20212	GE203	200			GF203			GF201	GF201	

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1.08279685	1.09671953 1.24280152	-1.1122862		-1.1642365		1.36177861			1.25014718			1.18212646					1.05934062			-1.4458194		1.24727766		-1.353508						-1.3460159		1.01230021
2179.545	2177.66 2177.607	2176.981		2176.833	2176.048	2175.585		2169.893	2169.141			2168.491	2168.36				2168.305	2167.331	2166.463	2166.226		2165.97	2165.562	2165.125			2165.081			2163.681	2163.104	2162.746
LTBP4												ACADM																				
latent transforming growth factor beta binding protein 4 Homo sapiens mRNA,	clone:RES4-4 ESTs	ESTs	Homo sapiens chromosome	19, cosmid R28379	ESTs	EST	H.sapiens mRNA for hcgVIII	protein	EST	acyl-Coenzyme A	dehydrogenase, C-4 to C-12	straight chain	EST	Homo sapiens cDNA	FLJ11110 fis, clone	PLACE1005921, weakly	similar to AIG1 PROTEIN	ESTs	ESTs	EST	ESTs, Weakly similar to CGI-	73 protein [H.sapiens]	ESTs	ESTs	Homo sapiens cDNA	FLJ20749 fis, clone	HEP05301	ESTs, Highly similar to	hypothetical protein	[H.sapiens]	ESTs	ESTs
Hs.85087	Hs.80306 Hs.202737	Hs.98122		Hs.22049	Hs.244487	Hs.86786		Hs.153618	Hs.83617			Hs.79158	Hs.260789				Hs.30822	Hs.58440	Hs.12253	Hs.94942		Hs.44114	Hs.151363	Hs.101773			Hs.8203			Hs.166406	Hs.268595	Hs.44380
Hs.85087	R69355 Hs.80306 AA132409 Hs.22268	4A412259 Hs.98122		4A427947 Hs.22049	4A121504 Hs.83888	4A219047 Hs.86786		4A701554 Hs.80234	Hs.83617			Hs.79158	Hs.92174				AA406363 Hs.30822	4A004684 Hs.58440	AA114864 Hs.12253	Hs.94942		Hs.44114	Hs.55590	Hs.101773			Hs.106250			Hs.131710	Hs.51693	Hs.44380
R87406	R69355 AA132409	AA41225		AA427947	AA121504	AA219047		AA701554	W90002			N70794	N30316				AA406363	AA004684	AA114864	W90105		N63448	W37721	H23270			R31681			W88753	T86687	N93122
166004	142122	731456		773512	489881	629885		435855	417307			298155	258033				753213	428811	491157	418113		278004	321931	52232			134419			417803	115114	304927
GF200	GF200	GF202		GF202	GF201	GF202		GF201	GF202			GF200	GF201				GF203	GF201	GF201	GF202		GF203	GF201	GF202			GF201			GF203	GF204	GF202

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1,34992452 1,28364129 1,13246091 -1,3421237 1,38492256 -1,2414879 -1,6579625	-1.0581976 -1.6283545 -1.1205793 -1.5797483	1,31758538	1.00432019 1.60083109 1.13495549 1.3026755 1.06656328
2151.399 2150.775 2150.504 2150.464 2148.865 2144.65 2143.448 2143.213 2142.973 2142.973	2139.291 2138.242 2135.706 2135.915 2133.879 2132.25 2131.038	2130.583 2124.8 2124.757 2124.339	2123.858 2120.721 2120.553 2119.707 2118.352 2118.352
TXNL2 XPO1 SPF31	HIP2 DKFZP586G1122 PKM2	MKP-L CARS ARL3	NFKBIA RANBP2 KIAA0574
ESTs ESTs thioradoxin-like ESTs ESTs ESTs ESTs ESTs exportin 1 (CRM1, yeast, homolog) splicing factor similar to dnaul	huntingtin-interacting protein 2 HIP2 DKFZP586G1122 protein EST ESTs pyruvate kinase, musole ESTS ESTS ESTS MKP-1 like protein brossine	phosphatase ESTs cysteinyl-tRNA synthetase ADP-ribosylation factor-like 3 nuclear factor of kappa light polypeptide gene enhancer in	B-cells inhibitor, alpha RN binding protein 2 ESTs, Weakly similar to APOLIPOPROTEIN(A) PRECURSOR [H.sapiens] KIAA0574 protein ESTs
Hs. 109302 Hs. 70944 Hs. 261162 Hs. 22646 Hs. 27463 Hs. 54901 Hs. 79090 Hs. 74711 Hs. 75611	Hs.155485 Hs.278422 Hs.47996 Hs.198281 Hs.110298 Hs.120860	Hs.91448 Hs.24611 Hs.159604 Hs.182215	Hs.81328 Hs.199179 Hs.166402 Hs.7132 Hs.56045 Hs.269341
N58372 Hs.108302 AA126694 Hs.70944 AA004811 Hs.18157 H17827 Hs.42844 H28458 Hs.113867 N03141 Hs.54901 AA47584 Hs.121222 AA57464 Hs.121222 AA57569 Hs.15681	178483 Hs.84713 182124 Hs.81980 456906 Hs.47996 100766 Hs.18965 153827 Hs.78035 M42736 Hs.40810	AA129677 Hs.91448 N32860 Hs.24611 AA464147 Hs.16642 AA644191 Hs.82105	2 Hs.81328 5 Hs.47908 07 Hs.119645 2 Hs.7132 2 Hs.55045 5 Hs.102812
N58372 A412669 A400481 H17927 H28458 N93141 A44758 T59055 AA28726	H78483 R92124 N56906 R00766 R53927 W42736	AA129677 N32860 AA464147 AA644191	W55872 N77205 A1023507 R60152 N94404 N67305
248027 490536 428912 50743 181805 304963 782669 74566 395898	233581 195330 280022 123858 39811 323260 856958	565493 259301 810321 845453	340734 245426 1643514 43022 309556 286566
GF202 GF202 GF201 GF203 GF204 GF202 GF201 GF200 GF203	GF200 GF203 GF202 GF200 GF204 GF204	GF200 GF201 GF200 GF201	GF200 GF200 GF204 GF202 GF202 GF202

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	-1.4921246 -1.2407983	1.22610886	1.06055343 -1.0999198	-1.1065774		1.98105295 -1.3093132	-1.1164622	-1.1353403	-1.1635579	
2116.202 2115.676	2115.588	2113.201 2112.756 2112.236	2112.212 2111.933	2111.717	2111.05	2110.971 2108.182	2107.799	2107.536	2107.058 2106.735 2105.734	2105.479 2105.473
	TLE2 PRED22	KIAA0631 CUL2				TOB1	KIAA0441	DLST	CD4 KIAA0468	
Homo sapiens partial mRNA for choline dehydrogenase (chdh gene) ESTs Tansducin-like enhancer of spilt 2, homolog of Drosophila	E(sp1) TI hypothetical protein Pł	ESTs KIAA0631 protein KI		Homo sapiens cDNA FLJ20185 fis, clone COLF0307 ESTs	ESTs ESTs, Weakly similar to	_DOC1 protein [H.sapiens] ransducer of ERBB2, 1 Tr	t tarate	complex) EST, Moderately similar to collagen alpha 5(IV) chain precursor, renal splice form		PLACE1005623 ESTs
Ho. 131668 (cf. Hs. 194305 ES	Hs.173063 E(Hs.167130 hy	Hs.269511 ES Hs.277543 KI Hs 82019 CU		Hc FL Hs.272972 CC Hs.10852 EE		Hs.41528 LE Hs.178137 tra		Hs.250801 co	Hs.133707 [H Hs.17483 Cl Hs.158287 Kl	Hs.58382 PI Hs.128757 E
AA878213 Hs.68848 AA706094 Hs.120887	AA873564 Hs.76103 W47366 Hs.10452	AA663552 Hs.116915 T95668 Hs.56712	AA447598 Hs.99122 AA416552 Hs.104793	W19329 Hs.7134 AA293206 Hs.10852	AA676636 Hs.130186	N22828 Hs.41528 AA490213 Hs.79558	V24789 Hs.32511	AA456824 Hs.401	R61877 Hs.91843 AA476285 Hs.105014 AA167273 Hs.28047	AA447579 Hs.77570 AA922703 Hs.128757
1416092 /	1473131 / 324719 \	853493 <i>f</i>				265627 1		815564	42864 770681 595593	782684 1474331
GF204 GF204	GF203 GF203	GF204 GF200	GF202	GF201	GF204	GF203	GF203	GF200	GF203 GF201 GF202	GF201 GF204

	-1.2341537	-1.1079579	1.02921109 -1.04461	1.13210763 1.00342448	-1.0043393	1.19254434	1.19254434 -1.3250478 -1.0349012
2105.312	2105.111	2104.45 2104.07 2103.407 2103.148 2103.137	2103.09 2102.115 2101.031 2100.637	2099.455 2099.455	2099.127 2098.488 2097.138	2095.044	2095.044 2093.795 2093.409 2091.097
WAS	PPP4C KIAA0344	KDELR2 CAPN3	GDF11	JUP		BAP1	BAP1 TCF21
Wiskott-Aldrich syndrome (ecezema-thrombocytopenia) profein phosphatase 4	(formerly X), catalytic subunit KIAA0344 gene product KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein	retention receptor 2 ESTs ESTs calpain, large polypeptide L3 ESTs	growth differentiation factor 11 GDF11 Homo sapiens mRNA; cDNA DKF2p564C1416 (from clone DKF2p564C1416) ESTs	EST junction plakoglobin ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING FNTRY !!!!	[H.sapiens] [H.sapiens] EST EST BRCA1 associated protein-1	hydrolase) BRCA1 associated protein-1	(any drawn carbox) (any drawns) ESTs ESTs transcription factor 21
Hs.2157	Hs.2903 Hs.184592	Hs.118778 Hs.22347 Hs.42683 Hs.40300 Hs.14070	Hs.34941 Hs.25910 Hs.268843 Hs.236438	Hs.2340	Hs.183969 Hs.230068 Hs.231043	Hs.106674	Hs.106674 Hs.119647 Hs.55200 Hs.78061
Hs.2157	AA405562 Hs.2903 AA677083 Hs.19092	AA416664 Hs.111238 H18936 Hs.22347 H99430 Hs.42683 AA426053 Hs.40300 AA894965 Hs.131928		Hs.93817 Hs.2340	3 Hs.95911 Hs.15132 Hs.113049	Hs.106674	H09065 Hs.75777 AA701931 Hs.119647 N98513 Hs.55200 AA699782 Hs.78061
H61193	AA40556 AA67708	AA41666 H18936 H99430 AA42605 AA89496	W49583 R54494 H58004 AA460826	N36873 R06417	Al005513 T90369 R02381	H09065	H09065 AA70193 N98513 AA69978
236282	772455 454190	731002 51606 262268 757248 1492382	325001 39725 204437 796266	273421 126320	1637279 110987 124611	46154	46154 435567 310501 461351
GF201	GF200 GF201	GF201 GF201 GF203 GF201 GF204	GF201 GF204 GF203 GF202	GF202 GF200	GF204 GF200 GF204	GF200	GF200 GF203 GF202 GF204

-1.2986949	1.59703498 1.12510642 -1.3135163 -1.1551626	1.31785808 -1.1772521 1.30645469	1.07022931	1.0042970 -1.4004249	-2.2390808
2090.322 2089.776 2088.124	2086.915 2086.736 2086.56 2086.302	2083.786 2082.887 2081.392	2080.885	2078.25 2076.336 2075.37 2075.97	2075.267 2075.087 2074.385 2073.62
PCANAP1 L1RL1LG	12AFL	TRIP7	РОН1	PTMS	RARRES3 AKAP2
te cancer associated 11 16 T1/ST2 receptor g protein	ESTs H2A histone family, member L H2AFL ESTs	I hormone receptor dor 7	_	TESSI Darathynosin ESTS Homo sapiens CDNA HOMO Sapiens CDNA FL110820 fis, Johne PLACE1002046, highly similar IO LIGATIN	Horno sapiens cDNA FLL20590 fis, clone KAT09052 ESTs retinoic acid receptor responder (tazarotene induced) 3 A kinase (PRKA) anchor A kinase (PRKA) anchor
Hs.118258 F Hs.54411 b Hs.13996 E	Hs.43213 E Hs.28777 H Hs.19985 E Hs.26344 E	0		Hs.45059 Hs.171814 FHs.22545 H Hs.274151 Hs.10018	Hs. 169549 Hs. 48349 Hs. 17466 Hs. 42322 Hs. 269060
AA149579 Hs.71990 AA285073 Hs.54411 AA463961 Hs.13996	AA496955 Hs.109008 AA453105 Hs.28777 AA678386 Hs.19985 AA0885 Hs.26344	AAA31611 Hs.77558 H83310 Hs.83796 AA437099 Hs.45032	Al024655 Hs.95631 R08876 Hs.76887	440202 Hs.45059 411526 Hs.2032 743910 Hs.22545 44133165 Hs.5693 N27829 Hs.108844	AA708989 Hs.10064 N59249 Hs.48349 W47350 Hs.17466 N51499 Hs.108870 N33228 Hs.108804
AA149579 AA285073 AA463961	AA496955 AA453105 AA678386 BA0885	AA431611 H83310 AA437099	AI024655 R08876	N40202 R11526 R43910 AA13316E N27829	AA706969 N59249 W47350 N51499 N33228
504290 700699 810305	823609 789091 431974	781704 222022 757337	1641737	276438 128302 32962 490766 270038	451911 289530 324225 282108 270535
GF202 GF200 GF201	GF203 GF200 GF203	GF200 GF203 GF202	GF204 GF200	GF202 GF200 GF201 GF204 GF204	GF203 GF201 GF201 GF201 GF201

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Att	2072.841 2072.009	2071.291	2070.922		2070.017 2069.164	2068.5 2067.436	2067.243 2066.471	2065.419	2065.419 2065.117	2062.429 2062.354
		РНАХ					NCYM	CD59	CD59	NMOR2
FUCULU EDZZEBEU APPENDIXA	ESTs ESTs	prospriory rated adaptor for RNA export ESTs, Weakly similar to similar to Glutaredoxin Zino	finger, C3HC4 type (Celegans) ESTs Homo sapiens cDNA FLI10052 fis. clone	HEMBA1001286, weakly similar to COMPLEMENT DECAY-ACCELERATING	FACTOR PRECURSOR ESTs	ESTs ESTs	DNA-binding transcriptional activator ESTs	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.345, EJ16, EJ30, EL32 and G344)	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.345, EJ16, EJ30, EL32 and G344)	NAD(P)H menadione oxidoreductase 2, dioxin- inducible ESTs
	Hs.19383 Hs.265640	Hs.267527	Hs.11307 Hs.103189		Hs.26244 Hs.32244	Hs.272739 Hs.113344	Hs.103989 Hs.94875	Hs.119663	Hs.119663 Hs.268061	Hs.73956 Hs.117823
	Hs.19383 Hs.55762	AA430653 Hs.102795	3 Hs.11307 3 Hs.103189		R54822 Hs.26244 AA447610 Hs.32244	AA608556 Hs.108689 AA700935 Hs.113344	AA609982 Hs.103989 AA457162 Hs.94875	9 Hs.77904	9 Hs.119663 4 Hs.35255	AA491124 Hs.73956 N59109 Hs.117823
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ok et al.	124014 347613	770398	37823 199334		40364	950678 383900	1031203 810497	208001	208001 248912	824024 246851
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-1.7506288 1.10182654 -1.2723497 1.05032695	1.55781639 -1.2765786 2.25127677	1.66594928	2.12945536	1.26690215	-1.143822	-1,6844444
2062.156 2061.872 2061.518 2060.955 2060.962	2060.167 2059.807 2059.262	2059.05 2057.904 2057.754 2055.782	2055.774 2055.049 2054.84	2054.463	2050.213 2049.359 2048.573 2042.731	2041.051 2040.542 2040.402
	KIAA0993	PPID KIAA0771 INSM1	KIAA0582	CSNK2B	Je FGG	
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Hs.58925 ES Hs.119187 ES Hs.55375 ES Hs.220963 ES Hs.209639 ES	Hs.17529 ES Hs.198135 KI/ Hs.182014 ES	Hs.143482 (c) Hs.6162 KI/ Hs.89584 ins Hs.269016 ES	Hs.274417 mF Hs.79507 KI Hs.180391 ES	Hs.165843 po Ho.165843 po Ho.	Hs.75431 ffb Hs.230143 ES Hs.163630 ES Hs.222079 ES	Hs.270404 PF Hs.25314 EU Hs.176583 ES
W88801 Hs.58925 AA778683 Hs.119187 W16792 Hs.55375 AA450353 Hs.48448 AA655185 Hs.116866 N74014 Hs.118181	T95238 Hs.17529 R09873 Hs.70457 N67006 Hs.33985	AA629987 Hs.75776 AA634466 Hs.6162 R38640 Hs.89584 H91245 Hs.41389	AA152202 Hs.76281 AA463630 Hs.79507 AA774159 Hs.10788	AA774638 Hs.84316 AA446016 Hs.75425	162652 Hs.81827 AA136541 Hs.71647 R96586 Hs.33583 AA909912 Hs.128617	T99719 Hs.129586 AA453473 Hs.25314 H17024 Hs.64000
417497 W 1049048 A 320345 W 785537 A 1031007 A 296669 N	120631 T8 128260 R6 295866 N	884500 A 743884 A 22895 R 241330 H	491500 A 811840 A 858567 A	399318 A. 781012 A.	67187 Ti 565949 A 199602 R 1505857 A	T22782 T1 795181 A 50782 H
GF201 GF203 GF202 GF203 GF204 GF203	GF200 GF200 GF200	GF202 GF204 GF201 GF201	GF204 GF202 GF204	GF203 GF202	GF201 GF202 GF200 GF204	GF203 GF201 GF202

	1.15426888 -1.7399148 1.07941994 1.18826518	1.07309073 -1.201435	1.54258524 1.17142176 -1.4122181 -1.112641 1.97620759	-1.0707406 -1.63728944 1.24542142
2040.299	2037.935 2036.825 2035.949 2035.686	2032.782 2031.658 2031.308	2027.989 2028.545 2024.426 2023.776 2022.109 2021.707 2020.902	2019.045 2018.868 2017.87 2017.673
	1.18	СТВР2	HSU53209 HFE ZNF35 FOSL1	
ESTS, Weakry similar to Yola/72wp (S. cerevisiae) ESTS, Weakry similar to ESTS, Weakry similar to FESTRADIOL THE BETA-DEHYDROARNASE A	Left broadland 4 H. sapiens) EST's Homo sapiens mRNA for KIAA1336 protein, partial cds merleukin 1, beta	ESTS C-terminal binding protein 2 ESTs	transformer-2 alpha (ritra-2 alpha) hemochromatosis ESTS ESTS Homo sapiers mRNA for Homo sapiers mRNA for MRA1399 protein, partial cds zino fringer protein 35 (clone HF.10) FOS-like artirien-1	ESTs, Weakly similar to Vsophospholipase [H sapiens] EST, Highly similar to R28830, 2 [H sapiens] Homo sapiens mRNA from chromosome 5q21-22, since:FBR89
Hs.71657 E Hs.108082 Y E E E	Hs.124696 [F Hs.112893 E Hs.145365 K Hs.126256 ir		HS.119523 a a HS.20019 E HS.39001 E HS.98006 E HS.6159 X HS.41732 HS.4245 F F HS.4245 F F	- 20 9 - 21 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
AA136699 Hs.71657 AA670353 Hs.108082	N65985 Hs.124696 AA620736 Hs.112893 N59131 Hs.11672 W47101 Hs.126256	H60514 Hs.108206 W49715 Hs.108956 AA128462 Hs.53446	R09691 Hs.24411 AA876054 Hs.20019 N21592 Hs.39001 AA406081 Hs.98006 R38369 Hs.66159 NG4607 Hs.41732 NR2617 Hs.4245	9 9
490994 AA1. 878403 AAG	293819 N65985 1049257 AA6207; 287634 N59131 324655 W47101		127677 R09691 1161797 AA87602 266161 N21592 743054 AA40602 23588 R38369 289923 N64607 110503 TR9817	
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ACADS		on EIF1AY	CDK4	į	IL4H	CALT	POU4F1	PPIF	E E	Ď.
acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain ESTs ESTs, Weakly similar to similar to SP:YR40_BACSU	[C.elegans] ESTs	eukaryotic translation initiation factor 1A, Y chromosome ESTs	cyclin-dependent kinase 4 ESTs, Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII	[H.sapiens]	interleukin 4 receptor caltractin (20kD calcium-	binding protein) POU domain, class 4,	transcription factor 1 peptidylprolyl isomerase F	(cyclophilin F) Human DNA sequence from clone RP5-876B10 on	Chromosome 1942.12-43. Contains the 3 end of the GNPAT gene for glyceronephosphate O-sayltransferase (DHAPAT, BAPAT, dihydroxyacetone phosphate acyttransferase, EC and the Annual Archandar and the Annual A	z.s.1.4z), ure gene ror a no protein (ortho
Hs.127610 Hs.269069	Hs.103147 Hs.269386	Hs.155103 Hs.191599	Hs.95577	Hs.175652	Hs.75545	Hs.82794	Hs.211588	Hs.173125		Hs.23971
AA676663 Hs.73966 H56088 Hs.34498	AA448189 Hs.57436 AA205838 Hs.96278	N92611 Hs.108575 AA416753 Hs.124069	AA486312 Hs.95577	AA063608 Hs.23817	AA292025 Hs.75545	N72193 Hs.82794	AA428196 Hs.74095	AA404286 Hs.111874		R46825 Hs.23971
896962	782787 647598	305122	842806	365990	714453	291216	773568	758343		36495
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1.18597804	-1.5506256	-1.2711102 1.87766057	2.29792996	-1.4026837	1 1975388	-1.4895161
2011.398	2008.372	2006.896 2004.795	2004.229	2003.662	2002.275 2001.763 2001.346 2001.052	1997.81 1997.557 1997.358 1997.359
АРРВР2		ALDH4	HADHSC		CAMKK2	
amyloid beta precursor protein (cytoplasmic tall)-binding protein 2 ESTs ESTs ESTs Abakky similar to IIII ESTs, Waakky similar to IIII	ENTRY III [H.sapiens] ESTs aldehyde dehydrogenase 4 (glutamate gamma- semialdehyde dehydrogenase;	pyrroline-5-carboxylate dehydrogenase) ESTs	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain FESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING FNTRY !!!!	[H.saplens] ESTs ESTs, Weakly similar to CYSTATIN SA PRECURSOR	[H.sapiens] calcium/calmodulin-dependent protein kinase kinase 2, beta (ESTs	ESTS Homo sapiens cDNA FLZ20731 fis, clone HEP10272 ESTS
Hs.84084 Hs.84469	Hs.173705 Hs.188614	Hs.77448 Hs.132230	Hs.7153	Hs.47334 Hs.119394	Hs.121554 Hs.108708 Hs.226422	Hs.22516 Hs.284636 Hs.98144 Hs.108887
AA046411 Hs.84084 R17746 Hs.84469	Hs.9069 Hs.16917	Hs.77448 Hs.42897	AA668230 Hs.7153	AA071045 Hs.109836 AA458879 Hs.98046	AA608859 Hs.121554 W70128 Hs.107703 AA875960 Hs.24142 DE3723 Lb. 35724	01
AA04641 R17746	T49854 N67553	H11346 N20810	AA66823	AA0710∠ AA45887	AA608859 W70128 AA875960	M42674 AA412512 H99704
380057 25395	68667 285076	47853 265087	853006	529827 810803	1048592 345793 1492251	49472 323084 730294 262927
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	1996	RASA1 1996	1995	H4FG 1995	FOXF1 1995	FOXF1 1995			1993	1992	DKFZP434I116 1990	DKFZP434C171 1989	1987			1987	SNX4 1987		RBMX 1986	•	AXL 1985	CD59 1985		CD59 1985	1982
APPENDIX A	ESTs	(GTPase activating protein) 1 F	ESTs	H4 histone family, member G F	forkhead box F1 F	forkhead box F1	Homo sapiens cDNA	FLJ10632 fis, clone	NT2RP2005637	ESTs	_	DKFZP434C171 protein	ESTs	Homo sapiens mRNA; cDNA	DKFZp564G212 (from clone	DKFZp564G212)		motif protein, X	osome		AXL receptor tyrosine kinase A	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16:345, EJ16, EJ30, EL32 and G344)	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5, EJ16,	EJ30, EL32 and G344) C	EST
	Hs.220482	Hs.758	Hs.269648	Hs.46423	Hs.155591	Hs.155591			Hs.202596	Hs.32062	Hs.16621	Hs.209100	Hs.122364			Hs.58662	Hs.267812		Hs.146381	Hs.268768	Hs.83341	Hs.119663		Hs.119663 Hs.83313	Hs.88033
	AA707781 Hs.120045	AA457027 Hs.758	AA777873 Hs.121961	AA868008 Hs.46423	AA112660 Hs.23269	AA112660 Hs.77288			Hs.102260	Hs.32062	Hs.17927	Hs.107365	AA788767 Hs.122364			Hs.58662	Hs.93345		Q		Hs.83341	Hs.77904		Hs.119663 Hs.12157	O
	AA70778	AA45702	AA77787	AA86800	AA11266	AA11266			H82421	N52980	H58884	H04771	AA78876			W81606	H73661		AA46109	H01068	H15718	H60549		H60549 T72825	AA25647
k et al.	413027	815507	449420	1461138	563444	563444			240109	244205	207379	152293	1240385			347763	214614		796161	149855	49318	208001		208001	682073
Westbrook et al.	GF203	GF200	GF203	GF203	GF200	GF200			GF201	GF200	GF200	GF203	GF203			GF202	GF200		GF202	GF203	GF201	GF200		GF200 GF201	GF203

1.42453117	1.06168921	-1.0449145	1.19615442	-1.3468114	1.37130364	1.06106505 -1.2546735	-1.2798883	-1.0754274
1982.72 1980.062	1978.951 1977.701 1977.367	1976.746 1976.687 1976.113	1975.708	1974.726 1974.442 1974.37 1973.947	1973.209 1972.57 1972.455 1970.383 1968.847	1968.835 1968.081	1967.869 1967.641	1967.19
SLC25A14	CLONE25003	KIAA0637	NAP1L1 FLJ20494	600	NDP52 RPS24 CALU		KLK10	отс
solute carrier family 25 (mitochondrial carrier, brain), member 14 ESTs	thiopurine S-methytransierase TPMT hypothetical protein CLON ESTs ESTs, Moderately similar to alternatively similar to	using exon 134 [H.saplens] KIAA0637 gene product Homo sapiens clone 23716 mRNA sequence	1-like 1 similar to mouse neuronal	ESIs ESTs EST CD9 antigen (p24)	nuclear domain 10 protein ribosomal protein S24 ESTs calumenin ESTs	ESTs ESTs	ESTs, Weakly similar to cDNA EST EMBL:C08125 comes from this gene [C.elegans] kallikrein 10 omithine	carbamoyltransferase
Hs.194686 Hs.188532	Hs.202669 Hs.22241 Hs.8116	Hs.269629 Hs.13604 Hs.12214	Hs.179662 Hs.111497	Hs.169104 Hs.15833 Hs.125483 Hs.1244	Hs.154230 Hs.180450 Hs.192124 Hs.7753 Hs.11859	Hs.18459 Hs.187459	Hs.16361 Hs.69423	Hs.117050
AA404241 Hs.22681 AA678058 Hs.117380	AA47098 Hs.78634 AA629251 Hs.22241 AA416631 Hs.8116	AA629668 Hs.121675 AA521298 Hs.13604 AA431773 Hs.12214	ιχ	0 0	H72030 HS.75406 AA626146 HS.116126 H10661 HS.30988 R78585 HS.7753 H17634 HS.31497	AA479148 Hs.18459 AA703640 Hs.121060	N58073 Hs.16361 AA459401 Hs.69423	AA677326 Hs.117050
758304 431843	784319 744044 731283	884951 827165 782503	275871	288849 246143 1466598 727251	214985 1055201 46236 144881 50805	754218 450353	247469 810960	454466
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Hs. 68398 Period (Drosophila) homolog 1 PER1 1964.989	-	H16769 HS.100873 AA219282 HS.110503	Hs.185689 Hs.172506	ESIS myosin VB	MYO5B	1966./31 1965.115	1.43348629 1.38843857
Hs.182280		T95053 Hs.105363 AA495809 Hs.105363	Hs.68398 Hs.105363	period (Drosophila) homolog 1 EST MADS box transcription enhancer factor 2, polypeptide A frovocyte enhancer factor	PER1	1964.999 1964.968	1.02944691
Hs.75643 Hs.75643 derived 2), 45kD NFE2 1964.89 Hs.30174 Hs.30174 Hs.30174 Hs.22479 Hs.22479 Hs.22479 Hs.22479 Hs.22479 Hs.1314 Hs.11314 Hs.11314 Hs.11314 Hs.11314 Hs.11314 Hs.11314 Hs.11319 Hs.25689 Hs.26889 Hs.26899 Hs.268999 Hs.26899 Hs.26899 Hs.26899 Hs.26899 Hs.26899 Hs.2		AA290847 Hs.78657	Hs.182280	2A) nuclear factor (erythroid-	MEF2A	1964.966	1.04520636
Hs. 20174 Hs. 30174 Hs. 30174 Complex, polypeptide 5, 19kD, SNAPCS 1961.393 34 Hs. 22479 Hs. 22479 KIAA111 ponolain (N-acelyl)-6- statistase (Sanfilippo disease lighted by the statistase (Sanfilippo disease) 1960.684 24 Hs. 15095 Hs. 164036 IIID 1950.684 14 Hs. 1514 Hs. 11314 Hs. 15095 1957.883 14 Hs. 1513 Hs. 1514 Hs. 1513 1958.062 14 Hs. 1514 Hs. 1514 Hs. 1514 1958.062 15 Hs. 1513 Hs. 1513 Interferon (alpha, beta and one-prior 1 linetreton (alpha, beta and one-		H59000 Hs.75643 AA668684 Hs.116609	Hs.75643 Hs.187807	derived 2), 45kD ESTs	NFE2	1964.89 1963.156	1.09247529
Hs. 3774 Hs. 164036 IIID) GNS 1958.052 45. 15.1596 Hs. 168036 IVID/Input/entical protein FL/20247 1957.833 14 Hs. 11314 DKFZP564N1383 protein DKFZP564N1383 1957.833 14 Hs. 1513 Initialicano (alpha, beta and morgal neceptor i DKFZP564N1383 1956.807 18 Hs. 1513 polymerase (RNA) POLR2D 1956.807 18 Hs. 1548 EST POLR2D 1956.415 19 Hs. 13189 EST 1956.415 1956.415 19 Hs. 13189 EST 1956.419 1956.419 19 Hs. 108023 ESTS 1954.419 1954.383 47 Hs. 30808 Hs. 108023 ESTS 1954.419 19 Hs. 30809 Hs. 2445 FOS-Ille antigen-1 FOSL1 1954.08 19 Hs. 3258 Hs. 2227571 signaling 4 1955.468 1955.468 19 Hs. 32997 ESTs EHDT 1956.408 1956.577 19 Hs. 32997 ESTs 1956.577 1956.577		W39639 Hs.30174 AA056734 Hs.22479	Hs.30174 Hs.22479	small nuclear RNA activating complex, polypeptide 5, 19kD KIAA110 protein glucosamine (N-acetyl)-6- sulfatase (Sanfilippo disease		1961.393 1960.694	1.1093673
22 Hs. 115095 Hs. 26533 hypothetical protein FLI20247 1957 833 (Hs. 115095 Hs. 115095 Hs. 11504 DKFZP564N1363 protein DKFZP564N1363 protein Interferont clains, beta and Hs. 1513 Hs. 1513 omega) receptor 1 FINAR1 10NA Hs. 15536 Hs. 194638 directed) polynepatide D POLR2D 1956.415 1956.435 Hs. 12799 Hs. 112799 EST Hs. 15268 Hs. 112799 EST Hs. 15636 Hs. 16923 Hs. 112799 FST Hs. 156303 Hs. 2465 Hs. 24		W56627 Hs.3774	Hs.164036	(QIII	GNS	1958.052	1.44746624
Hs.1513 Hs.1513 minchron rapiding, board and propertied by the properties of the polymentase (RNA) II (DNA POLRED 1956,752 polymentase (RNA) II (DNA POLRED 1956,493 polymentase (RNA) II (DNA POLRED 1956,493 polysidise hs.13198 ESTs polymentase (RNA) II (DNA POLRED 1956,493 polysidise hs.10822 hs.10823 hs.2055 ESTs polymental RS.3 hs.2055 ESTs polymental RS.3 hs.2055 Hs.20		AA677562 Hs.115095 AA465214 Hs.11314	Hs.96593 Hs.11314	hypothetical protein DKFZP564N1363 protein	FLJ20247 DKFZP564N1363	1957.833 1956.807	
Hs.194638 directed) polypeptide D POLR2D 1956.415 1956.415 1851.3189 ESTs 1955.433 1851.429 EST 1955.4819 1955.4819 EST 1955.4819 EST 1955.4819 1955.4819 EST 1955.4819 EST 1955.4819 1955.4819 EST 1955.4819 1955.4819 1955.4819 EH domain containing 1 EHD1 1955.481 1955.481 1855.97 EST 1955.77 1955.605 Hs.59997 EST 1955.77 1955.77 1955.605 Hs.59997 EST 1955.77 1955.77 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955.577 1955			Hs.1513	omega) receptor 1 polymerase (RNA) II (DNA	IFNAR1	1956.752	
Hs.11189 ESTs 1955.489 145.14289 ESTs 1955.489 145.14289 ESTs 1955.489 145.10823 ESTs 1955.389 1955.489 15.95289 ESTs 1955.389 1955.289 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.299 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 1955.279 19		H15431 Hs.15355	Hs.194638	directed) polypeptide D	POLR2D	1956.415	
Hs.112799 EST 1954.819 1 Hs.34665 ESTs 1954.889 1 Hs.04652 ESTs 1954.889 1 Hs.4245 FOS-like antigan-1 FOSL1 1953.173 1 Hs.4245 FOS-like antigan-1 FOSL1 1953.173 1 Hs.227571 signalling 4 1952.468 Hs.53997 ESTs 1953.78 1 Hs.05576 ESTs 1954.577 1955.65 1		AA165313 Hs.55468	Hs.131189	ESTs		1955.493	1.57893264
Hs.05829 ESTs		AA610000 Hs.112799	Hs.112799 Hs.34665	EST		1954.819	1.35694356
Hs.4245 ESTS FOS-like anigen-1 FOSL1 1959.173 1 1959.173 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		MA461749 IIS.340003	118.34000	EST.		1934.363	00000
Hs.4245 FOS-like antigen-1 FOSL1 1953.134 1 1 1953.134 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		N20045 HS.108923 AA059347 HS.95369	Hs.108923 Hs.95369	ESTS		1954.098 1953.173	-1.338502 1.51575669
Hs.227571 signalling 4 RGS4 1952.468 Hs.185119 EH domain containing 1 EHD1 1951.605 Hs.6997 ESTs 1950.378 Hs.106576 ESTs 1949.577			Hs.4245	FOS-like antigen-1 regulator of G-protein	FOSL1	1953.134	1.55291392
Hs.15519 EH domain containing 1 EHD1 1951-605 Hs.5997 ESTs 1950.378 Hs.106576 ESTs 1945.577		AA007419 Hs.4758	Hs.227571	signalling 4	RGS4	1952.468	
Hs.106576 ESTs 1949.577		AA626028 Hs.7214	Hs.155119	EH domain containing 1	EHD1	1951.605	1 0005150
		R56793 Hs.52454	Hs.106576	ESTs		1949.577	-1.000013

	1.09596549 1.87192788			1.29253949		1.02463129	-1.3073588			1.23042878					1.20921287		1.24368503	1.54424686		-1.1468526	1.102644	1.21791438	-1.1235452		-1.118295
	1948.979 1947.581	1946.648	1946.519	1946.368		1946.302	1946.03	1945.726		1944.972			1944.563		1942.381		1942.197	1942.083	1941.966	1941.933	1941.927	1940.436	1939.659		1939.347
	TCN2			DNCLI2		-				MOBP					SET		HMG14	KIAA0429	NEO1	C190RF3				į	RTVP1
transcobalamin II. macroovdio	anemia ESTs	ESTs	ES I S dynein, cytoplasmic, light	intermediate polypeptide 2	ESTs, Highly similar to	KIAA0793 protein [H.sapiens] FSTs. Highly similar to CGI-78	protein [H.sapiens]	ESTs	myelin-associated	oligodendrocyte basic protein	ESTs, Moderately similar to !!!!	WARNING ENTRY !!!!	[H.sapiens]	SET translocation (myeloid	leukemia-associated)	high-mobility group (nonhistone chromosomal)	protein 14	KIAA0429 gene product	neogenin (chicken) homolog 1 NEO1	chromosome 19 open reading frame 3	ESTs	ESTs	ESTs	glioma pathogenesis-related	protein
	Hs.84232 Hs.268751	Hs.124965	HS.42635	Hs.194625		Hs.101709	Hs.108408	Hs.122014		Hs.169309			Hs.182476		Hs.145279		Hs.251064	Hs.77694	Hs.90408	Hs.6454	Hs.42932	Hs.179750	Hs.48485		Hs.64639
	AA490680 Hs.84232 768245 Hs.28856		HS.42635	AA454959 Hs.43003		Hs.101709	Hs.109468	AA778303 Hs.122014		Hs.57707			AA464739 Hs.96337		AA608548 Hs.75055		Hs. 83477		AA454591 Hs.14379	AA878576 Hs.6454	Hs.42932	Hs.18015	Hs.48485		AA251800 Hs.64639
	AA490680 R68245	AA8574	N33224	AA4549		H14342	T55608	AA7783		H23310			AA4647.		AA6085		B53889	N78895	AA4545	AA8785	N21043	R00594	N62206		AA2518
	823864	1475410	270538	811870		48299	73600	378905		51974			810609		950607		138139	300012	811562	1492426	264858	123439	290158		684661
	GF200 GF200	GF204	GFZ01	GF200		GF202	GF202	GF204		GF200			GF201		GF200		GF200	GF202	GF201	GF203	GF202	GF200	GF203		GF200

1.32800227	1.13662767	-1.297584		-1.3327021	-1.177274			1.770619						1.26087277	1.10001201	1.06058962						1.13681906	-1.1271484	1.53175623	1.34348645	-1 5216879	6/00/201-	1.20180126
1938.963	1936.601	1936.411		1936.184	1935.871	1935.811	1934.577	1934.35	1933.223	1933.183			1932.868	1931.966	1931.818	1928.967	1928.923				1928.716	1928.364	1927.334	1927.15	1926.704	1926 631	1950.001	1926.339
NCOR1					DLX5	LOC51704	CHAD		VHL	TKTL1			SCYA3			TNNT3									UGB			HOXBS
nuclear receptor co-repressor	ESTS, Moderately similar to dJ83L6.1 [H.sapiens] Homo saniens clone 24828	mRNA sequence, partial cds	ESTs, Weakly similar to LYSOSOMAL PRO-X CARBOXYPEPTIDASE	PRECURSOR [H.sapiens]	distal-less homeo box 5	G protein-coupled receptor	chondroadherin	ESTs	von Hippel-Lindau syndrome	transketolase-like 1	small inducible cytokine A3	(homologous to mouse Mip-	1a)	EST	ESTs	troponin T3, skeletal, fast	ESTs	ESTs, Weakly similar to !!!!	ALU SUBFAMILY SB2	WARNING ENTRY !!!!	[H.sapiens]	ESTs	EST	ESTs	uteroglobin	Homo sapiens mRNA for KIAA1144 protein partial ods	יייייייייייייייייייייייייייייייייייייי	nomeo box 65
Hs.144904	Hs.11488	Hs.21708		Hs.14089	Hs.99348	Hs.242407	Hs.97220	Hs.21550	Hs.174007	Hs.102866			Hs.73817	Hs.105306	Hs.45091	Hs.73454	Hs.30880				Hs.113660	Hs.31297	Hs.102676	Hs.268620	Hs.2240	He 22675	113.6207.0	Hs.22554
T99688 Hs.108232	AA487433 Hs.11488	Hs.21708		AA418395 Hs.14089	Hs.99348	Hs.82945	2	Hs.118042	Hs.51238	AA919020 Hs.102866			Hs.119089	AA490058 Hs.105306	Hs.45091	AA449932 Hs.73454	Hs.30880				Hs.5499		Hs.102676	Hs.111675	Hs.2240	He 91718	01/15.61	Hs.22554
T99688	AA48743	H51336		AA41839	N74882	R43873	AA93721	N51657	R54177	AA91902			R47893	AA4900E	N40949	AA44993	H29257				N30639	AA457501	N52883	T90360	T63761	B16167	101011	H84287
122822	841327	179426		767268	299600	33603	1507713	280537	41607	1543346			153355	839903	277181	788695	49631				257823	838446	283633	110980	81336	53379	27000	222527
GF200	GF202	GF200		GF202	GF200	GF201	GF204	GF203	GF201	GF204			GF201	GF202	GF202	GF200	GF201				GF201	GF202	GF202	GF200	GF200	CE203	50215	GF203

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	-1.2397913	1.10056845	-1.1432835	-1.6848622 1.45870997 -1.2589365	1.28919582	-1.0637456 1.42169259 1.9662693 1.02335173	1.54425357 1.89000976
1926.227	1926.021 1922.705	1922.063	1921.54 1921.381	1921.372 1920.38 1919.494	1918.13	1917.497 1917.424 1917.064 1916.368	1916.299 1916.03
DDX17	EIF2S1 KIF5C	PPP2R5C	KCNK4 DKFZP434C211	MINK			NAP1L1
DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 17 (72kD) eukaryotic translation initiation	factor 2, subunit 1 (alpha, 35kD) kinesin family member 5C protein phosphatase 2,	regulatory subunit B (B56), gamma isoform potasslum inwardly-rectifying channel suhfamily K. member	4 DKFZP434C211 protein	Misshapen/NIK-related kinase MINK ESTs ESTs ESTs FLJ10937 fis, clone FLJ10937 fis, clone OVARCIO01094, mighty	mRNA ESTs ESTs, Weakly similar to IIII WARNING ENTRY IIII	H.sapiens] ESTs ESTs ESTs	nucleosome assembly protein 1-like 1 EST
Hs.6179	Hs.81613 Hs.6641	Hs.171734	Hs.97174 Hs.17270	Hs.112028 Hs.194620 Hs.268836	Hs.168640 Hs.38501	Hs.124841 Hs.93740 Hs.53127 Hs.238797 Hs.122001	Hs.179662 Hs.237339
Hs.108900	AA669452 Hs.81613 N66104 Hs.6641	W32943 Hs.118970	AA406036 Hs.97174 AA04447 Hs.17270	Hs.112028 Hs.18619 Hs.34212	Hs.108510 Hs.38501	AA032084 Hs.124841 V30205 Hs.93740 H39287 Hs.53127 V30704 Hs.7402 AA777949 Hs.12001	Hs.103144 Hs.93141
N22684	AA669452 N66104	W32943	AA406036 AA04447	R02058 R02716 R89567	H81907 N68424	AA032084 N30205 R99287 N30704 AA777949	R93829 H54764
266483	884894 278430	321661	743016 486493	124605 124087 195340	239889	470914 258860 201203 257387 449538	275871 203302
GF201	GF201 GF203	GF200	GF202 GF204	GF200 GF200 GF200	GF201 GF200	GF202 GF202 GF200 GF202	GF200 GF200

ESTs, Highly similar to zinc

		00070200	2.0334888			1.01049367	-1.0336148	1.29355061				1.83828796				-1.3173484		1.31395579	1.00151646			1.3037472		-1.811395	-1.017541	-1.017541	-1.4444744		-1.23771				
	1916.029	104	1915.193			1914.692	1913.427	1913.303			1913.14	1913.014		1912.119	1911.479	1909.855	1909.614	1908.913	1908.309	1908.249		1907.418		1907.349	1906.308	1906.308	1906.111	1904.628	1903.942	1903.755		1903.67	
		0 4 0 4 4 4	HADIIA			GCN5L2					GR01			×			ZNF297					CNN1		SUPT6H								KIAA0735	
finger protein 106	[M.musculus]	HABIIA, member hAS	Oricogene rannily	GCN5 (general control of	amino-acid synthesis, yeast,	homolog)-like 2	ESTs	ESTs	GRO1 oncogene (melanoma	growth stimulating activity,	alpha)	ESTs	GLUCOSE TRANSPORTER	×	ESTs	ESTs	zinc finger protein 297	ESTs	ESTs	ESTs	calponin 1, basic, smooth	muscle	suppressor of Ty	(S.cerevisiae) 6 homolog	ESTs	ESTs	ESTs	ESTs	EST	ESTs	KIAA0735 gene product;	homolog	•
	Hs.268226	10.75040	HS./3018			Hs.101067	Hs.184581	Hs.25087			Hs.789	Hs.97814		Hs.10574	Hs.20432	Hs.97313	Hs.206770	Hs.55977	Hs.268992	Hs.192245		Hs.21223		Hs.12303	Hs.86489	Hs.86489	Hs.97610	Hs.112876	Hs.48494	Hs.114172		Hs.8071	
	AA180214 Hs.57665		H0/695 HS.Z0018			AA452872 Hs.101067	AA447507 Hs.106385	R36181 Hs.25087			W46900 Hs.83333	AA400495 Hs.97814		59518 Hs.10574	4A677661 Hs.107397	4A402483 Hs.97313	4A455280 Hs.4945	W46955 Hs.55977	98529 Hs.18398	AA460281 Hs.14697		AA399519 Hs.21223		38625 Hs.105914	W52273 Hs.54485	V52273 Hs.86489	AA398327 Hs.97610	4A620638 Hs.112876	N62231 Hs.48494	4A703201 Hs.114172		R56082 Hs.25229	
	611472 A		1,55/39			788574 A	784289 A	136801 F			324437 V	743309 A		76049 T	897287 A	727202 A	810037 A	324593 V	123065 T	795726 A		726779 A		22991 H	325365 V	325365 V	726690 A	1048713 A	_	435976 A		40893 F	
	GF204		GF 200			GF200	GF202	GF200			GF201	GF202		GF201	GF204	GF203	GF201	GF202	GF200	GF201		GF200		GF202	GF200	GF200	GF203	GF204	GF202	GF204		GF201	

-1.0702694 1.22982039 1.03827685	1.32704796	1.15124819 -1.4322783 -2.0018061	1.36923973	1.01689322	1,22838532 -1,4011296 1,16445856	-1.1195067	1.10055017
1902.577 1902.144 1902.015 1901.128 1900.823	1899.281 1899.017	1898.509 1898.387 1897.192	1894.057	1892.451 1891.986	1891.082 1890.855 1890.311	1889.861 1889.14	1888.751 1888.519
JUND KIAA0786	CDC10	PIM2	SLC16A4		KIAA0246	KIAA0800	PSEN2 DKFZP586I1023
ESTs. Weakly similar to dul170K4.1 H.sapiensj jun D prote-oncogene latrophilin ESTs ESTs	ESTs cell division cycle 10 (homologous to CDC10 of S. cerevisiae)	Homo sapiens mRNA; cDNA DKFZp434G1919 (from clone DKFZp434G1919); partial cds pim-2 oncogene ESTs	solute carrier family 16 (monocarboxylic acid transporters), member 4 ESTs, Weakly similar to IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	[H.saplens] EST EST, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING FNTRY !!!!	[H.sapiens] ESTs KIAA0246 protein	ESTs KIAA0800 gene product presenilin 2 (Alzheimer	disease 4) DKFZP586I1023 protein
Hs.23406 Hs.2780 Hs.24212 Hs.123877 Hs.20685 Hs.32478	Hs.271627 Hs.184326	Hs.7256 Hs.80205 Hs.116415	Hs.23590	Hs.226142 Hs.103939	Hs.268231 Hs.62528 Hs.84753	Hs.102756 Hs.118738	Hs.25363 Hs.111515
H19105 Hs.23406 N66278 RG.31 A4598999 Hs.102604 R51871 Hs.123877 R10860 Hs.20685 AA029314 Hs.32478	AA130986 Hs.60509 AA205818 Hs.104136	N26515 Hs.57444 AA863383 Hs.80205 AA609189 Hs.112660	H73003 Hs.23590	N92804 Hs.54848 AA167500 Hs.103939	AA487297 Hs.35218 AA457485 Hs.62528 R42815 Hs.84753	AA460702 Hs.102756 R93309 Hs.13928	AA450249 Hs.25363 AA461309 Hs.5190
50914 285226 897731 39265 129088	586947 645315	266259 1469292 1031446	141562	308620 609047	838999 838287 32231	796711 275653	789253 796309
GF201 GF200 GF202 GF203 GF201 GF204	GF202 GF203	GF203 GF203 GF202	GF200	GF202 GF202	GF202 GF202 GF200	GF202 GF203	GF200 GF201

	-1.3224886	1.03784988		1.04039493	1.12776827	2.07410828	1.56737327	1.51154108	-1.2712339						1.23397626	-1.3584985						1.15831965			1.13401398		00000011	1.77833999
	1888.355	1886.233		1885.888	1884.869	1884.233	1883.638	1883.192	1882.982	1882.869				1882.703	1881.683	1879.683			1879.097	1878.967	1878.658	1878.513			1877.727		010	1877.612 187 6. 483
		PACE4														DKFZP58611023											15300	COXTS
ESTs, Weakly similar to SODIUM- AND CHLORIDE- DEPENDENT GLYCINE	TRANSPORTER 1 [H.sapiens] paired basic amino acid	cleaving system 4	alternatively spliced product	using exon 13A [H.sapiens]	EST	ESTs	Homo sapiens GT212 mRNA	ESTs	ESTs	ESTs	ESTs, Weakly similar to !!!!	ALU SUBFAMILY J	WARNING ENTRY !!!!	[H.sapiens]	ESTs	DKFZP58611023 protein	ESTs, Weakly similar to	similar to cell division control	protein [C.elegans]	ESTs	ESTs	ESTs	Human clone 161455 breast	expressed mRNA from	chromosome X	COX15 (yeast) homolog,	cytodillollie c sandase	assembly protein EST
	Hs.107854	Hs.170414		Hs.272068	Hs.93743	Hs.106843	Hs.83086	Hs.118208	Hs.93842	Hs.93828				Hs.191987	Hs.10432	Hs.111515			Hs.62918	Hs.20450	Hs.269882	Hs.54530			Hs.92683		1000	Hs.226581 Hs.120010
	Hs.129884	AA251457 Hs.77234		AA486185 Hs.125176	Hs.93743	4A424790 Hs.108465	Hs.83086	Hs.118208	Hs.117628	Hs.93828				AA776813 Hs.20535	AA488636 Hs.10432	Hs.23099			4A620831 Hs.62918	Hs.20450	Hs.51893	Hs.54530			Hs.92683		,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	AA455163 Hs.108991 AA707448 Hs.120010
	H81036	AA251457		AA486185	N30713	AA424790	H82977	N75318	H11369	N52136				AA776813	AA488636	N33054			AA620831	N62522	T95815	N89735			H25551			AA455163 AA707448
	230496	684626		842766	257414	768172	198917	298779	47853	284355				1291666	843250	270365			1055547	288807	120717	302004			161455		, 000,0	813304 1291946
	GF203	GF203		GF202	GF202	GF202	GF200	GF203	GF200	GF201				GF204	GF202	GF203			GF204	GF201	GF201	GF202			GF203		0000	GF202 GF204

Westbrook et al.

APPENDIX A

ESTs. Weakly similar to

1.29726864 1.41220812 .02622672 .02556039 2.10880915 2.07483492 1.53900547 1.12327591 -1.0448731 2.4206073 1 1133383 1.21726981 1.0860396 1.1429557 1.5164164 -1.043862 -1.169259 1865.003 1873.467 1870.637 875.158 872.784 870.978 869.214 867.445 864,949 874.627 872.727 872.554 872.006 1871.676 870.55 869.897 869.564 869.231 867.767 867.657 867.583 KIAA0205 KIAA0553 KIAA0057 HOXB6 GRB10 PVALB IFRD1 HLA-A USP4 LM04 ARF1 SOS1 CTH INHIBITOR, MUSCLE/BRAIN son of sevenless (Drosophila) growth factor receptor-bound ubiquitin specific protease 4 cystathionase (cystathionine Similarity to Yeast D-lactate dehydrogenase [C.elegans] developmental regulator 1 ADP-ribosylation factor 1 ESTs, Weakly similar to KIAA0057 gene product; KIAA0205 gene product major histocompatibilitv CAMP-DEPENDENT PROTEIN KINASE complex, class I, A FORM [H.sapiens] -IM domain only 4 **FRAM-like** protein **<1AA0553 protein** (proto-oncodene) nterferon-related omeo box B6 gamma-lyase) parvalbumin 1 polomor protein 10 ESTS ESTS ESTS ESTS EST 4s.106106 ls.119473 4s.105749 4s.181244 4s.153954 4s.102383 4s.19904 4s.50476 **1s.94869 1s.98428** 4s.77500 Hs.3844 **4s.81875 1s.46879** -ls.81849 ls.16979 1s.74571 4s.21371 4s.3610 4s.5672 4s.7879 Hs.106181 Hs.117890 AA704171 Hs.119473 Hs.105749 Hs.109956 AA700167 Hs.106520 Hs.102383 AA610066 Hs.93176 Hs.76813 AA454143 Hs.77500 AA136336 Hs.81875 Hs.46879 AA010609 Hs.81849 Hs.25592 Hs.19904 AA682626 Hs.50476 AA412520 Hs.16979 AA669557 Hs.74571 Hs.3610 AA443946 Hs.5672 Hs.3844 W60701 R48587 R91264 T74606 130669 178609 H27986 N56891 R07167 N32095 H98987 1031076 234965 565379 277506 430318 153614 126795 431284 260216 730313 341774 856800 452423 195138 258265 95288 460881 261441 757157 162533 34820 GF200 GF200 GF204 GF204 GF201 GF204 GF203 GF200 GF202 GF200 GF202 GF203 GF200 GF203 GF202 GF202 GF202 GF203 GF203 GF200 GF202

1.15623488	1.08607447		-1.5213151	-1.0657336	-1.0467256 1.55266143	1.11462203	1.26450508	-1.6333186		1.84426643 2.05182191
1864.945	1864.84 1864.678	1864.559	1863.773	1863.339	1863.185 1862.745	1862.471	1860.362	1859.62	1859.2	1858.852 1858.216
	KIAA0215	19713		АТР6Н	МАДН6	змР6		DR1		C8ORF2
Homo sapiens cDNA FLJ11041 fis, clone PLACE1004405 ESTs, Moderately similar to !!!! ALU SUBFAMILY SX	بر و الأه	=:	H.sapiens] ATPase, H+ transporting, vsosomal (vacuolar proton	a	_	bone morphogenetic protein 6 BMP6 Human clones 23667 and 23775 zinc finger protein	mRNA, complete cds down-regulator of transcription 1, TBP-binding (negative	≣ .⊓	ENTRY !!!! [H.sapiens] chromosome 8 open reading	-
Hs.28792 F	Hs.206088 [I	Hs.170116 P	Hs.222631 [I	Hs.24322 p	Hs.153863 h Hs.98636 E	Hs.6101 b	Hs.7137 n d d	Hs.16697 CHs.118156 E	Hs.269180 E	Hs.125849 fi
Hs.28792	Hs.9582 Hs.82292	Hs.73803	AA708058 Hs.120080	Hs.24322	Hs.23341 Hs.98636	Hs.6101	Hs.7137	AA043503 Hs.16697 N70688 Hs.118156	Hs.59342	AA679448 Hs.125849 N80361 Hs.14248
R66924	R39769 H14804	W73790	AA708058	AA486112 Hs.24322	AA235597 Hs.23341 AA429856 Hs.98636	AA424833 Hs.6101	R40324	AA043503 N70688	W93074	AA679448 N80361
140301	26267 49117	344134	392711	840803	724052 780964	768168	28098	487797 294244	415076	432227 292482
GF200	GF204 GF200	GF201	GF203	GF202	GF200 GF202	GF200	GF200	GF201 GF203	GF204	GF203 GF200

	1.1742837	1.0386526	-1.10791	1.15145374 -1.1758133		1.10661539 1.10003854 1.02848309 1.02588751	-1.0057733	1.1721095	1.01373546
1857.907	1857.526 1857.468	1857.424	1857.363	1857.33 1857.138	1856.231	1856.043 1855.193 1855.524 1853.195 1853.195	1852.67	1851.337	1851.195
NEURL	SFRS2IP DKFZP586N1922	HLA-DPB1	LIMS1	COL7A1 GPC4	CIT			SCD	LRP2
neuralized (Drosophila)-like	splicing factor, arginine/serinerich z, interacting protein DKFZP586N1922 protein maior histocompathility	complex, class II, DP beta 1	antigen-like domains 1 collagen, type VII, alpha 1 (epidermolysis bullosa,	dystrophic, dominant and recessive)	citron (mo-interacting, serine/theorine kinase 21)	Homo sapiens cDNA PLACE1010053, highly similar PLACE1010053, highly similar to M.muesoulus Spor mRNA for RETs ESTs ESTs ESTs ESTs, Weakly similar to problein-tyrosine phosphatase H. sapiens ESTs, Weakly similar to ALU SUBFAMILY.	WARNING ENTRY IIII [H.sapiens]	steartyr-CoA desaturase (delta-9-desaturase) Iow density linoprotain-ralated	protein 2
Hs.172700	Hs.51957 Hs.7357	Hs.814	Hs.112378	Hs.1640 Hs.58367	Hs.15767	Hs.8215 Hs.191194 Hs.8899 Hs.112804 Hs.20281	Hs.269390	Hs.119597	Hs.153595
Hs.34343	R85367 Hs.92847 AA488178 Hs.7357	7 Hs.814	AA609556 Hs.112378	AA598507 Hs.1640 W95636 Hs.58367	Hs.107817	AA465704 Hs.99653 R00262 Hs.121051 AA418875 Hs.31336 AA610016 Hs.112804 H00288 Hs.20281	AA489768 Hs.112230	Hs.119597	Hs.79722
N30706	R85367 AA488178	AA486627 Hs.814	AA609556	AA598507 W95636	N33778	AA465704 R00262 AA416875 AA610016	AA489768	R00707	R76808
257391	274578 877638	840942	1031698	897768 358217	272951	814915 123039 730016 1032015	839807	123474	143846
GF201	GF200 GF201	GF200	GF202	GF203 GF202	GF201	GF203 GF202 GF202 GF202 GF204	GF202	GF200	GF200

1.64332441	-1.2530666	1.16458855	1.30320032 -1.2772525 -1.762766		-1.0019484	-1.9401257
1850.896	1850.777 1850.101 1849.705 1849.67	1849.242	1848.001 1847.657 1847.465 1845.714	1845.341 1845.016 1844.685	1844.355 1843.699	1842.889 1842.078 1842.078
STAU		MUC1	SLC17A3	DSP G18 NSF	MTHFS DVETDERA/C198	2010
staufen (Drosophila, RNA- binding protein) Homo sapiens cDNA FLJ10669 its, done NTZRP2008275, weakly similar to MICROTUBULE- SASOCIARTE PROTEIN 1B	LC31 ESTs ESTs EST	mucin 1, transmembrane solute carrier family 17 (sodium phosphate), member	3 ESTs EST ESTs	desmoplakin (DPI, DPII) cytokine-inducible SH2- containing protein N-ethylmaleimide-sensitive factor	5,10-methenylletrahydrofolate synthetase (5- formylletrahydrofolate cyclo- ligase) ligase) For Standard Records	ESTS ESTS ESTS, Weakly similar to dd393P12.2 [H.sapiens] ESTs
Hs.6113	Hs.66048 Hs.6592 Hs.97804 Hs.116151	Hs.89603	Hs.104635 Hs.268948 Hs.43886 Hs.9016	Hs.74316 Hs.8257 Hs.108802	Hs.118131 Hs.6112	Hs.43687 Hs.117170 Hs.65588 Hs.167598
AA669068 Hs.6113	AA461521 Hs.66048 AA150015 Hs.6592 AA400469 Hs.97804 AA626325 Hs.116151	AA488073 Hs.89603	AA858296 Hs.104635 N66070 Hs.115276 N27108 Hs.43886 AA460965 Hs.9016	N54244 Hs.109322 AA427521 Hs.8257 H97488 Hs.108802	AA777551 Hs.118131 AA427921 Hs.6112 AAA77657 Us.01626	AA427678 Hs.117170 AA677578 Hs.117170 AA278780 Hs.55379 AA453470 Hs.96784
854450	795856 504516 742772 745577	840687	1323539 293991 258118 796127	247582 771058 251936	448432 773487	703751 703751 795171
GF203	GF201 GF201 GF202 GF204	GF200	GF203 GF203 GF202 GF201	GF201 GF201 GF201	GF203 GF201	GF202 GF204 GF203 GF203

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APPENDIX A

Westbrook et al.

	1.11747342 1.33354922	1.08626361	-1.2275961	-1.9037513	-1.5136346	-1.4649451 -1.1562651 1.73392086	1.02384493	1.18499582	-1.3039175
1840.917 1840.425 1840.12	1839.649 1839.125	1838.921	1838.005 1837.27 1836.999	1836.372	1833.173	1833.068 1831.215 1831.192	1830.732	1830.277 1828.501	1827.55 1826.632
DKFZP586G011	FHIT GAS1	RBMX	KIAA0950 FSP-2		ALPL	YDD19	МЕР1А	CYP1B1	DPM2
ESTs, Weakly similar to SODIUM- AND CHLORIDE- DEPENDENT GLYCINE TRANSPORTER 1 [H.sapiens] DKFZP586G011 protein ESTs	fragile histidine triad gene growth arrest-specific 1 RNA binding motif protein, X	chromosome Homo sapiens mRNA; cDNA DKFZp564M0616 (from clone	DKFZp564M0616) lifeguard fibrousheathin II	ESTs ESTs	alkaline phosphatase, liver/bone/kidney	YDD19 protein ESTs ESTs	meprin A, alpha (PABA peptide hydrolase) cytochrome P450, subfarnily I cifoxin-inducible), polypeptide I changowa 3 primary I changowa 3 primary	infantile) ESTs Colichyl-phosphate mannosyltransferase	polypeptide 2, regulatory subunit ESTs
Hs.107854 Hs.234265 Hs.63187	Hs.77252 Hs.65029	Hs.146381	Hs.21195 Hs.182859 Hs.252716	Hs.267027 Hs.9176	Hs.250769	Hs.25615 Hs.17850 Hs.191901	Hs.179704	Hs.154654 Hs.19167	Hs.108973 Hs.122986
N34637 Hs.44613 N32281 Hs.53086 AA055449 Hs.63187	4A256123 Hs.77252 4A292054 Hs.65029	AA487651 Hs.82083	R42922 Hs.21195 R88440 Hs.107819 H22927 Hs.6903		85 1	AA411556 Hs.90031 AA398420 Hs.17850 AA704688 Hs.120898	AA454113 Hs.73763	AA448157 Hs.82009 N69989 Hs.19167	R78591 Hs.29783 AA431192 Hs.122986
271280 N 272658 N 377515 A		841352 /	32331 F 166616 F 51920 H				788269	782760 <i>A</i> 296057 N	144887 F 782145 A
GF201 GF201 GF204	GF200 GF203	GF200	GF201 GF203 GF204	GF203 GF201	GF203	GF203 GF203 GF203	GF203	GF200 GF203	GF201 GF202

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1.10859864 1.17943647 -1.0960349 -1.0698708 2.13262341	1,12172363 1,48096519 1,270387 1,18505351 -1,0189267 -2,352692 -1,0725783 -1,2118182 1,00454185
1826.02 1824.784 1822.642 1821.78 1821.78 1820.446	1818.799 1815.589 1815.589 1814.614 1813.884 1813.862 1813.802 1810.201 1810.20 1807.406 1807.218 1807.218
PSMB7 ME1	1 WNT-4 HPS6KA3 OIP5 DKFZP564C1940 ADCY7 UBE2A DKFZP564D166
ESTs protessome, protessome, macropain) subunit, beta type, TS TS malic enzyme 1, NADP(+)-dependent, cytosolic ESTs ESTs	Human DNA sequence from clone 22446 on chromosome 1935.1-36.23 Contrains part of a gene similar to Mouse Witt-4 protein, the gene for CDC42 (cell division cycle 42 (ESTs, GSSs and a CpG Island WNT-4 ESTs, GSSs and a CpG Island WNT-4 ESTs, GSSs and a CpG Island WNT-4 ESTs (GNC), polypeptide 3 RPS6K ESTs (GNC), polypeptide 3 ADCY7 Ubquildin-conjugating enzyme CSTs adenylate cyclase 7 ADCY7 Ubquildin-conjugating enzyme CSTs ESTs ESTs ESTS ESTS ESTS
Hs.266868 Hs.118065 Hs.22010 Hs.14732 Hs.268051 Hs.32687 Hs.32687	Hs. 146409 Hs. 53112 Hs. 17366 Hs. 116766 Hs. 116206 Hs. 10817 Hs. 30812 Hs. 80612 Hs. 20871 Hs. 29903 Hs. 29903 Hs. 29903 Hs. 47248 Hs. 173317
AA489400 Hs.91876 W88466 Hs.22010 AA689689 Hs.14732 N48909 Hs.129893 W48708 Hs.32587 H47542 Hs.33962	AA008697 Hs.107354 H91065 Hs.53112 R95841 Hs.35462 H940144 Hs.91695 H54393 Hs.116206 AA420506 Hs.119398 AA42505 Hs.19320 AA601173 Hs.80612 AA621188 Hs.4996 AA706203 Hs.2986 AA706203 Hs.2986 AA706203 Hs.2986 AA706203 Hs.2986 AA706203 Hs.2986 AA70620 Hs.2986 AA708203 Hs.2986 AA7082 Hs.2097 N627767 Hs.4298 N627767 Hs.4298
214158 H77 843352 AAA 417388 W81 857264 AAE 279481 N8E 325079 W44 193533 H47	365531 AAC 240796 H91 199198 R85 38816 R85 38816 R85 5202958 H54 57833 AAA 57437 AA 74437 AA 392463 AA 757137 AA 757137 AA 757137 AA 757137 AA 757137 AA 757137 AA
GF200 GF201 GF201 GF203 GF203 GF203 GF203	6F201 6F204 6F203 6F203 6F203 6F202 6F200 6F200 6F201 6F201 6F203 6F201 6F201 6F203

1.14323295 -1.3377209 -1.1719644 -1.0507764	1.10594355 1.92875075 -1.1631109 -1.191249	-2.0001299 2.18891535 1.1411564 -1.0951042 1.8510007	1.76590542 -1.150779 -1.150779	1.39227901 1.13647818 -1.06263 1.0784757
1806.124 1805.799 1805.753 1804.334 1804.182 1803.75	1803.659 1803.635 1803.215 1802.953	1802.032 1801.492 1801.418 1801.305 1800.678 1799.401 1799.365	1797.131 1796.638 1796.169 1796.169	1795.841 1795.719 1795.44 1794.69
RBM9 KIAA0805 CRYAA	KISS1 PIPOX HSPCA	KIAA0625 KIAA0173 DATF1 BUP	GPR39 RAB2 KIAA0217 KIAA0217	YDD19 E46L UREB1
ESTs ESTs RNA binding motif protein 9 F RAAA6005 protein 6 K ESTs Crystallin, alpha A	KiSS-1 metastasis-suppressor H L-pipecolic acid oxidase ESTs heat shock 90kD protein 1, heat shock 90kD protein 1, plipha ESTs, Weakly similar to !!!!	tion	G protein-coupled receptor 39 C AMB2, member RAS oncogene femily KIAA0217 protein KIAA0217 protein Promo spelnes cDNA	itein E46 element
Hs.55153 Hs.112805 Hs.5011 Hs.55947 Hs.21860 Hs.184085	Hs.95008 Hs.271167 Hs.67552 Hs.180532	Hs.188834 Hs.154919 Hs.169910 Hs.37978 Hs.25373 Hs.155313 Hs.35660	Hs.85339 Hs.78851 Hs.78851	Hs.67619 Hs.25615 Hs.13493 Hs.158101 Hs.3383
R78589 Hs.55153 AA610036 Hs.112805 AA454681 Hs.5011 W46420 Hs.55947 R41227 Hs.21860 H95633 Hs.81923	AA464595 Hs.95008 H37880 Hs.52899 AA071514 Hs.67552 N62339 Hs.48517	AA478603 Hs.125174 AA490490 Hs.14623 AA682815 Hs.78145 H69275 Hs.37978 AA004823 Hs.58460 AA700739 Hs.35660	AA626797 Hs.116175 W60890 RG.43 AA491206 Hs.119441 AA491206 Hs.119441	AA446898 Hs 6584 R19406 Hs.44680 AA449943 Hs.111357 R23215 Hs.100931 AA446600 Hs.3383
144885 1032041 809645 323968 30114 220851	812955 191572 366057 290399	753657 823895 450453 213118 221776 429173 435351	877789 342069 824044 824044	784258 130027 788714 131024 783681
GF200 GF202 GF201 GF201 GF203	GF202 GF200 GF202 GF202	GF202 GF203 GF201 GF200 GF203 GF201 GF201	GF204 GF200 GF200	GF201 GF200 GF203 GF203 GF200

1.05543171 1.17603555 2,44995607 .45202741 -1.8173255 -1.4588036 74194109 1.06666889 1.29956714 -1.0790094-1.3333561 -1.1493661 793.274 790.675 790.659 1789.199 788.715 787.253 1785.573 793.229 792.401 792.207 790.322 789.727 1788.664 786.654 1786.044 790.16 1789.24 KIAA0253 ZNFN1A1 YWHAQ HBOA DEHYDRATASE (EC 4.2.1.55) nonooxygenase/tryptophan 5-ZINC FINGER PROTEIN 135 peta-tubulin mRNA, complete KIAA1225 protein, partial cds zinc finger protein, subfamily ESTs, Moderately similar to ESTs. Moderately similar to Homo sapiens clone 24703 HYDROXYBUTYRYL-COA nonooxygenase activation nistone acetyltransferase Homo sapiens mRNA for protein, theta polypeptide PLACE1000142, weakly autoantigen [H.sapiens] diabetes mellitus type I Homo sapiens cDNA FLJ10948 fis, clone KIAA0253 protein A, 1 (Ikaros) similar to 3-H.sapiens yrosine 3-ESTS ESTS ESTS ESTS ESTS ESTS ESTS EST Hs.102558 Hs.125249 Hs.193358 4s.62510 -ls.17966 4s.54452 4s.23972 **-18.58330** ls.31396 Hs.56187 -Is.99550 1s.21907 4s.97725 Hs.74405 Hs.9670 Hs.4788 Hs.8117 AA774047 Hs.121716 AA496884 Hs.101645 Hs.102558 Hs.125249 Hs.104151 4A280931 Hs.54452 Hs.62510 Hs.58330 4s.31396 Hs.56187 AA461515 Hs.99550 AA598797 Hs.21907 AA401377 Hs.97725 AA633997 Hs.74405 Hs.9670 Hs.4788 AA446451 Hs.8117 AA868748 W56810 H37989 N62487 N57798 172850 N73753 396527 115913 1460661 711680 199645 340926 344126 858488 340855 742696 781046 288748 159470 191603 858293 84264 397587 95844 898083 GF204 GF202 GF202 GF202 GF200 GF204 GF202 GF203 3F201 3F201 3F203 GF200 GF202 GF202 GF201

2.5676889		1.0216329		-1.2373653		-1.2303615	1.52582361	1.3563804		1.27710177
1784.955	1784.171	1783.533	1783.35	1783.043 1782.552		1779.523	1777.791 1776.559	1775.807	1774.484	1773.627
Q. Q.	ARNTL		ATP1A2	s KIAA0135			KIAA0929	KIAA1286 -	EIF3S4	
Homo sapiens clone 669 unknown mRNA, complete sequence CD3D antigen, delta nolynentide (TIT3 complex)	ary hydrocarbon receptor nuclear translocator-like Homo sapiens cDNA FLJ10931 fis, clone	OVARC1000564 ESTs ATPase. Na+/K+ transporting.	alpha 2 (+) polypeptide Homo sapiens mRNA; cDNA	DKFZp761E13121); partial cds KIAA0135 protein	Homo sapiens cDNA FLJ10782 fis, clone NT2RP3004480, weakly similar to VACUOLAR PROTEIN SORTING- ASSOCIATED PROTEIN	VPS35 KIAA0929 protein Msx2 interacting nuclear target	(MINT) homolog ESTs	KIAA1286 protein eukaryotic translation initiation factor 3, subunit 4 (delta,	44kD) ESTs	ESTs
Hs.180378 Hs.95327	Hs.74515	Hs.13794 Hs.44066	Hs.34114	Hs.4749 Hs.79337		Hs.264190	Hs.184245 Hs.104892	Hs.42179	Hs.28081 Hs.123645	Hs.62800
AA490243 Hs.26106 AA056946 Hs 95327	H17528 Hs.74515	AA459393 Hs.102986 N29638 Hs.44066	R73570 Hs.119068	AA773304 HS.4749 AA427740 HS.79337		N47691 Hs.106255	T96987 Hs.17961 AA479912 Hs.104892	AA235112 Hs.42318	AA668703 Hs.28081 R88992 Hs.107783	AA047008 Hs.62800
823755		810945 257342	156437	845037 770837		281010	120277			376893
GF202	GF201	GF201 GF202	GF201	GF203 GF201		GF203	GF204 GF202	GF203	GF201 GF201	GF202

Atty Docket No. 21 / 26/92	1.26163488	-1.1248031	-1.2506618	1.24474832	-1.17178 -2.3829597		1.03111625 1.44464639	1.62784823	-1.2106103	1.02128581 1.0284093 1.05071591
Ащу	1773.492 1773.43	1773.27 1772.701 1772.639 1772.576	1768.732	1768.549 1767.936 1767.927	1767.307 1766.472	1766.444	1766.314 1765.984 1765.313	1764.957	1764.852	1764.02 1763.362 1763.064
) ZNF36 KIAA0275	SAE1		TNFRSF12		0.9P.0	i 5	MAP2K3	GGTLA1
APPENDIX A	ESTs ESTs	zinc finger protein 36 (KOX 18) ZNF36 ESTs ESTS ESTS KIAA0275 gene product KIAA0275 Sene product SIMO-1 activatine enzyme	subunit 1	EST's, Weakly similar to cDNA EST EMBL-T00822 comes from this gene (Calegans) Home saplens GTL2 gene EST's tumor necrosis factor receptor superfamily, member 12 curanicarizing chain-	protein) ESTs Weakly similar to serine/threonine kinase	[M.musculus] Himan Chromosome 16 BAC	clone CIT987SK-A-362G6 ESTs fibrousheathin II	ESTs mitogen-activated protein	kinase kinase 3 gamma-glutamyltransferase-	like activity 1 ESTs ESTs
	Hs.163348 Hs.172971	Hs.132390 Hs.21835 Hs.6052 Hs.74583	Hs.250747	Hs.52891 Hs.105509 Hs.42946	Hs.180338 Hs.48818	Hs.97684	Hs.6349 Hs.15043 Hs. 252716	Hs.271689	Hs.180533	Hs.1675 Hs.170252 Hs.14662
	AA884321 Hs.125722 AA149061 Hs.103873	AA211508 Hs.363 AA454605 Hs.21835 AA463504 Hs.6052 AA398230 Hs.74583	AA598486 Hs.7600	N30222 Hs.52891 AA454710 Hs.101029 AA039857 Hs.42946	R34121 Hs.23741 N63543 Hs.48818	AA626260 Hs.97684	AA432023 Hs.6349 AA598809 Hs.15043	N74942 Hs.36648	H08749 Hs.2151	AA150859 Hs.1675 N50556 Hs.47076 AA706822 Hs.14662
k et al.	1466893 504859	562115 811581 797012 726678	898121	256975 809703 375853	136317 278198	745556	782497 897926 745468	295527	45641	504774 280758 451812
Westbrook et al.	GF204 GF202	GF201 GF201 GF201 GF200	GF203	GF203 GF201 GF201	GF200 GF202	GF204	GF200 GF203	GF200	GF200	GF200 GF202 GF203

1.52637903

1.32672994

-1.0316508

-1.386315 -1.0770531 -1.0475034

ŧ	ť	1762.322	1761.298	1760.423		1760.131	1759.546		1758.267	1758.005				1757.144	1757.032			1757.024	1756.707	1755.932	1755.834	1755.791		1755.742	1753.62			1752.929		1752.574	1/52.510
						SNRP70	KIAA0307	t)	CAPZB		.1.								KIAA1105					GAB1							
10.070204	APPENDIX A	ESTs	ESTs	ESTs	small nuclear ribonucleoprotein 70kD	polypeptide (RNP antigen)	KIAA0307 gene product	capping protein (actin filament)	muscle Z-line, beta	ESTs	ESTs, Moderately similar to C-	1-TETRAHYDROFOLATE	SYNTHASE, CYTOPLASMIC	[H.sapiens]	ESTs	Homo sapiens cDNA	FLJ10959 fis, clone	PLACE1000562	KIAA1105 protein	ESTs	EST	ESTs	GRB2-associated binding	protein 1	ESTs	Homo sapiens mRNA; cDNA	DKFZp434H1419 (from clone	DKFZp434H1419); partial cds Homo saniens mRNA: cDNA	DKFZp564E153 (from clone	DKFZp564E153)	ESIS
		Hs.90363	Hs.105695	Hs.46908		Hs.174051	Hs.6111		Hs.76368	Hs.112952				Hs.202437	Hs.21580			Hs.7041	Hs.23440	Hs.121528	Hs.18190	Hs.116104		Hs.239706	Hs.99361			Hs.56876		Hs.8769	HS.46472
		Hs.90363	Hs.38120	Hs.46908		Hs.83252	Hs.6111		4A430524 Hs.76368	AA621216 Hs.112952				AA609608 Hs.112733	Hs.21580			Hs.7041	4A496875 Hs.23440	4A757672 Hs.121528	Hs.18190	4A625899 Hs.116104		Hs.46455	Hs.99361			AA032198 Hs.56876		Hs.45108	HS.464/2
		H09971	133808 H62838	N49213		R02346	AA019774 Hs.6111		AA430524	AA621216				AA609608	H09748			R43609	AA496875	AA757672	T97931	AA625899		N68193	AA454186 Hs.99361			AA032198		W47641	N45091
	7 el al.	46584	208375	280257		124261	363590		769911	744413				1031745	46452			32801	897586	395485	121600	744943		292272	795452			375650		324307	282810
In to showthat M	westploo	GF201	GF200	GF202		GF200	GF200		GF201	GF202				GF202	GF201			GF204	GF203	GF203	GF200	GF204		GF200	GF202			GF202		GF201	GFZ01

-1.0233494 -1.4006024 -1.2064039

1.44596676

-1.5153175

1.16343468

GF201 GF201 GF202 GF203 GF201 GF201

GF200

Ally Downer INO. 2 17 2		1.23642534 -1.8601869		-1.1189806		1.33268189 -1.0960226	1.18471034	-1.1054614	1.21845846	1.27344444	36002001				-1.2824742	
Aut)	1751.26 1750.613	1749.825 1748.477	1747.459 1746.298	1745.738		1745.69 1745.433	1745.429	1744.946	1744.442	1744.184	1743.856	1739.879	1738.486	1737.724	1737.403	1735.695
	HBG2	ARL5	KIAA0479	NEFL				TNFRSF10B		2	TEO 25		MYO1B	KIAA0086		GRIK1
APPENDIX A	ESTs, Highly similar to PROTEIN ARGININE N- METHYLTRANSFERASE 2 [H.sapiens] hemodlobin, qamma G	ESTs ADP-ribosylation factor-like 5	ESTs KIAA0479 protein neurofilament, light	polypeptide (68kD) Homo sapiens cDNA	FLJ10894 fis, clone NT2RP4002888, highly similar to Homo sapiens mRNA;	cDNA DKFZp434F172 EST	EST temperature recentor	tunor necosso racor receptor superfamily, member 10b ESTs, Moderately similar to IIII ALU SUBFAMILY SB WARNING ENTRY IIII	[H.sapiens]	EST	ESTs	ESTs	myosin IB	KIAA0086 gene product	ESTs	kainate 1
	Hs.169396 Hs.272812	Hs.98348 Hs.42500	Hs.23823 Hs.158244	Hs.211584		Hs.31532 Hs.48943	Hs.54643	Hs.51233	Hs.103913	Hs.102298	Hs.83259	Hs.262212	Hs.34160	Hs.1560	Hs.25120	Hs.181581
	N52195 Hs.46661 AA454566 Hs.14938	AA421469 Hs.98348 AA424568 Hs.98417	R27319 Hs.23823 AA431435 Hs.41429	R14230 Hs.6625		15	N90688 Hs.54643	AA453410 Hs.51233	ß	H90573 Hs.102298		AA777233 Hs.122624	AA485871 Hs.75795	N30156 Hs.106277	AA496881 Hs.25120	R44776 Hs.22631
. et al.	284292	731037 767167	132307 782452	28422		450781 277871	306351	788185	591116	241794	321456	448205	840474	268176	897577	33096

GF203 GF202 GF202

GF200

GF202 GF200 GF202 GF201 GF201 GF201 GF201 GF201

GF201

1.42296827	1.22450258	-1.1088836	1.49158564	1.10258153 1.42850127	1.20456984
1735.477 1735.339 1734.487 1734.481	1733.363	1731.656 1730.816	1730.626 1730.299 1729.689 1729.592	1729.344 1729.326 1728.958	1727.947 1727.659 1727.412
	GTF2F1	KIAA0576		YWHAG ТН	CLU ELK4
ESTS ESTS ESTS ESTS ESTS ESTS ESTS ESTS	[H.sapiens] general transcription factor IIF, polypeptide 1 (74kD subunit)	ESTs KIAA0576 protein Homo sapiens mRNA; cDNA DKFZp434M0435 (from clone	DKFZp434M0435) ESTS EST ESTS Wrosine 3- monoxygenase/tryptophan 5- monooxygenase activation	protein, gamma polypeptide yrosine hydroxylase ESTs ESTs clusterin (complement lysis rinhibitor, SP-40,40, sulfated plycoprotein 2, testosterone-pressed prostite message	2, apolipoprotein J) ELK4, ETS-domain protein (SRF accessory protein 1) ESTs
Hs.13815 Hs.56178 Hs.40696 Hs.191889 Hs.24817	Hs.268677 Hs.68257	Hs.97779 Hs.172329	Hs.25700 Hs.25880 Hs.99688 Hs.24005	Hs.25001 Hs.178237 Hs.3769	Hs.75106 Hs.169241 Hs.87507
4 th 8	R08755 Hs.51926 AA282092 Hs.68257	(O N	N94435 Hs.25700 AA778560 Hs.25880 AA287948 Hs.9688 R26813 Hs.24005	AA432085 Hs.25001 AA447751 Hs.2031 R38289 Hs.124950	AA130017 Hs.75106 H61758 Hs.200 AA236015 Hs.87507
110167 340806 795280 1292880 855739	127408	743242 769773	309603 1048916 701409 132623	784129 813654 23572	5893 6 2 236155 684277
GF202 GF202 GF201 GF204 GF204	GF200 GF200	GF202 GF203	GF201 GF204 GF200 GF200	GF202 GF202 GF204	GF200 GF201 GF203

	1.26461416 1.01079647 -1.0165974	-1.735536 1.18274252	2.05784294	1.0440923	z.u9 ləsəu8 -1.7177263	1.22401212	1.52692055
1727.12	1726.808 1725.891 1725.72	1724.263 1723.992 1723.794 1723.684	1723.673	1722.365 1722.365 1722.348	1721.457 1721.065 1720.998 1720.304	1719.644 1719.16 1718.991	1717.694
			MAN2A2	TNFSF10	KIAA1104 AES MAP2K2	CCNT2 NUBP1 KIAA0620 SH3BGBI	10000
ESTs	flow or sapiens cDNA LL20463 fis, clone KAT06143 STs SSTs form sapiens cDNA flow sapiens cDNA LL20366 fis, clone	HEP18008 Homo sapiens mRNA for consistency partial cds segs segs segs and anosidase, alpha, class 2A, mannosidase, alpha, class 2A, mannosidase, alpha, class 2A,	nember 2 ESTs umor necrosis factor (ligand)	superfamily, member 10 ESTs Homo sapiens cDNA FLJ10724 fis, clone NT2RP3001176	KIAA 1104 protein EST amino-terminal enhancer of split mitogen-activated protein misse kinase 2	oyclin 72 nucleotide binding protein 1 (E.coli MinD like) KIAA0820 protein SH3-binding domain glutamic	ESTs
Hs.43558 E	Hs.120769 F Hs.170268 E Hs.271879 E	Hs.8358 H Hs.7871 K Hs.231072 E Hs.37745 E			Hs.260116 K Hs.28225 E Hs.244 si Hs.72241 ki		Hs.61568 E
N51365 Hs.43558	AA047275 Hs.109069 W45025 Hs.55784 N72252 Hs.102815	T61269 Hs.8358 AA487210 Hs.7871 N21688 Hs.43050 H59595 Hs.37745	75	H54629 Hs.83429 T72555 Hs.12573 AA011335 Hs.58650	AA447691 Hs.4812 AA417354 Hs.98225 AA443157 Hs.4312 AA425826 Hs.72241	~ m -	AA029561 Hs.61568
283204 N51	488555 AAC 322926 W44 291323 N72	77911 T61 841295 AA4 266455 N21 206755 H59	-		813609 AA4 731196 AA4 796775 AA4 769579 AA4		366708 AAC
GF204	GF202 GF202 GF203	GF201 GF201 GF203 GF203	GF201 GF200	GF201 GF201 GF201	GF202 GF202 GF201 GF201	GF200 GF201 GF201	GF202

-1.0853963	1.1042814	-1.4842727	1.85883918	-2.838595	1.79419287	-1.3470719	2.2745654					-1.1533571			1.02052452				.6125695	1.40201645	.32645092	
1717.452	1716.982 1716.896	1716.723	1716.331	1715.585	1715.481	1714.642		1712.888		1712.451			1710.453		1709.151	1707.918			1707.627	1707.424	1707.336	1707.306
	GGT1	SQI			KIAA0892					IFI30	DKFZP434A0131					KIAA1097			SNRPC		DKFZP586K0524	RPS6KC1
ESTs, Highly similar to SKD3 PROTEIN [M.musculus]	gamma-glutamyltransferase 1 GGT1 ESTs	syndrome)	Human glucocorticoid receptor alpha mRNA, variant 3' UTR	ESTs, Weakly similar to KIAA0745 protein [H.sapiens] Homo sapiens mBNA for	KIAA1211 protein, partial cds KIAA0892 protein	ESTs	ESTs	ESTs	interferon, gamma-inducible	protein 30	DKFZp434A0131 protein	ESTs	ESTs	Homo sapiens cDNA FLJ11219 fis. clone	PLACE1008122	KIAA1097 protein	small nuclear	ribonucleoprotein polypeptide	ပ	EST	DKFZP586K0524 protein	ribosomal protein S6 kinase, 52kD, polypeptide 1
Hs.21263	Hs.135 Hs.101064	Hs.172458	Hs.102761	Hs.15032	Hs.205293 Hs.4864	Hs.38455	Hs.112083	Hs.184233		Hs.14623	Hs.61950	Hs.269385	Hs.20085		Hs.40337	Hs.173694			Hs.1063	Hs.36094	Hs.27239	Hs.30352
AA127442 Hs.21263	AA620715 Hs.135 AA922858 Hs.101064	H14810 Hs.75429	N66871 Hs.102761	AA495804 Hs.15032	AA598594 Hs.112475 H98706 Hs.4864	166542 Hs.38455	V23885 Hs.112083	4A777138 Hs.122657		AA630800 Hs.119114	762577 Hs.61950	4A481770 Hs.100465	491961 Hs.20085		W06875 Hs.40512	AA917376 Hs.9011			4A411107 Hs.1063	H48467 Hs.36094	4A455663 Hs.109910	AA670286 Hs.30352
565653 AA	1049230 AA6 1457396 AA9	48801 H14	287125 N66	768381 AA	898204 AA	_	_	378157 AA		·		838831 AA	306919 N91		299663 W0	•			724387 AA	200604 H48	_	878281 AA6
GF202	GF203 GF204	GF203	GF202	GF202	GF203	GF200	GF202	GF204		GF201	GF201	GF202	GF201		GF200	GF204			GF200	GF200	GF203	GF204

ıtal. 19212 182547 Hs.76473 H		Ĩ	Hs.76473	APPENDIX A Insulin-like growth factor 2 receptor 105P2R	∠∠OSEDIU IGF2R	Atty 1707.208	Atty Docket No. 21726
5 N30372 Hs.54434 Hs.54434 i	HS.54434		inter	oceptor nterferon regulatory factor 5 ESTs	IRF5	1706.552	-1.7402112
N21056 Hs.42936 Hs.42936 I	Hs.42936		ESTs Novel	ESTS Novel human gene mapping to		1703.544	-1.1954848
AA699390 Hs.117318 Hs.184938 R43566 Hs.119029 Hs.119029	Hs.184938 Hs.119029	0	chom	chomosome 13 ESTs		1703.537	
491184 AA137072 Hs.44892 Hs.111915 UNT-ZP360 Homo sapic FL20767 Hs.24192 O.0.06896	Hs.44892 Hs.111515 Hs.24192 Hs.24192		Homo FLJ20 COL0	UKFZF38611023 protein Homo sapiens cDNA FLJ20767 fis, clone COL06986	UNFZF3ddi 1023	1701.987	1.09639597
AA663435 Hs.66369 Hs.228059	Hs.228059		KRAB- ligase	KRAB-associated protein 1 igase III, DNA, ATP-	TIF1B	1701.773	0000000
	Hs.100299		depend ESTs, I ALU SU WARNI	dependent ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!	LIG3	/6:10/1	1.72278133
530197 AA111975 Hs.118626 Hs.234035 [H.sapiens] 243638 N49883 Hs.33384 Hs.33384 ESTs	Hs.234035 Hs.33384 Hs.6368		[H.sapi ESTs	[H.sapiens] ESTs Poll-like recentor 2	TI R2	1701.344 1700.524 1700.01	1.3007402
15/791 HS.53505 HS.53505 3 AA256458 HS.44811 HS.44811	Hs.44811		ESTs	leceptor z	207	1699.919	1.38666624
Polygiur 859025 AA666078 Hs.30570 Hs.30570 1 Homo s	Hs.30570		polyglu 1 Homo s DKFZp	polyglutamine binding protein 1 Homo sapiens mRNA; cDNA DKF7n43401317 (from clone	PQBP1	1699.573	
712454 AA281729 Hs.25362 Hs.25362 DKFZp	Hs.25362		DKFZp	DKFZp43401317)		1698.016	-1.319737
ESTS.N 345051 W72803 Hs.57858 Hs.57958 KNA07 thyroid associa	Hs.57958		ESTs, V KIAA07 thyroid associa	ESTs, Weakly similar to KIAA0768 protein [H.sapiens] thyroid hormone receptorassociated protein, 95-kD		1696.196	
767315 AA418545 Hs.31659 Hs.31659 subunit 627508 AA192268 Hs.61645 Hs.4864 KIAA08 815794 AA485214 Hs.3164 Hs.3164 nucleoò	Hs.31659 Hs.4864 Hs.3164		subunit KIAA08 nucleob	subunit KIAA0892 protein nucleobindin 2	TRAP95 KIAA0892 NUCB2	1695.448 1695.046 1694.756	1.67623135 1.94838752 1.46353035

				_
	TACC2			HLA-DRB
APPENDIX A	transforming, acidic colled-coil containing protein 2	ESTs	major histocompatibility	complex, class II, DR beta 1 HLA-DRB1
	Hs.272023	Hs.11556		Hs.180255
	4458796 Hs.6145	30436 Hs.11556		88967 Hs.109129
	4458796	30436		88967

	1.07342217	-1.0891221				1.17678092		2.03541197	-1.3998254		-1.723272			1.76251486		1.3150319		1.02494375				2.1410045			1.52857025	-1.2908533			-1 6809885	200	1.10463853	
	1694.603	1694.422		1694.222		1693.253	1692.832	1692.62	1691.391		1690.073			1689.648	1688.961	1688.929		1688.869		1687.227	1686.066	1685.843			1685.761	1684.853	1683.716	1683 647	1682.38	200	1682.333	1682.201
	TACC2			HLA-DRB1		LGALS8					RTVP1									IL6					SGCB		DHPS				IL13RA1	IFNG
ransforming, acidic colled-coll	containing protein 2	ESTs		-	ecili, galacioside-biliding,	soluble, 8 (galectin 8)	ESTs	ESTs	ESTs	glioma pathogenesis-related		Homo sapiens mRNA; cDNA	OKFZp564D0472 (from clone	OKFZp564D0472)	ESTs	ESTs	ESTs, Highly similar to CGI-22	protein [H.sapiens]	nterleukin 6 (interferon, beta	(i	ESTs	ESTs	sarcoglycan, beta (43kD	dystrophin-associated	glycoprotein)	ESTs	deoxyhypusine synthase ESTs, Weakly similar to	B0041 5 [C elecans]	= ST	-	interleukin 13 receptor, alpha 1 IL13RA1	nterferon, gamma
_	Hs.272023	Hs.11556	-	Hs.180255		Hs.4082	Hs.43679	Hs.226666	Hs.34460		Hs.64639	_	_	Hs.208414	Hs.20969	Hs.98002		Hs.55041		Hs.93913		Hs.14599	•		Hs.77501	Hs.98696	Hs.79064	He 108812		18.12123	911	Hs.856
	AA458796 Hs.6145	N30436 Hs.11556		W88967 Hs.109129		397340 Hs.4082	V30157 Hs.43679	V57848 Hs.24897	AA490616 Hs.34460		H97597 Hs.114583			AA465188 Hs.90566	420522 Hs.20969	AA406062 Hs.98002		N94366 Hs.55041		V98591 Hs.93913	V26175 Hs.93405	R45632 Hs.14599			355105 Hs.77501	AA432246 Hs.98696	4A496046 Hs.79064	N95497 Hs 49594		7,01,927,118.12.12.03	AA598577 Hs.112474	AA969504 Hs.856
	838384 AA	271219 N3		417711 W		199403 RS	268178 N3	247082 NE	824115 A/		260696 HS			815069 AA	51308 HZ	743032 AA		309494 NS		310406 NS	269433 NZ	35620 R ²			40562 RE	782294 AA	759200 A/	267638 N				1579639 AA
	GF203	GF202		GF201		GF200	GF201	GF200	GF203		GF202			GF203	GF201	GF202		GF202		GF201	GF201	GF202			GF200	GF202	GF201	CE201	0000	61203	GF202	GF204

	-1.4319458	-1.5801792		1.13451799	-1.1320962		1.59944291	1.08377437	-1.0897364	
1682.168	1681.609	1681.521	1681.192	1680.591	1679.258 1679.007	1678.175	1677.382	1677.324 1677.228	1676.12	1675.262
	ATP5JD		AGTA2		DDX19 NRG2	UBE2G2	MYC	DKFZP434L243 LAMB2	DKFZP434K1772	
Homo sapiens cDNA FLJ11290 fis, clone PLACE1009622, weakly similar to MATERNAL EFFECT PROTEIN STAUFEN ATT synthase, H+ transnorfin, mitochondrial	F1F0, subunit d ESTs, Weakly similar to	TYPE II [H.sapiens] actin, alpha 2, smooth muscle,	aorta Homo sapiens cDNA FLJ10842 fis, clone	NT2RP4001343 DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 19	(Dbp5, yeast, homolog) neuregulin 2 ubiquitin-conjugating enzyme	UBC7)	v-myc avian myelocytomatosis viral oncogene homolog ESTs	DKFZP434L243 protein laminin, beta 2 (laminin S)	ESTS hyothetical protein Homo sapiens mRNA for	KIAA1340 protein, partial cds
Hs.96870	Hs.64593	Hs.58043	Hs.195851	Hs.260238	Hs.226396 Hs.113264	Hs.192853	Hs.79070 Hs.41840	Hs.21695 Hs.90291	Hs.96657	Hs.51743
Hs.127295	AA504246 Hs.64593	W69778 Hs.58043	AA634006 Hs.119122	AA446901 Hs.46541	AA857827 Hs.18665 AA706226 Hs.113264	Hs.102785	W87741 RG.52 AA703159 Hs.41840	AA400512 Hs.21695 AA156802 Hs.90291	AA463449 HS.104607 R96552 Hs.96657	Hs.125105
R39821	AA50424	W69778	AA63400	AA44690	AA85782 AA70622	N69044	W87741 AA703159	AA40051 AA15680	AA46344 R96552	R76890
25440	825386	343923	868304	784264	1418726 1240116	298097	417226	743382 502518	199610	143989
GF204	GF203	GF203	GF201	GF202	GF204 GF203	GF201	GF200	GF202 GF203	GF203	GF204

-1.1527334	1.14171021 1.55718479	1.45672936	-1.376436	-1.2963484	1.5899223	1.04746766	1,20960586 1,87396311 1,25714534
1674.519	1674.056 1674.054	1673.274 1672.912 1672.478	1672.461 1671.934	1670.89	1669.755 1669.129	1666.498	1666.309 1666.209 1666.013
		NNAT	KIAA1069	KIAA0735	TCF4		GALNT1
Homo sapiens cDNA FLJ10110 fis, clone HEMBA1002688 FSTs, Weakly similar to partial	CDS [C.elegans] ESTs	Hormo sapiens done 24422 FSTs FSTs Feuroratin ESTs, Weakly similar to uniquations TPR motif. Y	isoform [H.sapiens] KIAA1069 protein Homo sapiens cDNA	PLACE 10043, 900 KIAA0735 gene product; synaptic vesicle protein 28 homolog Homo sapiens mRNA; cDNA	DKFZp586F1122 (from clone DKFZp586F1122) transcription factor 4 Homo sapiens cDNA El 1994 of the clone of the	FLAZO 109 118, GIOTE COLL05067 UDP-N-acetyl-alpha-D- galactosamine:polypeptide N-	e 1 (GalNAc-T1) EST ESTs
Hs.264363	Hs.18349 Hs.47094	Hs.109268 Hs.85862 Hs.117546	Hs.118756 Hs.193143	Hs.16580	Hs.5306 Hs.75356	Hs.118194	Hs.80120 Hs.17922 Hs.38961
Hs.15769	Hs.18349 Hs.47094	AA599072 Hs.109268 AA194189 Hs.85862 R63918 Hs.117546	Hs.118756 Hs.26467	AA443193 Hs.16580 R53963 Hs.8071	AA454969 Hs.5306 AA669136 Hs.75356	Hs.118194	AA706987 Hs.7498 T96919 Hs.17922 H70942 Hs.38961
N62535	W32403 N50684	AA59907 AA19418 R63918	N20247 N62619	AA44319 R53963	AA45496 AA66913	N67797	AA70698 T96919 H70942
288827	321354 280831	950407 665738 139681	264627 288894	813195 39933	811888 854581	291548	431397 121415 239199
GF203	GF200 GF203	GF202 GF203 GF201	GF203 GF201	GF203 GF204	GF202 GF201	GF203	GF203 GF200 GF202

-1.3888129	2.26000127	1.12434353 -1.5064877	1.15747861	1.16899063		-1.1419531	1.05933345	-1.4681318	-1.1138137 -1.3584903
1665.531 1665.146 1664.629	1663.91	1663.889 1663.385	1663.203	1661.878	1661.023	1660.312	1659.868 1659.727 1658.476	1658.298	1657.465 1657.278 1657.211
	DKFZP586I1419 MAPK10						SLC7A8 KIAA0337	GDBR1	SOD3
platelet-den/ved growth factor beta polypeptide (simian sarcoma viral (v-sis) oncogene homolog) ESTs	DKFZP58611419 protein mitogen-activated protein kinase 10	ESTs EST ESTs, Weakly similar to IIII ALU SUBFAMILY SC WARNING ENTRY IIII	[H.sapiens] Homo sapiens mRNA; cDNA DKFZp566D224 (from clone	DKFZp566D224) Homo sapiens cDNA FLJ10120 fis, clone	HEMBA1002863 Homo sapiens mRNA, exon 1,	2, 3, 4, clone:RES4-24A solute carrier family 7 (cationic amino acid transporter, y+	system), member 8 ESTs KIAA0337 gene product putative glialblastoma cell	differentiation-related superoxide dismutase 3,	extracellular ESTs ESTs
Hs.1976 Hs.99689 Hs.119118	Hs.24341 Hs.151051	Hs.191582 Hs.251574	Hs.260556	Hs.28425	Hs.15953	Hs.104258	Hs.22891 Hs.91582 Hs.45180	Hs.9194	Hs.2420 Hs.54751 Hs.97737
	H94043 Hs.41949 T75436 Hs.89661	AA401438 Hs.97741 T55197 Hs.110326	R83853 Hs.57138	R63528 Hs.28425	W37841 Hs.103017	AA431970 Hs.104258	N23174 Hs.22891 AA743240 Hs.91582 AA187340 Hs.45180	AA026605 Hs.9194	AA454160 Hs.99358 N91914 Hs.54751 AA401409 Hs.97737
343320 701411 714151	242797	743197 73953	193937	138752	322154	782199	267666 1272428 624577	366518	795309 306829 743184
GF200 GF203 GF204	GF200 GF200	GF202 GF202	GF200	GF200	GF201	GF200	GF203 GF204 GF201	GF203	GF201 GF202 GF202

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1.08569689 -1.0029438 1.39025841 -1.2230391	-1.2268416 -1.20155479 -1.7192871	1,91350971	1.63970313 2.26887603 -1.6052929	2.19804181
1656.774 1656.686 1656.178 1655.474	1655.358 1654.681 1654.58 1654.445	1653.973 1653.486 1653.365	1652.593 1652.559 1651.883 1651.822 1651.632	1651.099
PDHB DKFZP564F0923	PHLDA1	ADTB1	POLL	
pyruvate dehydrogenase (lipoamide) beta ESTs DMF72564F0923 protein ESTs pleckstrin homology-like	domain, family A, member 1 ESTs, Weakly similar to retinal rod Na+/Ca+, K+ exchanger [H.sapiens] nel (chicken)-like 1 ESTs	adaptor-related protein complex 1, beta 1 subunit ESTS ESTS ESTS Human DNA sequence from chromosome 20. Contains the 3 and of the gene for a novel protein kinsee with Src homology domain 2. Such browned domains, a fleeringeneous nuclear infortuceloprotein A3 inclear infortuce	pseudogene, the gene for a novel protein similar ESTs ESTs polymerase (DNA-directed), almoda ESTs Homo sapiens TTF-1 incracting peptide 20 mRNA,	partial cus Homo sapiens mRNA for KIAA1219 protein, partial cds
Hs.979 Hs.110039 Hs.25524 Hs.123784	Hs.82101 Hs.173896 Hs.21602 Hs.30654	Hs.89576 Hs.120260 Hs.221498	Hs.184062 Hs.221754 Hs.268724 Hs.129903 Hs.16488	Hs.25431
AA521401 Hs.979 W74462 Hs.110039 AA419026 Hs.25524 AA454163 Hs.123784	H26271 Hs.32185 AA461505 Hs.14765 W16715 Hs.21602 AA428368 Hs.30654	H41489 Hs.89576 45904824 Hs.120260 H52623 Hs.53161	AA706829 Hs.3307 R84407 Hs.33451 R51535 Hs.25803 W89567 Hs.129903 N62832 Hs.16488	AA434139 Hs./9531 AA283091 Hs.115197
826077 346612 755564 795314	162077 795825 301504 773605	192569 1504481 202414	451805 194656 38691 344168 278564	713147
GF200 GF202 GF203 GF202	GF203 GF201 GF200 GF202	GF201 GF204 GF200	GF203 GF200 GF203 GF204 GF201	GF203

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1.59817891	1.32146359	1.16159943	1.08185751	-1.0183038 1.79701683	1.73304248 1.75029439 -1.3783876	1.03227351 -1.2158998 1.04218091 -1.6145584	1.26248668
1650.615 1650.58	1650.361 1649.987 1649.398	1649.362	1648.961 1648.059 1647.921	1647.56 1647.153 1646.682 1645.462	1645.217 1643.465 1643.438	1643.126 1642.598 1641.313 1641.285	1640.859
	ZNF9	rsta3	ART3	YDD19	KIAA1275 RNF13	SSB	НМG17
ESTs ESTs zinc finger protein 9 (a cellular retroviral nurlair and hinding			ase 3	ESIS YDD19 protein ESTs ESTs	275 protein ger protein 13 sapiens cDNA 3801 fis, clone A2001256 birchly similar		ESTs, Weakly similar to KIAA0924 protein IH.sapiens] nigh-mobility group (nonhistone chromosomal) protein 17
Hs.221849 E	Hs.2110 Hs.130873 Hs.268961	Hs.264428		Hs.120306 Hs.25615 Hs.58076 Hs.51574	ω – ω	Hs.40137 t Hs.32060 E Hs.83715 (Hs.112640 E	Hs.121830 P
R95132 Hs.56185 AA621291 Hs.88111	AA625995 Hs.2110 AA897765 Hs.130873 H77772 Hs.18046	AA421687 Hs.75801	W38022 Hs.39094 740025 Hs.106551 AA884935 Hs.24976	AA176156 Hs.73363 H60163 Hs.37811 W69912 Hs.58076 R38264 Hs.51574	2 5	N68492 Hs.40137 AA401452 Hs.32060 H29484 Hs.83715 AA609088 Hs.112640	AA775830 Hs.121830 H93087 Hs.57431
198694 R6 744605 AA	745503 A/ 1504340 A/ 214165 H7	739126 AA	> L 4.	610342 AA 207538 H6 344262 W 23529 R3		292567 NE 742030 AA 49970 H2 1031309 AA	878500 AA 241826 HE
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1,77655626 -1,0882522 1,18199401 -1,0745298 1,16627853	-1.1547361	-1.2681016		-1.4464847
1625.296 1625.024 1624.911 1624.766 1624.084 1622.766 1622.766 1622.767	1621.89 1621.582 1620.181	1619.94 1619.093 1618.644 1618.31	1618.29 1618.159 1617.956	1617.714 1617.701 1617.667
KIAA0821 TLOC1 PRKCZ		KIAA0962 RPL28	GNG2	COMP
ESTS ESTS EST EST EST EST KIAA0821 protein Translocation protein 1 protein knase 6, zeta ESTS	ESTs, Weakly similar to coded for by C. elegans cDNA M473c12.5 [C.elegans] ESTS Homo sapiens full length insert cDNA YNSBE09	ESTS, Moderately similar to KIAA1016 protein [H.sapiens] KA40962 protein ESTS ribosomal protein L28 graphine nucleodide-binding protein GIN/GIO) namna-2 protein GIN/GIO) namna-2	subunit Homo sapiens cDNA FLJ1074 fis, clone PLACE1005027 ESTs ESTs	orden (pseudoachondroplasia, epiphyseal dysplasia 1, multiple) ESTs growth hormone receptor
Hs. 256301 Hs. 33855 Hs. 94486 Hs. 116624 Hs. 107054 Hs. 107054 Hs. 107054 Hs. 8146 Hs. 8146 Hs. 78793 Hs. 94814	Hs.110407 Hs.227182 Hs.143330	Hs.42643 Hs.9059 Hs.124036 Hs.4437	Hs.23767 Hs.7904 Hs.17884	Hs.1584 Hs.116946 Hs.125180
AA430409 Hs.27217 44175 Hs.33855 WSDOT Hs.94486 AA688219 Hs.116624 AA458911 Hs.124830 H91861 Hs.125009 AA450205 Hs.8146 AA458933 Hs.115627 H9152 Hs.8853	AA421482 Hs.110407 AA128017 Hs.61597 H41196 Hs.33035	H99202 Hs.42843 H80637 Hs.40164 W86387 Hs.18132 AA486919 Hs.4437	AA425438 Hs.124215 AA487457 Hs.7904 W87371 Hs.17884	N94385 Hs.109691 AA680250 Hs.116946 R40357 Hs.106565
769945 AAA 192477 H41 305243 N96 852975 AAG 814406 AAA 221237 H91 789204 AAA 814266 AAA	731086 AA4 501890 AA1 175528 H41	261827 H96 239862 H80 415894 W8	773337 AA4 841610 AA4 417043 W8	309515 N94 869449 AA6 28705 R40
GF203 GF204 GF202 GF204 GF204 GF200 GF200 GF200	GF204 GF201 GF200	GF203 GF201 GF200 GF200	GF204 GF201 GF201	GF201 GF204 GF203

1.25618083 -1.405446 -1.5169635	-1.186886	-1.4809454 -1.072485 -1.6653373 1.3638981	1.81562395	-2.7859704
1617.663 1617.654 1617.14 1616.627 1615.514	1614.533 1613.28 1612.756	1611.269 1611.381 1611.391 1611.206	1610,254 1610,151 1609,293	1609.245 1607.837 1607.816 1607.548
PIASX-BETA SCP2 KIAA0989	KCNK3 DLX4 KIAA1109		CDC45L B4-2	SSSCA1 CRABP1 MRS1
Protein Inhibitor of activated STAT X ESTs ESTs sterol carrior protein 2 ESTs KIAA0989 protein	potassium channel, subfarnily K, member 3 (TASK) distal-less homeobox 4 KIA4109 protein ESTs, Waakly similar to IIII	WARNING EN I HY !!!! [H.sapiens] ESTS ESTS EST Homo sapiens mRNA; cDNA DKFZp434H0820; (from clone DKFZp434H0820; partial cots	CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like ESTs proline-rich protein with nuclear targeting signal Sjognen's	syndrome/scleroderma autoantigen 1 cellular retinoic acid-binding protein 1 EST MRS1 protein
Hs.111323 Hs.56025 Hs.22481 Hs.75760 Hs.271305 Hs.92186	Hs.24040 Hs.172648 Hs.6606	Hs.33827 Hs.98079 Hs.112603 Hs.112603	Hs.114311 Hs.269005 Hs.75969	Hs.25723 Hs.7678 Hs.116160 Hs.30985
N95048 Hs.32167 AA284261 Hs.56025 H23330 Hs.22481 AA664009 Hs.75760 AA521370 Hs.104423 W46944 Hs.112453	T49657 Hs.100401 R92495 Hs.96042 N90419 Hs.54619	W96174 Hs.33827 AA704698 Hs.120800 H98963 Hs.108854 AA608852 Hs.112603 N34466 Hs.109857	AA700904 Hs.114311 H70163 Hs.114253 AA669637 Hs.75969	AA456077 Hs.25723 AA454702 Hs.75602 AA626362 Hs.116160 AA464606 Hs.30985
305271 325169 51992 855395 826985	67769 196444 305920	361642 450924 261393 1048671 271115	453107 213575 857002	813499 809694 745097 812976
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-1.2893764	-1.5304346	1.80145709	1.74245064 1.43097537 1.19842116	1.52207726	-1.9729481 1.15931379	1.27894435
1606.957 1606.934 1606.445	1606.365 1606.272	1605.891	1604.206 1604.187 1603.877	1603.86 1603.802 1603.768	1602.714 1602.407 1601.661	1601.638 1600.828 1598.541
	MNT	LAF4	HSPA2 SF3B1	NFX1	TNFSF11 DKFZP434B103	
Homo sapiens mRNA; cDNA DKFZp564A2164 (from clone ESTE2p564A2164) ESTS ESTS, Weakly similar to transformation-related motain	transconnation rouses process. [H.sapiens] MAX binding protein Homo sapiens cDNA	PLOZOGO IIS, GOIRE PECOGS42 Iymphoid nuclear protein related to AF4 ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARDSHINC ENTEX	WAHNING ENTRY !!!! [H.sapien2] heat shock 70kD protein 2 splicing factor 3b, subunit 1, 155kD	ESTs, Weakly similar to KIAA0727 protein [H.sapiens] nuclear transcription factor, X- box binding 1 ESTs	tumor necrosis factor (ligand) superfamily, member 11 DKFZP434B103 protein EST ESTs, Highly similar to 5-	aminolevulinate syntrase [H.sapiens] ESTs ESTs
Hs.19150 Hs.112915 Hs.121817	Hs.265398 Hs.25497	Hs.99829 Hs.38070	Hs.24104 Hs.75452 Hs.13453	Hs.37617 Hs.3187 Hs.4958	Hs.115770 Hs.158196 Hs.116799	Hs.114018 Hs.20432 Hs.71947
AA425653 Hs.19150 AA620862 Hs.112915 AA775427 Hs.121817	AA682861 Hs.118133 AA455509 Hs.25497	AA490319 Hs.99829 H99588 Hs.38070	AA455102 Hs.75452 AA421230 Hs.13453	AA932955 Hs.37617 N59790 Hs.3187 R43915 Hs.4958	AA504211 Hs.115770 W81229 Hs.58641 AA633887 Hs.116799	AA699919 Hs.114018 W89107 Hs.20432 AA149121 Hs.71947
773214 1049336 878138	450398 809731	824460	123817 809838 739247	1565445 248583 33066	825287 347472 858199	435314 417706 504545
GF202 GF202 GF204	GF203 GF201	GF203	GF200 GF200 GF203	GF204 GF203 GF201	GF203 GF202 GF204	GF203 GF203 GF201

1.13518119		-1.1335758	-1.2361337	-1.5523954			-1.0096973		-1.2417033		-1.2417033	-1,098975					1000	-2.3184505		1.13561308	1.4868351	-1.8218288			-1.9772914					1.30788445			-1.010701	
1598.526	1598.073	1597.875	1597.813	1597.317			1597,241		1596.952		1596.952	1594.418			1594.393	1594.32		1594.048	1593.828	1592.527	1592.19	1592.129			1591.994	1590.731		1589 956		1589.385		1589.143	1589.013	
MUC2	CDC25C			YDD19			TNP1		TRIP6		TRIP6	OTOF						MINK		MCT-1										GFRA2		76		
mucin 2, intestinal/tracheal	cell division cycle 25C	ESTs	ESTs	YDD19 protein	transition protein 1 (during	histone to protamine	replacement)	thyroid hormone receptor	interactor 6	thyroid hormone receptor	interactor 6	otoferlin	Homo sapiens mRNA; cDNA	DKFZp434B1620 (from clone	DKFZp434B1620)	ESTs	,	Misshapen/NIK-related kinase MINK	ESTs	MCT-1 protein	ESTs	ESTs	Homo sapiens mRNA,	chromosome 1 specific	transcript KIAA0487	ESTs	ESTS, Weakly similar to !!!!	FINT BY III I'M sapiens)	Circle iii [iii:delcirc]	GDNF family receptor alpha 2 GFRA2	ECTs Weakly similar to	antigen NY-CO-33 [H.sapiens]	ESTs	
Hs.315	Hs.656	Hs.98168	Hs.102495	Hs.25615			Hs.3017		Hs.119498		Hs.119498	Hs.91608			Hs.43112	Hs.29696		Hs.112028	Hs.120340	Hs.102696	Hs.90725	Hs.270256			Hs.92381	Hs.146907		He 53565	200000	Hs.19317		Hs.31451	Hs.33412	
AA857748 Hs.315	01 Hs.656	AA416874 Hs.98168	4A487248 Hs.102495	21 Hs.23764			AA707545 Hs.3017		AA485677 Hs.78614		AA485677 Hs.119498	36 Hs.91608			AA029993 Hs.26774	97 Hs.29696		AA481868 Hs.89738	AA693513 Hs.120340	84 Hs.102696	AA486084 Hs.90725	40 Hs.114299			AA425630 Hs.92381	59 Hs.116339		109 He 53565		81 Hs.19317		AA406371 Hs.31451	AA125825 Hs.33412	
1435339 AA85	415102 W95001	730014 AA41	841485 AA48	35392 R45221			1292073 AA70		811108 AA48		811108 AA48	38517 R51236			470006 AA02			-	1276352 AA69	142586 R70784	840786 AA48				768643 AA42	121873 T97359		397337 WN09109		43207 H12981		753232 AA40	548693 AA12	
GF203	GF201	GF202	GF202	GF203			GF203		GF200		GF200	GF203			GF201	GF204		GF200	GF204	GF200	GF202	GF202			GF203	GF204		CE201	20 10	GF200		GF204	GF200	

Ally Docket No. 21	.3 -1.5622849 .4 -1.234086	9 -1.7617285	-1.2383907 7 -2.9090932	q	1.99967637		99		90			31 -1.0239578	1 2810223		2	3 1 2182615		3 2.15863671	-1.6862323	22
	1588.803 1588.604	1587.989	1587.751 1587.417	1607 148	1586.72	1586.17	1585.956		1585.866	1585.47	1584.716	1584.181	1589 594	1581 963		1581.93	00000	1580.43	1579.729	15/9./05
		NDUFC1			DPYSL2					FUS1		DKFZP586A0522		CAMO				RREB1	, MAD1L1	
APPENDIX A	ESTs ESTs NADH dehydrogenase (ubiouinone) 1, subcomplex	unknown, 1 (6kD, KFYI) Homo sapiens mRNA; cDNA DKFZp564O1016 (from clone	DKFZp564O1016) EST	kynurenine 3-monooxygenase	(kynurenine 3-nydroxylase) dihvdropvrimidinase-like 2	ESTs	ESTs	ESTs, Weakly similar to type 1 RNA helicase pNORF1	[H.sapiens]	lung cancer candidate	ESTs	DKFZP586A0522 protein ESTs Weakly similar to	protoin 4.1 G [H conjons]	sterol-C4-methyl oxidase-like	ESTS, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	[H.sapiens]	ras responsive element	binding protein 1	MAD1 (mitotic arrest deficient, yeast, homolog)-like 1	ESTs
	Hs.169119 Hs.23023	Hs.84549	Hs.15787 Hs.37844	0,000	HS.10/318 Hs.173381	Hs.86458	Hs.31783		Hs.20725	Hs.8186	Hs.178318	Hs.108740	112.074.400	Hs.271400	0.250.0350	Hs.82590	US. IOIOUS	Hs.204304	Hs.7345	Hs.194114
	AA394108 Hs.24725 AA456135 Hs.23023	AA460251 Hs.84549	N48361 Hs.15787 H60523 Hs.37844	000000	AA485429 Hs.33003	4A883660 Hs.86458	420826 Hs.31783		4A459402 Hs.20725	4A496147 Hs.8186	AA460846 Hs.99568	AA704713 Hs.108740	000000011000000000000000000000000000000	4A41/940 HS.01653	00.1		HU1940 HS.19239	AA757764 Hs.59472	AA718910 Hs.7345	AA443967 Hs.125884
ok et al.	725727 A 796366 A	796513 A	279810 N 207952 H		486/10 A		51548 H		810962 A	757220 A	796275 A	450938 A		/6/423 A			700471	395711 A	01	757200 A
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-1.1499227		-1.0019313	1.17059488		-1.3912217		1.40587731	-1.0180186	-1.0971526	-1.3635377				-1.3351869					1.10847703	1.62165765	2.00693589		1.55096761				1.29843785	-1.0178699	-1.1215124		1.21359418
1578.81	1578.299	1576.623	1575.259	1575.239	1574.707	1574.666	1574.393	1572.455	1572.016	1571.76		1571.091		1570.961				1570.788	1570.784	1570.624	1570.447		1570.325			1570.316	1570.197	1569.683	1569.482		1569.153
PC4	PTRF				TBCE			PCBP1				HAOX2		HNRPA2B1				NDUFS5					HLA-DQB1				RFP2	CRTL1			YES1
activated RNA polymerase II transcription cofactor 4 FANA POLYMERASE I AND TRANSCRIPT RELEASE	FACTOR	ESTs	ESTs	ESTs	tubulin-specific chaperone e	ESTs	ESTs	poly(rC)-binding protein 1	ESTs	ESTs	long-chain L-2-hydroxy acid	oxidase	heterogeneous nuclear	_	NADH dehydrogenase	(ubiquinone) Fe-S protein 5	(15kD) (NADH-coenzyme O	reductase)	ESTs	ESTs	ESTs	major histocompatibility		ESTs, Moderately similar to !!!!	WARNING FNTRY ##	[H.sapiens]	otein 2	otein 1	ESTs	па	viral oncogene homolog 1
Hs.74861	Hs.29759	Hs.55305	Hs.269099	Hs.125384	Hs.32675	Hs.213207	Hs.180060	Hs.2853	Hs.196008	Hs.99395		Hs.236545		Hs.75598				Hs.80595	Hs.185940	Hs.54888	Hs.20300		Hs.73931			Hs.271925	Hs.151428	Hs.2799	Hs.107375		Hs.194148
Hs.84521	4A443119 Hs.29759	Hs.55305	Hs.124726	4A878195 Hs.125384	AA504713 Hs.25995	Hs.107678	Hs.110535	AA490047 Hs.2853	Hs.100608	4A455133 Hs.99395		AA919149 Hs.118315		Hs.75598				4A214053 Hs.80595	4A757711 Hs.121594	Hs.54888	Hs.20300		AA442984 Hs.73932			Hs.45582	Hs.96830	Hs.2799	Hs.107375		RG.25
N51590	AA443119	W04687	N54783	AA878195	AA504713	N66068	N70791	AA490047	T84084	AA455133		AA919149		W02101				AA214053	AA757711	N93057	R09153		AA442984			N71080	R07594	AA115901 Hs.2799	H14988		N36882
280465	809473	320424	244300	1415732	825585	293985	298162	839890	111264	809869		1535106		327350				562409	396085	307774	127943		809298			299465	125685	531739	48662		273435
GF202	GF201	GF202	GF202	GF204	GF200	GF201	GF202	GF200	GF200	GF203		GF204		GF200				GF201	GF203	GF202	GF200		GF200			GF201	GF200	GF200	GF203		GF200

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	1.0739957	-2.0876589				1.17188405	1.03291522		1.13748718			1.43715085	-1.2277712		1.11168096	1.09953103											-1.0188885			2.46264103	
	1568.495	1568.323			1568.04	1567.931	1567.595		1567.141	1566.945	1566.893	1566.793	1566.164		1566.08	1565,476		1565.435				1564.792		1562 871		1562.79	1562.349			1562,182	1560.533
	PIK3C3		=:				CDK6		SAP18	KIAA0472					1351			RAB32								NFYA					
phosphoinositide-3-kinase,	class 3	EST	ESTs, Moderately similar to !!!! ALU SUBFAMILY SP	WARNING ENTRY !!!!	[H.sapiens]	ESTs	cyclin-dependent kinase 6	sin3-associated polypeptide,	18kD	KIAA0472 protein	ESTs	ESTs	ESTs	tetratricopeptide repeat	domain 1	ESTs	RAB32, member RAS	oncogene family	ESTs, Moderately similar to	PROTEIN-TYROSINE	PHOSPHATASE 1B	[H.sapiens]	Homo sapiens cDNA	COLORS	nuclear transcription factor Y,	alpha	ESTs	Homo sapiens cDNA	FLJ20071 fis, clone	COL01887	ESTs
	Hs.32971	Hs.97608			Hs.54073	Hs.104866	Hs.38481		Hs.23964	Hs.6874	Hs.7154	Hs.110044	Hs.114236		Hs.7733	Hs.98155		Hs.32217				Hs.175550		Hs 116470	2	Hs.797	Hs.162604		:	Hs.14328	Hs.82302
	AA455605 Hs.32971	AA398360 Hs.97608			N62404 Hs.106301	AA426038 Hs.104866	H73724 Hs.38481		AA133155 Hs.23964	N72307 Hs.53824	H17800 Hs.7154	T52700 Hs.110044	H75776 Hs.114236		AA291821 Hs.7733	AA412419 Hs.98155		AA057378 Hs.32217				W92859 Hs.33773		NE1006 He 47905		AA412691 Hs.797	AA504132 Hs.71725			AA485137 Hs.14328	AA633866 Hs.82302
		GF203 726857			3F201 288683				GF203 490729	GF201 291417	GF201 50250	3F202 67237	3F202 233246		GF200 725274	GF202 730530		GF201 472186				GF201 418366		303030		GF201 731648	-				GF204 858188

	1.08627741	-2.9395111			1.02553308				-1.2154171		-1.1847256		-2.2749787	-1.187969				1.58408756				1.58408756		-1.6439818	-1.290333						-1.1121259			1.37392411
	1558.549	1558.442	1558.439		1557.855	1557.831			1557.411	1557.121	1554.985		1554.775	1554.211				1554.007				1554.007		1553.867	1553.354	1552.413				1552.254	1552.063	1551.108	1551.045	1550.687
	SNRPG				COX6A1													YWHAB				YWHAB		DJ402G11.8										RFP
small nuclear ribonucleoprotein polypeptide		ESTs	ESTs	sytochrome c oxidase subunit	Vla polypeptide 1	ESTs	Homo sapiens mRNA; cDNA	OKFZp434E0517 (from clone	DKFZp434E0517)	ESTs	ESTs	Human gene from PAC	262D12, chromosome 1	ESTs	yrosine 3-	nonooxygenase/tryptophan 5-	nonooxygenase activation	protein, beta polypeptide	yrosine 3-	monooxygenase/tryptophan 5-	nonooxygenase activation	protein, beta polypeptide	novel protein similar to mouse	MOV10	ESTs	ESTs	ESTs, Moderately similar to !!!!	ALU SUBFAMILY SO		H.sapiens	ESTS	ESTs	ESTs	ret finger protein
	Hs.77496	Hs.59741	Hs.144651		4	Hs.96642				6	Hs.21657		Hs.247324	Hs.88537	_	_		Hs.182238	_	_	_	Hs.182238	_		9	Hs.47554	_				_			Hs.142653
	AA405809 Hs.91073	N95876 Hs.59741	R02329 Hs.17607		4A482243 Hs.2609	V89673 Hs.96642			4A460848 Hs.23360	AA707598 Hs.120029	W47100 Hs.21657		4A460831 Hs.125159	AA481493 Hs.88537				594 Hs.108250				594 Hs.5049		0	_	V52875 Hs.47554					102612 Hs.30333		37	108725 Hs.6253
		358357 W95	124229 R02:			307050 N89					324653 W47		-	815130 AA4				208161 H62594				208161 H62594			_	283617 N528			•	_	_	_	~	45525 H08;
	GF202	GF202	GF201		GF200	GF201			GF202	GF204	GF203		GF202	GF203				GF200				GF200		GF202	GF200	GF201				GF204	GF203	GF201	GF204	GF200

1.20067236	1,01293925	-1.0620678	-1.015282 -1.5030813	-1.4204145	1.8302373	-1.2376984		1.02372311	2.11006533	1.17504769	1 0700238	-1.0334779 1.08318874	-1.27 6203
1550.665 1550.38 8 1549.832	1549.167 1548.871	1547.735	1547.078 1547.069	1546.853 1546.363	1545.933 1545.281	1545.124 1544.691	1544.242	1544.167	1543.415	1542.275	1542.166	1541.969	1541.004
	СБНЗ	NDUFS8	LCK KIAA0183		RAD23A TPM2	PCBP2					FRI 4	SDF1	
ESTs, Weakly similar to XY40 protein [R.norvegicus] ESTs ESTs cadherin 3, P-cadherin	(placental) EST NADH dehydrogenase (ubiquinone) Fe-S protein 8	reductase) lymphocyte-specific protein	tyrosine kinase KIAA0183 protein	ESTs ESTs RAD23 (S. cerevisiae)	homolog A tropomyosin 2 (beta)	poly(rC)-binding protein 2 EST	Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA	ESTs	ESTS	Homo sapiens mRNA for KIAA1146 protein, partial cds ESTs, Weakly similar to ZINC FINGER PROTEIN 7	[H.sapiens] E-boy protein FBI 4	ESTs stromal cell-derived factor 1	ENIS
Hs.262716 Hs.32538 Hs.240833	Hs.2877 Hs.207688	Hs.90443	Hs.1765 Hs.76666	Hs.96418 Hs.117825	Hs.180455 Hs.180266	Hs.63525 Hs.29036	Hs.103391	Hs.121178	Hs.104825 Hs.269400	Hs.153489	Hs.58377 He.40526	Hs.237356	Hs.98154
N72210 Hs.94273 AA432074 Hs.32538 AA025274 Hs.61202	AA425556 Hs.2877 N66866 Hs.49278	AA127014 Hs.90443	AA420981 Hs.1765 AA434369 Hs.76666	AA447780 Hs.96418 AA700865 Hs.117825	AA476274 Hs.76157 AA477400 Hs.118772	AA431841 Hs.63525 R69798 Hs.29036		R64449 Hs.28448	AA469972 Hs.104825 H69653 Hs.38886	R53578 Hs.107459	AA074620 Hs.58377	H56453 Hs.37310 AA447115 Hs.77423	AA412418 Hs.98154
291241 784128 364932	287122	502141	730410	813821 452351	770674	782449	68049	141366	730438	40178	366093	203878	730528
GF201 GF202 GF202	GF200 GF202	GF203	GF200 GF200	GF203 GF204	GF203	GF200 GF200	GF201	GF200	GF202 GF200	GF202	GF201	GF203 GF200	GF202

Atty Docket No. 21725	1.09998096	1.16686556	1.12147664		1.11000134		1.16301143	4 077000	607//01-	1.0210384		1.35931843	1.56245961	1.51737823	1.1017009			1.84425091		4 700000	5000067.1-	1.65/13/4/		1.32412446	1.60680996	-1.6811833			1.35917562	-2.5511217	2.00963008	
Affy	1539.964	1539.042	1538.791	1538.371	1538.326		1538.278	700	1537.883	1537.765	1537.403	1537.047	1536,607	1536.118	1536.025			1535.952		1525 700	1000/188	1535.184		1535.08	1534,571	1533.665			1533,583	1533.291	1533.191	
	DKEZDE8611093	CTRB1						04000	SLC30A3		KIAA0972				EFNB2							BGN		MIC2						PCTK1		
APPENDIX A	EST DVEZDE9811033 protoin	chymotrypsinogen B1 FSTs Highly similar to C8	[H.sapiens]	ESTs	ESTS Homo saniens mRNA: cDNA	DKFZp761A07121 (from clone	DKFZp761A07121)	solute carrier ramily 30 (zinc	transporter), member 3	ESTs	KIAA0972 protein	ESTs	ESTs	ESTs	ephrin-B2	ESTs, Weakly similar to	allernatively spliced product	using exon 13A [H.sapiens]	Homo sapiens mRNA; cDNA DKFZp434,10650 (from clone	OVEZAVA 10650): postiol ode	UNFZP434J065U); partial cus	biglycan	monoclonal antibodies 12E7.	F21 and O13	ESTS	ESTs	ESTs, Weakly similar to !!!!	ALU SUBFAMILY SP WARNING ENTRY !!!!	[H.saniens]	PCTAIRE protein kinase 1	EST	
	Hs.48336	Hs.74502	Hs.30114	Hs.14825	Hs.1/1268		Hs.10177		Hs.11196/	Hs.105378	Hs.75264	Hs.54773	Hs.269416	Hs.48474	Hs.30942			Hs.30211		11- 40700	HS.48389	Hs.821		Hs.177543	Hs.29075	Hs.269340			He 269709	Hs.171834	Hs.20273	
	Hs.48336	AA845168 Hs.74502	AA634371 Hs.30114	Hs.14825	Hs.505//		AA455237 Hs.10177		4A621201 Hs.111967	4A496141 Hs.105378	Hs.75264	Hs.54773	4A505003 Hs.105747	V62074 Hs.48474	AA461424 Hs.30942			Hs.93122		00707	HS.48589	Hs.17184		AA937895 Hs.118618	Hs.29075	Hs.109331			He 15207	Hs.9704	Hs.20273	
	N59194	AA845166	AA634371	H81214	N/499/		AA455237		AA621201	AA496141	R53059	N92310	AA505003	N62074	AA461424			N71365		0000014	Nezeza	W70065		A A 93789	N34786	N54855			T91057	N93661	R08866	
etal.	288668	1412504	743810	241391	2995/0		814779		744391	757199	40537	308031	839764	289847	796198			294127		00000	288899	343974		1435862	271421	248397			112525	307013	127514	
Westbrook et al.	GF202	GF203	GF203	GF204	GF202		GF203		GF202	GF202	GF201	GF202	GF202	GF202	GF200			GF200		00010	GF203	GF203		GE203	GF203	GF202			GESON	GF203	GF200	

1.22968381 1.81165211 1.03100217	1,43451813 1,43844241 -1,7391464		-1.6610803	-1.2481072 2.80274261
1532.812 1532.135 1531.814 1531.729 1531.267	1530.753 1530.496 1530.293 1529.601 1529.019	1528.024	1526.853	1526.844 1526.715
PSMD9 TAX40 SMP-1	SGK AQP3 KIAA0652	SREB2 LY6E	SORL1	IL2RG SELL
ESTS, Moderately similar to TUBULIN BETA-2 CHAIN [H.saplens] ESTS ESTS protessome (prosome, macropain) 26S subunit, non-farration protein 40 sperm membrane protein 1 9	Homo sapiens cDNA FLJ 10849 its, clone NT2RP4001144, highly similar to SEPTIN 2 HOMOLOG serum/glucocorticoid regulated finase aquapoin 3 KIAA0652 gene product Homo sapiens (clone p5-23-3) mRNA ESI's	super conserved receptor expressed in brain 2 (ymphocyte antigen 6 complex, locus E	sortilin-related receptor, L(DLR class) A repeats-containing interleukin 2 receptor, gamma (souchs combined) cyte e 1)
Hs.23189 Hs.37268 Hs.112970 Hs.5648 Hs.112933 Hs.256747	Hs.8768 Hs.159640 Hs.234642 Hs.78672 Hs.193384 Hs.12316	Hs.152009 Hs.77667	Hs.278571	Hs.84 Hs.82848
AA629908 Hs.23188 AA448849 Hs.37268 AA621313 Hs.112970 AA4018S3 Hs.5648 AA621019 Hs.112933 N63260 Hs.118128	Hs.34614 Hs.35752 Hs.94306 Hs.79672 Hs.52363 Hs.12316	N62306 Hs.118103 AA773987 Hs.59763	Hs.129951	Hs.84 Hs.82848
AA629906 AA443849 AA621313 AA401853 AA621019 N63260	H81313 H75599 R91904 N51771 H68370 R43675	N62306 AA773987	N48698	N75745 H00756
884653 784085 744641 758662 1056200	239575 232946 196005 281793 211843 22840	290375	279388	244355
GF204 GF202 GF202 GF200 GF201 GF201	GF204 GF200 GF200 GF203 GF204 GF204	GF204 GF204	GF202	GF200 GF200

-1.1036248 1.00131195	1.16400753	1.23544287	1.24399918	1.27170944	-1.4279521 1.3875758 1.55635041 1.20106962 -1.0084289	-1.5038732
1526.684 1526.666 1525.306	1525.198 1524.865 1524.337 1523.35	1522.724 1522.616	1521.954	1521.049 1521.017	1520.488 1520.244 1520.136 1519.956	1519.415 1519.101 1518.609 1517.28
		SCYA11			RALBP1 KIAA0966 H3F3A	S ATF6 KIAA0999 IDE KIAA0169
ESTS, Weakly similar to !!!! ALU SUBFAMILY J ALU SUBFAMILY J [H.sapiens] ESTS ESTS Human 40871 mRNA partial	sequence ESTs ESTs ESTs small inducible cytokine subfamily A (Vos-Cys),	member 11 (eotaxin) ESTs ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	[H.sapiens] Homo sapiens mRNA; cDNA DKFZb434E082 (from clone	DKFZp434E082) ESTs ESTs, Weakly similar to !!!! ALU SUBFAMILY SB2	[H.sapiens] ralA binding protein 1 KIAA0966 protein ESTs H3 histone, family 3A	activating transcription factor 6 ATF6 KIAA0999 protein insulin-degrading enzyme IDE KIAA0169 protein KIAA0169 protein
Hs.269642 Hs.112950 Hs.126083	Hs.234216 Hs.58585 Hs.26026 Hs.47191	Hs.54460 Hs.191186	Hs.272173	Hs.30504 Hs.193984	HS.167619 HS.75447 HS.52463 HS.177217 HS.181307	Hs.247433 Hs.4278 Hs.1508 Hs.30002
AA776893 Hs.121882 AA621200 Hs.112950 AA428240 Hs.126083	R56251 Hs.91802 W79524 Hs.58585 H10156 Hs.26026 N51117 Hs.47191	W69211 Hs.54460 AA487501 Hs.112329	R98957 Hs.36035	H06525 Hs.30504 AA779520 Hs.131246	H68394 Hs.23813 AA085990 Hs.75447 H69354 Hs.52463 R25464 Hs.23875 AA668811 Hs.118838	AA707661 Hs.74938 AA446193 Hs.4278 W86199 Hs.1508 AA976525 Hs.79414
858914 / 744385 / 773575 /	40871 F 347064 V 46994 H 282007 N	343736 \	200847 F	44387 H	137918 562983 142120 132323 884272	451711 / 781151 / 415899 / 1587852 /
GF204 GF202 GF202	GF201 GF202 GF201 GF201	GF201 GF202	GF200	GF203 GF204	GF200 GF200 GF200 GF200 GF202	GF203 GF201 GF201 GF204

	1.07600887	1.46913809	1.88583966	1.04063053 1.29869239	-1.3607125	-1.9884922	90200340	-1.2586932	1.45058688	-1.8623159	-1.7876176			-1.3686553	-2.0657557	1.22517242
1516.824	1516.408 1516.212	1515.532 1515.194	1514.482	1514.094 1513.9	1512.817 1512.465	1512.457	1512.153	1511.333	1511.307	1510.897	1510.657	1510.506 1510.478	1510.091	1509.673	1509.018	1508.736
	GNG2 USP8	KIAA0226		FXYD3	SALL2		ZNF6	UKFZp564CZ46			RAC3		KIAA1081	UXT	DMWD	CBX1
Homo sapiens mRNA; cDNA DKFZp434K0172 (from clone DKFZp434K0172) guanine nucleotide-binding guanine nucleotide-binding guaning GIVIG(O) namma-2	subunit	KIAA0226 gene product ESTs	Homo sapiens mRNA for KIAA1287 protein, partial cds EXYD domain-containing ion	transport regulator 3 ESTs	ESTs sal (Drosophila)-like 2		(CMPX1)	nypometical protein ESTs	ESTs	ESTs	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3) ESTs. Weakly similar to	140G11.h [D.melanogaster] ESTs	KIAA1081 protein ubiquitously-expressed	transcript dystrophia myotonica-	containing WD repeat motif	(Drosophila HP1 beta)
Hs.121073	Hs.23767 Hs.152818	Hs.141296 Hs.47003	Hs.50187	Hs.92323 Hs.260579	Hs.43744 Hs.79971	Hs.98851	Hs.75839	Hs.48699	Hs.184260	Hs.105653	Hs.45002	Hs.74346 Hs.21433	Hs.141709	Hs.172791	Hs.275924	Hs.77254
AA774082 Hs.121073	T80932 Hs.14811 AA443908 Hs.3086	N36389 Hs.109120 W95480 Hs.47003		AA126115 Hs.92323 H81104 Hs.19674	N67808 Hs.43744 H23365 Hs.79971	22	AA680306 Hs.124769	AA48/552 HS.61628 N63049 HS.48699		AA485117 Hs.105653	N54221 Hs.45002	AA284245 Hs.74346 R20763 Hs.21433		AA401736 Hs.14369	R00855 Hs.75706	AA448667 Hs.77254
858510	109309	273024	291062	511428 241288	291575 52430	730606	869504	278944	362773	815665	281978	325606 26410	324679	727305	123916	786084
GF204	GF200	GF202 GF201	GF202	GF200 GF200	GF201	GF202	GF204	GF202	GF203	GF203	GF200	GF201 GF204	GF201	GF202	GF203	GF200

	-1.6399318	1.28267716	-2.1400507	-1.4048011					1.3593224	-1.0681145				1.85765198			1.55273195		1.54585389	1,03543135	1.48646013		4 9344609	70044071	-2.7116462	-1.1270053	1.04056474			1.27152353
1508.467	1508.342	1507.939	1507.44	1507.349				1507.325	1507.129	1506.822				1506.285			1505.841		1505.694	1505.132	1504.248		1500 040	1303.340	1503.866	1503.528	1503.461	1503.084		1502.93
		RAGE						SLC25A5												•	RANBP2L1		i con							MLLT2
ESTs	ESTs	renal tumor antigen	ESTs	ESTs	solute carrier family 25	(mitochondrial carrier; adenine	nucleotide translocator),	member 5	ESTs	ESTs	ESTs, Moderately similar to !!!!	ALU SUBFAMILY J	WARNING ENTRY !!!!	[H.sapiens]	Homo sapiens mRNA; cDNA	DKFZp434M1317 (from clone	DKFZp434M1317)	ESTs Highly similar to protein	kinase JNK1 beta1 [H.sapiens]	ESTS	BAN binding protein 2-like 1		DNA2 (DNA replication	rencase, yeast, nornology-like ESTs, Weakly similar to hNB-	2s [H.sapiens]	ESTs	EST	ESTs	myeloid/lymphoid or mixed- lineage leukemia (trithorax (Drosophila) homolog);	translocated to, 2
Hs.42456	Hs.36341	Hs.104119	Hs.118598	Hs.85971				Hs.79172	Hs.16360	Hs.48050				Hs.209508			Hs.75497		Hs 190913	Hs 222088	Hs.179825		10000	HS. 194000	Hs.120079	Hs.237382	Hs.112777	Hs.206063		Hs.114765
N23940 Hs.42456	AA701483 Hs.36341	N77779 Hs.104119	AA490182 Hs.118598	AA195014 Hs.85971				AA404486 Hs.79172	AA682616 Hs.16360	AA398284 Hs.48050				R91986 Hs.34541			AA459364 Hs.75497		AA812676 Hs 859	H73178 Hs 199886			1000	AA9/4495 HS.8956/	AA757468 Hs.120079	AA456044 Hs.40367	-	H10036 Hs.27977		AA057425 Hs.114765
268650	435452	289666	840024	665361				772304	450860	726729				195232			814528		1377071	214512	198924	130001		13/2140	395885	812175	1032080	46620		381021
GF201	GF203	GF200	GF202	GF203				GF201	GF203	GF203				GF200			GF203		GF203	GE203	GE203	8	i d	GFZ03	GF203	GF203	GF202	GF201		GF203

-1.3897242	-1.1638029	-1.0096661	-1.5378935	1.55811741		1.10015732	1.7238/46	0.000000	1.50056671	1.45090485		1.05296064		1.24347849	-1.0763176	-1.8895272		1.71066288	1.50125174		
1502.574 1502.051	1502.04	1501.892 1501.067	1501.036	1501.023	1500.395	1500.372	1499.642	1498.837	1498.292	1498.075		1498.035		1497.883	1497.604	1497.418	1497.381	1497.108	1497.07	1496.97	1496.61
MLN64		RAB3-GAP150	POLB2L			KRT8		LOC51304	PCL1			HIF1A		MDM4	SMN1		SAS				
steroidogenic acute regulatory protein related ESTs ESTs, Moderately similar to RAS-RELATED PROTEIN	RAB-28 [H.sapiens] rab3 GTPase-activating protein, non-catalytic subunit	(150kD) ESTs	polymerase (RNA) II (DNA directed) polypeptide L (7.6kD) POLR2L	ESTs	ESTs	keratin 8	ES! ESTs	DHHC1 protein	prenylcysteine lyase	ESTs	hypoxia-inducible factor 1, alpha subunit (basic helix-loop-	helix transcription factor)	mouse double minute 4, human homolog of; p53-	binding protein	telomeric	ESTs	sarcoma amplified sequence	ESTs	ESTs	ESTs	ESTs
Hs.77628 Hs.151586	Hs.5018	Hs.197289 Hs.138809	Hs.71618	Hs.86248	Hs.91867	Hs.242463	HS.9893/ He 50450	Hs.14896	Hs.278627	Hs.101277		Hs.197540		Hs.101874	Hs.77306	Hs.98003	Hs.50984	Hs.269281	Hs.260977	Hs.95941	Hs.27358
AA504710 Hs.77628 W45568 Hs.55892	AA418876 Hs.5018	H82081 Hs.108524 N89812 Hs.54538	AA873691 Hs.71618	AA206370 Hs.86248	AA669464 Hs.91867	AA598517 Hs.78271	M43/13/ HS.9893/ W93/03 He 59/59		R78527 Hs.15686	R61866 Hs.101277		AA598526 Hs.82765		N66001 Hs.38168	AA448194 Hs.77306	AA406063 Hs.98003	AA664211 Hs.116941	AA169154 Hs.72798	H54423 Hs.36905	AA147642 Hs.15819	H19217 Hs.27358
825577 323457	767868	248886 305481	1325816	645628	884903	897781	/5/3//	50581	144852	43065		897806		293847	782797			609935	203122	505584	51103
GF200 GF201	GF202	GF201 GF202	GF203	GF203	GF204	GF200	GFZUZ	GF201	GF200	GF203		GF200		GF200	GF200	GF202	GF204	GF202	GF200	GF201	GF201

-1.0741534	1.03112541	1.03112541	1.71232235 1.37294628	1.33584999	1.14102156	1.16695568	1.10507988	-1.0829553 1.09312158 -1.3186668 -2.9389702 2.19760193
1496.439	1495.816	1495.685 1495.685	1495.214 1494.636	1494.246 1493.256	1492.762	1492.632 1492.148	1491,991	1491.557 1491.237 1490.877 1490.351
	FOP2A	rop2A		KIAA0040			KDELR2	
ESTs, Moderately similar to kinesin like protein 9 [M.musculus] Homo sapiens chromosome 19, cosmid R29368 cooxisomerase (DIA) Il alpha hoposisomerase (DIA) II alpha hoposisomerase (DIA) II alpha hoposisomerase (DIA) II alpha			HEP02567 ESTs	KIAA0040 gene product ESTs	ESTs ESTS, Highly similar to DPIOID BINDING PROTEIN/CELL ADHESION MOLECULE PRECURSOR	[H.sapiens] ESTs KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein		PRECURSOR EST ESTs ESTs
ES kin Hs.105187 [M. Ho. Hs.184950 19,00	Hs.156346 (17	Hs.156346 (17 Hs.116198 ES Hol	Hs.183860 HE Hs.35035 ES	Hs.158282 KIA Hs.191598 ES	Hs.24853 ES ES OP PR	Hs.273544 [H: Hs.167343 ES KD	Hs.118778 rett Ho HC. FL. PL. Sim	Hs.3781 PRE- Hs.66691 EST Hs.40479 ESTs Hs.28295 ESTs Hs.42736 ESTs
AA609473 Hs.105187 AA157797 Hs.129791	AA504348 Hs.3378	AA504348 Hs.119142 AA628128 Hs.116198	AA121360 Hs.27567 R92865 Hs.35035	AA465479 Hs.77526 AA416627 Hs.98252	R52965 Hs.24853	AA425422 Hs.115471 R58974 Hs.20931	AA485911 Hs.82032	AA452138 Hs. 3781 AA063577 Hs. 66691 AA424650 Hs. 40479 116179 Hs. 28295 199791 Hs. 42736
1031592 AA	825470 AA	825470 A/ 1055719 A/	564176 A/ 196837 RS	814054 A/ 731290 A/	40407 R&	773305 A/ 41137 RE	843140 AA	787854 AA 360035 AA 767222 AA 48610 H1 262940 H1
GF202 GF204	GF200	GF200 GF204	GF202 GF200	GF200 GF202	GF202	GF200 GF201	GF200	GF202 GF202 GF203 GF203 GF203

1.57070813 1.07017236 -1.5179714 1.5628041	1.27704764	-2.2064164	2.73349397	1.12019035	1.48508729 1.14765456	1.15933702 -1.5419513 1.16492524
1489.974 1489.414 1488.583 1488.583 1487.904	1487.613	1486.292	1484.909 1484.668 1484.647 1484.464	1482.142 1481.962 1481.889	1481.232 1481.101	1480.996 1479.357 1478.547
FAF1	NME5	-	LOC51295 CHD4	IRAK1	KIAA0878	SNRPD3 KIAA0186 TRA@
EST ESTS ESTS EST EST EST Fas (TNFRSF6) associated	non-metastatic cells 5, protein expressed in (nucleoside- diphosphate kinase) SRY (sex determining region	Y,box 4 ESTs. ESTs, Weakly similar to serin protease with IGF-binding motif [H.sapiens]	ESTs ECSIT chromodomain helicase DNA binding protein 4 ESTs	ESTs interleukin-1 receptor- associated kinase 1 ESTs ESTs, Weakly similar to Dof	protein [D.melanogaster] KIAA0878 protein small nuclear ribonucleoprotein D3	polypeptide (18kD) KIAA0186 gene product T cell receptor alpha locus
Hs.116179 Hs.124047 Hs.24808 Hs.130832 Hs.112755 Hs.250614	Hs.72050	Hs.83484 Hs.189780 Hs.60440	Hs.132940 Hs.22199 Hs.74441 Hs.27935	Hs.97570 Hs.182018 Hs.268645	Hs.86437 Hs.188006	Hs.1575 Hs.36232 Hs.74647
AA626854 Hs.116179 W15499 Hs.102978 AA489467 Hs.24808 H92571 Hs.130832 AA609734 Hs.112755 N34494 Hs.51750 W70189 Hs.29133	36	N23606 Hs.93668 R14858 Hs.105993 H29724 Hs.29261	52 9	AA421280 Hs.97570 AA169355 Hs.90930 T96605 Hs.13803	R62339 Hs.86437 AA599094 Hs.16056	R89363 Hs.16640 AA725561 Hs.36232 AA666096 Hs.97879
4 745185 1 322679 2 897415 3 231438 2 1031908 1 271165		3 250869 0 129514 4 186234	+1 91		0 139558 2 950450	3 196037 3 1343726 3 859383
GF204 GF201 GF202 GF203 GF202 GF201 GF201	GF202	GF203 GF200 GF204	GF201 GF203 GF201 GF201 GF201	GF202 GF202 GF201	GF200 GF202	GF203 GF203 GF203

eukaryotic translation initiation

-1.3860535	-1.142602	-1.1621138	1.90731342						-1.0235857	-1.1605875				1.09986215			1,27137581				
1478.51	1478.002	1477.982	1477.495	1477.417			1476.648	1476.626	1476.468	1476.292			1475.498	1475,244	1474.888		1473.632		1472.819	1472.22	1471.765
EIF2S3		KIAA0700	NCK1														SFRS8				
factor 2, subunit 3 (gamma, 52kD) Homo sapiens cDNA	FLJ11000 fis, clone PLACE1002794	Homo sapiens clone 23551 mRNA sequence KIAA0700 protein	NCK adaptor protein 1	ESTs	FLJ10697 fis, clone	NT2RP3000527, weakly	PROTEIN 43	ESTs	ESTs	ESTs	ESTs, Weakly similar to	thioredoxin-like protein	[H.sapiens]	EST	ESTs	splicing factor, arginine/serine- rich 8 (suppressor-of-white-	apricot, Drosophila homolog)	Homo sapiens mRNA; cDNA DKFZp7610031 (from clone	DKFZp7610031); partial cds	ESTs	ESIS
Hs.211539	Hs.77365	Hs.184019	Hs.54589	Hs.14217			Hs.104557	Hs.181895	Hs.55607	Hs.42463			Hs.13201	Hs.112899	Hs.269320		Hs.84229	18:00:44	Hs.274256	Hs.106293	Hs.169552
AA158258 Hs.34131	Hs.77365	Hs.44599		4A431746 Hs.14217			Hs.40177	6	Hs.55607	Hs.42463			AA677563 Hs.13201	AA620760 Hs.112899	AA284307 Hs.102966		AA702973 Hs.84229	44 L L R R R R R R R R R R R R R R R R R	_	_	Hs.96556
AA15825	N73248	N63539	N90137	AA43174			H80749	AA42936	M37776	H97921			AA67756	AA62076	AA2843(AA7029	AA4237	N91003	R38630	R32788
592807	246546	278188	302369	782269			248849	771130	322173	260718			455256	1049293	327239		447167	788877	306066	23095	135503
GF202	GF200	GF201	GF200	GF201			GF201	GF201	GF202	GF202			GF204	GF202	GF201		GF203	GF 202	GF201	GF204	GF201

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protein phosphatase 2,

1.342303	-1 2248002	20004-37:1-	1.61009766		1.60041836 -1.2070805		1.09185938	-1.497731	-1.6487309		1.61825022	-2.000871		1.21936399					1 78601450	1.10001-100		-5.0679099	-1.0287552	1.63005595	
1471.65	1471.414	1471.083	1470.74	1470.173	1469.598 1469.392		1468.814	1468.7	1468.696		1468.066	1467.788	1467.772	1467.507			1467.3		1/66 776	1400.7	1466.646	1465.345	1465.162	1464.981	
PPP2R5A		ACP1	MYC		GRP58		DIA4				RFC3		SNK	H326						!	GSTM5		PRKCH	CONI	
B56),	Homo sapiens cDNA FLJ20736 fis, clone HEP08473	phosphatase 1, soluble	osis	developmentally regulated protein [R.norvegicus] glucose regulated protein,		diaphorase (NADH/NADPH)	nrome b-5 reductase)	ESTs	EST	replication factor C (activator	1) 3 (38KD)	ESTs	serum-inducible kinase		Homo sapiens cDNA	FLJ10717 fis, clone	NT2RP3001084	ESTs, Weakly similar to MHC	ciass region promise non		ione S-transferase M5	ESTs	protein kinase C, eta	cyclin I	
Hs.155079	Hs.48712	Hs.75393	Hs.79070	Hs.38497	Hs.183760 Hs.154396		Hs.80706	Hs.46667	Hs.23654		Hs.115474	Hs.191887	Hs.3838	Hs.110707			Hs.25277		707777	HS. 141494	Hs.75652	Hs.60536	Hs.1880	Hs.79933	
R59164 Hs.79129	V63102 Hs.48712		AA464600 Hs.79070	AA453528 Hs.38497	AA115310 Hs.55074 H23091 Hs.31953		8	-	R44927 Hs.23654		194617 Hs.9969	4A778938 Hs.124870	4A460152 Hs.3838	W02116 Hs.110707			AA458491 Hs.25277				156898 Hs.75652	4A011684 Hs.60536	4A047803 Hs.89616	AA434408 Hs.119038	
41356 R56	284787 NG	_	812965	795427 AA	511459 AA		_	280324 N4	34093 R4		_	452609 AA	795877 AA	_			809620 AA				_	429727 AA	380245 AA	770888 AA	
GF200	GF201	GF202	GF200	GF201	GF202 GF203		GF200	GF202	GF202		GF200	GF203	GF201	GF200			GF201		200	GFZUZ	GF201	GF202	GF200	GF203	

-1.0357568	-1.0917427	-1.0555729 -2.1303673	-1 6522594		1.08395761					1.32578918			1.05714472		-1.3388453		-1.0477898		*	-1.0398336	
1463.749 1462.825	1462.623	1462.501 1462.564	1462 978		1461.99			1461 767		1461.139	1461.045		1460.678	1460.674	1460.538		1460.279	1460.237	0 0 0	1459.245	1459.24
IGL@		НСК	PEMT					FRAF			SPF31		TRIP10	KLF2			ALDH5A1			NOPS	MLLT4
immunoglobulin lambda locus IGL@ ESTs	ESTs	hemopoietic cell kinase EST	phosphatidylethanolamine N-	Homo sapiens cDNA FI.110158 fis. clone	HEMBA1003463	endometrial bleeding associated factor (left-right	determination, factor A;	transforming growth factor	Homo sapiens mRNA for	KIAA1273 protein, partial cds	splicing factor similar to dnaJ	thyroid receptor interacting protein 10 (CDC42-interacting	protein)	Kruppel-like factor 2 (lung)	ESTs	aldehyde dehydrogenase 5 family, member A1 (succinate-	semialdehyde dehydrogenase) ALDH5A1	Homo sapiens clone 23676 mRNA sequence	nucleolar protein (KKE/D	repeat) myeloid/lymphoid or mixed- lineage leukemia (trithorax	(Drosophila) homolog); translocated to, 4
Hs.181125 Hs.13291	Hs.268755	Hs.89555 Hs.105637	Hs 15100		Hs.104627			He 25195	2	Hs.23413	Hs.74711		Hs.73999	Hs.107740	Hs.5967		Hs.5299	Hs.100841		Hs.5092	Hs.100469
T67053 Hs.111572 AA127818 Hs.13291	Hs.113696	4A149096 Hs.89555 4A479285 Hs.105637	Lo 112066		AA486551 Hs.104627			He 25105	02:03:01	AA176164 Hs.23413	Hs.78949		Hs.73999	Hs.107740	Hs.5967		Hs.2494	Hs.100841		Hs.5092	Hs.100469
T67053 AA127818	R74206	AA149096 AA479285	DOMEAS	7	AA486551			W56771		AA176164	W37375		R49671	W69213	AA478452 Hs.5967		H06675	R38291		AA894577 Hs.5092	N26539
66560 501674	143380	504544	107707	3	840968			340657		610341	322067		37491	343731	786239		44505	23676		1492304	266318
GF200 GF201	GF202	GF200	0000	5	GF202			CE201	5	GF202	GF201		GF200	GF201	GF203		GF200	GF201		GF203	GF201

-1.4152309	1.08869599	1.3161837 1.34884211 -1.0918477 1.31073638	1.01263163	1.35225537	
1458.822 1457.288 1457.126	1456.824 1456.433	1456.182 1455.912 1455.241 1455.208 1454.719	1453.756 1453.711 1452.59	1452.446	1451.824
AP4		GACNA2D2	KIAA0573	PURA	
Homo saplens cDNA FLJ10191 fis, clone HEMBA1004756, weakly similar to Human transporter protein mFNA zinc finger protein ESTs	ESTs, Moderately similar to KIAA0961 protein [H.sapiens] ESTs Human HLA-DR alpha-chain mRNA acalcum channel, voltage- dependent, alpha 2/delta	subunit 2 ESTs ESTS ESTS ESTS	ESTS, Weakly similar to Prt1 mondog [H.sapiens] ESTS KIAA0573 protein ESTS, Weakly similar to !!!! ALU SUBFAMIL Y J WARNING ENTRY !!!!	[H.sapiens] purine-rich element binding protein A ESTs, Woakly similar to	nypoineucal protein [H.sapiens] Homo sapiens cDNA FLJ1132 fis, clone PLACE1006335
Hs.165655 Hs.90693 Hs.5806	Hs.192999 Hs.210209 Hs.76807	Hs.127436 Hs.176648 Hs.160881 Hs.262858 Hs.71528	Hs.111650 Hs.186544 Hs.154023	Hs.193452 Hs.25180	Hs.97141 Hs.106005
N88679 Hs.129545 AA482079 Hs.90693 W49491 Hs.5806	Hs.35461 Hs.94195 Hs.76807	N53512 Hs. 100541 R32723 Hs. 24548 AA404231 Hs. 91568 T41024 Hs. 8368 AA134595 Hs. 71528	AA446907 Hs.111650 R95867 Hs.16148 AA620519 Hs.80844	Hs.89709 Hs.25180	AA448168 Hs.97141 AA625621 Hs.106005
N68679 AA482079 W49491	N51097 N67810 R47979	N53512 R32723 AA40423 T41024 AA13459	AA44690 R95867 AA62051	W96268 H46663	AA44816 AA62562
293240 756418 325002	281982 291594 153411	284160 135212 758284 61626 502531	784255 199241 951304	361639	782761
GF203 GF204 GF203	GF201 GF201 GF200	GF201 GF200 GF202 GF202 GF202	GF201 GF201 GF202	GF200 GF200	GF201 GF204

	2.02310845	1.4687699	-1.1190874	1.03331604					1.39616443					1.19736264					-1.0928555														1.03275103		
	1451.653	1450.027	1449.536	1448.97	1447.658	1447.401		1447.293	1447.174	1446.8	1446.294			1445.537			1445		1444.767					1444.502	1444.44			1444.212		1443.343	000	1442.203	1440.808	1440.343	1440.122
	KIAA1004							HTATIP											AOE372											TPST2					SP4
APPENDIX A	F-box protein FBL11 FSTs	ESTs	ESTs	EST	ESTs	EST	HIV-1 Tat interactive protein,	60 kDa	ESTs	ESTs	ESTs	Homo sapiens mRNA; cDNA	DKFZp434O0515 (from clone	DKFZp43400515)	ESTs, Weakly similar to	similar to kinensin-like protein	[C.elegans]	thioredoxin peroxidase	(antioxidant enzyme)	Homo sapiens cDNA	FLJ11196 fis, clone	PLACE1007688, weakly	similar to LA PROTEIN	HOMOLOG	EST	Homo sapiens cDNA	FLJ20729 fis, clone	HEP11012	tyrosylprotein sulfotransferase	2	Homo sapiens HDCMD45P	mHNA, partial cds	ESTs	ESTs	Sp4 transcription factor
	Hs.219614 Hs 25088	Hs.21422	Hs.47359	Hs.46530	Hs.208514	Hs.126229		Hs.6364	Hs.156710	Hs.91678	Hs.46704			Hs.50094			Hs.43549		Hs.83383					Hs.6166	Hs.258822			Hs.5111		Hs.26350		Hs.103180	Hs.269047	Hs.26507	Hs.2982
	Hs.104763 Hs 25088	Hs.21422	Hs.47359	Hs.46530	Hs.90353	4A873172 Hs.126229		4A777540 Hs.113427	4A489791 Hs.105297	Hs.91678	Hs.46704			AA629517 Hs.50094			AA431199 Hs.43549		AA459663 Hs.83383					4A130193 Hs.6166	Hs.6537			Hs.5111		AA459389 Hs.26350		Hs.119459	Hs.43597	Hs.26507	4A772989 Hs.2982
	R32334	B37780	N51883	N48794	T47971	AA873172		AA777540	AA48979-	R41994	N52192			AA629517			AA431199		AA459663					AA130193	R40328			R52643		AA45938		W72911	N25049	R56134	AA77298
	134942	27072	282144	279464	71557	1472788		448409	839545	31969	284286			884328			782164		795543					503335	28203			39803		810937		344977	254694	41192	859660
	GF201	GF203	GF202	GF202	GF201	GF204		GF204	GF202	GF201	GF201			GF203			GF201		GF200					GF201	GF204			GF204		GF201		GF204	GF202	GF201	GF204

	-1.0976875	-1.0322046	-1.332884 -1.4713778 -1.4182415 2.0124114	1.3363361 -1.1379363 -1.7013843	1.06211406 -1.1680027 1.22845369	1.09240125 1.25787858 -1.3043265
1438.312	1437.445 1437.006	1436.55 1436.112	1435.841 1435.304 1435.148 1435.039	1434.881 1434.258 1433.14 1432.954	1432.512 1432.388 1430.339	1430.311 1429.897 1429.716
MADH3	PIK3R4	ABCA4 DAXX	PDGFB KIAA1020	EIF3S5 DKFZP586G1517	S100A11 CAPN5	EIF4E KIAA0204
Homo sapiens mRNA; cDNA DKFZp434C0328 (from clone DKFZp434C0328) MAD (mothers against decapentaplegic, Drosophila) homoloo 3	phosphoinositide-3-kinase, regulatory subunit 4, p150 ESTs	Arr-Unfully Cassette, sub- family A (ABC1), member 4 death-associated protein 6 platelet-derived growth factor beta polypeptide (simian carroma viral (vexis) monogene	Account what is a subject to the subject of the sub	ARKD) 47KD) 47KD) 65Ts 65Ts CSTs DKFZP586G1517 protein S100 calcium-binding protein	A11 (calgizzarin) calpain 5 ESTs eukarvotic translation initiation	factor 4E Ste20-related serine/threonine kinase ESTs
Hs.24583 Hs.211578	Hs.83050 Hs.65583	Hs.198396 Hs.180224	Hs.1976 Hs.109445 Hs.42964 Hs.177711	Hs.7811 Hs.268697 Hs.98857 Hs.44155	Hs.256290 Hs.6133 Hs.7104	Hs.79306 Hs.105751 Hs.106818
37 Hs.24583 114 Hs.83290		AA054358 Hs.40993 N73287 Hs.8181	T49539 Hs.1976 R39191 Hs.109445 N21233 Hs.42964 AA251363 Hs.87864	H67864 Hs.8249 R37690 Hs.125204 AA435996 Hs.98857 AA779617 Hs.122580	AA464731 Hs.76155 AA777637 Hs.6133 H97677 Hs.7104	AA193254 Hs.79306 AA454970 Hs.105751 H28738 Hs.106818
135106 R33037		380737 AA0543 292042 N73287	67654 T49539 23345 R39191 264449 N21233 684623 AA25136	238886 H67864 25309 R37690 730735 AA43591 1033229 AA7796	810612 AA4647; 448514 AA7776; 251529 H97677	665774 AA19325 811890 AA45497 49993 H28738
GF201 13		GF200 38	GF200 671 GF202 233 GF203 68	GF202 238 GF204 255 GF202 738 GF203 103	GF200 810 GF203 444 GF202 25	GF200 66 GF200 81 GF202 499

	-1.9856276	-1.6094097	-1.1033209	-1.0301536	-1.28153	1.15539192				2.29814396	1.06163515	1 076944	1.09945942				1.81634729		1.05263267	1.0274952		1.30953366	
	1429.128	1429.106 1428.635	1428.608	1428.587	1427.409	1427.381		1426.796	1426.751	1426.419	1426.129	1425.958	1425.315		1425.1	1424.867	1424.648		1424.6	1424.357	1424.274	1423.901	1423.349
				PDE6G							GS3955	DKFZP58600223			NNT								ĘĶ
Homo sapiens hepatic angiopoietin-related protein (ANGPTL2) mRNA, complete	cds Homo sapiens mRNA; cDNA DKFZp761B101 (from clone	DKFZp761B101) ESTs	ESTs phosphodiesterase 6G, cGMP-	specific, rod, gamma	ESTs	ESTs, Highly similar to SOUL protein [H.sapiens]	reverse transcriptase related	protein [H.sapiens]	ESTs	ESTs	GS3955 protein	hypothetical protein	ESTs	nicotinamide nucleotide	transhydrogenase	ESTs	ESTs ESTs Moderately similar to	glutathione-S-transferase	homolog [H.sapiens]	ESTs	ESTs	ESTs	integrin-linked kinase
	Hs.9613	Hs.235390 Hs.269509	Hs.46772	Hs.1857	HS.163731 HS.56219	Hs.111029		Hs.13477	Hs.103379	Hs.39311	Hs.155418	Hs.49005	Hs.261727		Hs.18136	Hs.125906	Hs.268647		Hs.44860	Hs.103535	Hs.19151	Hs.98786	Hs.6196
	298 Hs.110240	AA017301 Hs.60796 AA663254 Hs.118707	877 Hs.46772	4A074148 Hs.1857	W57712 Hs.56219	113 Hs.111029		W87826 Hs.13477	^	472290 Hs.39311	4A458653 Hs.75820	AA455284 Hs.49005	10		H22944 Hs.18136	9	309 Hs.18032		AA159327 Hs.44860	H24323 Hs.103535	AA004274 Hs.19151	AA433910 Hs.98786	AA148200 Hs.6196
	69002 T54298	361317 AA01 853280 AA66	_	-	340898 W57	83156 T68113		417081 W878	-	_	`	810047 AA45			51826 H229	-	121501 T97309		591422 AA15	52057 H243	429243 AA00	773678 AA43	590615 AA14
	GF202	GF203 GF204	GF202	GF200	GF204 GF202	GF202		GF201	GF201	GF200	GF200	GF201	GF202		GF201	GF204	GF200		GF202	GF202	GF201	GF202	GF201

-1.2115496	-1.0821231 1.64353237 -1.2974723	1.95312891	-1.3935183 1.1012035 1.80532604		-1.2741688		1.54065389	-1.379137	1.29704627	-1.1717513
1423.023	1422.383 1421.46 1420.166	1417.796 1416.93	1416.562 1416.483 1416.287 1416.036	1415.988	1415.183 1415.156	1414.203	1413.43	1413.34	1412.7 1412.598 1412.563	1412.487
BETA-4	COL5A2		PITPNB		PSMA4	SLC3A2		LY6E	GPS1 DKFZP586I1023	MAPRE2
adaptor-related protein complex 4, beta 1 subunit Homo sapiens mRNA for	UCC1 protein (UCC1 gene) ESTs collagen, type V, alpha 2	ESTs, Weakly similar to cytokeratin 20 [H.sapiens] ESTs phosphotidylinositol transfer	protein, beta ESTs ESTS	ESTs proteasome (prosome, macropain) subunit, albha	type, 4 type, 4 ESTs solute carrier family 3 (activators of dibasic and	member 2 potassium inwardly-rectifying channel, subfamily J, member	EST Iymphocyte antigen 6 complex,	locus E G protein pathway suppressor	1 ESTs DKFZP586I1023 protein microtubule-associated	protein, HP/EB tamily, member 2
Hs.28298	Hs.46721 Hs.29438 Hs.82985	Hs.59363 Hs.42392	Hs.7370 Hs.98209 Hs.99336 Hs.11371	Hs.31677	Hs.251531 Hs.107845	Hs.79748 Hs.11173	Hs.98001	Hs.77667	Hs.268530 Hs.192894 Hs.111515	Hs.78335
AA481045 Hs.28298	N47445 Hs.46721 H42967 Hs.29438 AA461456 Hs.82985	W93299 Hs.59363 AA148524 Hs.42392	AA679468 Hs.7370 AA417211 Hs.98209 AA453598 Hs.99336 T64012 Hs.11371	N52193 Hs.31677	AA449333 Hs.107325 AA007283 Hs.107845	AA630794 Hs.79748		AA865464 Hs.77667	AA521025 Hs.77196 AA701260 Hs.114492 AA062688 Hs.61169	AA704387 Hs.106531
814662	280699 183120 796613	356943 491367	859886 731154 795230 79817	284288	785701 429211	856454	743030	1470048	826350 434902 512751	383868
GF203	GF203 GF200 GF203	GF202 GF201	GF204 GF202 GF202 GF202	GF201	GF203 GF201	GF201	GF202	GF203	GF200 GF203 GF204	GF203

Atty Docket No. 2172			-1.2724804	-1.0521968		1.11969371	1.115/2554	1.06153328 1.21423877 1.06425507
∢		1412.123	1411.907	1411.39	1411.234	1410.804	1410.25/ 1410.196	1410.032 1409.738 1409.534
		SSX2		RBBP4			SHBG	FGFR2 DKFZp434B0435
	APPENDIX A	synovial sarcoma, X breakpoint 2 ESTs	ESTs	retinoblastoma-binding protein 4	ESTs	EST	sex hormone-binding globulin SHBG ESTs	fibroblast growth factor receptor 2 (bracteria-expressed kinase, karatinocyte growth factor receptor, cranidacial dysostosis 1. Crouzon exprdorme, Pfeiffer syndrome, Jackson-Weiss syndrome, Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-Jackson-
		Hs.166076 Hs.180848	Hs.26536	Hs.16003	Hs.5621	Hs.43275	Hs.46319 Hs.120893	Hs.278881 Hs.12900 Hs.240 Hs.144339
		N72228 Hs.42715 AA862484 Hs.127787	32 Hs.26536	AA429422 Hs.81058	AA863257 Hs.5621		T69346 Hs.46319 AA704443 Hs.120893	809464 AA443093 Hs.82775 50990 H18436 Hs.12900 292964 N91105 Hs.48860 1292856 AA776722 Hs.56159
_		291290 N72228 1456974 AA86248		773599 AA42		_		809464 AA44300 50990 H18436 292964 N91105
Westbrook et al.		GF201 291 GF204 145	4	GF200 773		•••	GF200 82871 GF203 45107	GF200 809 GF200 509 GF200 2920 GF204 129

1.23259394 1.26142601 1.18761257 -1.2518544 1.29504465 -1.0564736 1.08832647 -1.0536702 -1.1260971 1.1029892 -1.258999 1406.676 1409.269 1408.183 1407.334 1407.196 1406.384 406.364 409.187 409.089 407.437 1407.43 408.28 KIAA0614 AHCYL1 MAPRE1 **ZNF205** RER1 AIP-1 DBT ESTs, Highly similar to titin-like component of branched chain similar to S. cerevisiae RER1 novel genes, one similar to C. bacterial genes, and the first Human DNA sequence from clone 30M3 on chromosome Sp22.1-22.3. Contains three exon of the KIAA0319 gene. complex; maple syrup urine ESTs, Moderately similar to alternatively spliced product using exon 13A [H.sapiens] elegans Y63D3A.4 and one dihydrolipoamide branched similar to (predicted) plant, worm, yeast and archaea Homo sapiens mRNA full S-adenosylhomocysteine enath insert cDNA clone keto acid dehydrogenase microtubule-associated chain transacylase (E2 abl-interactor 12 (SH3zinc finger protein 205 EUROIMAGE 609395 protein, RP/EB family, protein [H.sapiens] containing protein) <IAA0614 protein</p> hydrolase-like 1 Contains E member 1 disease) ESTS Hs.173685 Hs.234279 Hs.256315 Hs.139410 Hs.267791 Hs.40500 Hs.28896 Hs.13128 Hs.99509 4s.19015 4s.7314 Hs.4113 AA176819 Hs.108489 Hs.89479 Hs.13128 AA459981 Hs.99509 AA922700 Hs.75346 AA425821 Hs.23588 AA479109 Hs.19015 Hs.86870 Hs.28896 AA418914 Hs.9345 Hs.7314 Hs.5852 N30811 190785 N21334 R68626 R89083 T99018 474323 195753 611324 796444 111492 769565 753946 122685 768059 138455 257136 265102 GF203 GF202 GF202 GF200 GF201 GF203 GF203 GF200 GF203 3F203 GF203 GF200

glutamic-oxaloacetic

16150400	2010	1.34218274												-1.4351088	1.07389436	-1.0177305				1.58124343		1.2012885		-1.5323157		1.15242562			4 0045766	-1.6943700
908	617.00	1405.822	1405.755	1405.209			1404.769	1404.609		1404.388		1403.532	1403.013	1402.485	1402.353	1402.302	1401.628	1401.541		1401.508	1401.268	1400.9		1400.776		1400.767		1400 461	1400.401	1400.278
, HOO			HSPCA					KIAA0419		HLA-DRB1		COVA1		HRIHFB2436			KIAA0555				HSPC121	DKFZP586I1023		POU2F2		U5-100K				
ransaminase 1, soluble	(asparate animotransierase 1) GOTT ESTs, Highly similar to	PTD016 protein [H.sapiens]	alpha	ESTs	Homo sapiens cDNA	FLJ10853 fis, clone	VT2RP4001502	KIAA0419 gene product	najor histocompatibility	complex, class II, DR beta 1	cytosolic ovarian carcinoma	antigen 1	ESTs	endocrine regulator	ESTs	ESTs	KIAA0555 gene product	ESTs	ESTs, Moderately similar to	hNKR-P1a protein [H.sapiens]	butyrate-induced transcript 1	DKFZP586I1023 protein	POU domain, class 2,	transcription factor 2	prp28, U5 snRNP 100 kd	protein	Homo sapiens mRNA; cDNA	DNTZP+04MO92 (:: 0:: 0:0::0	DKFZp434M09Z)	ESIS
	/SC:SL	Hs.30154	Hs.180532	Hs.117995			Hs.72085	Hs.236828		Hs.180255		Hs.155185	Hs.68624	Hs.48433	Hs.175034	Hs.98261	Hs.43107	Hs.124717		Hs.78628	Hs.84926	Hs.111515		Hs.1101		Hs.168103		00000	HS.260622	Hs. / 004
	Jac.sh	Hs.30154	Hs.84055	Hs.43551			Hs.11874	AA625653 Hs.112269		Hs.114929		4A156560 Hs.82137	4A634482 Hs.68624	4A443937 Hs.48433	4A418402 Hs.98292	4A416795 Hs.98261	Hs.27165	Hs.43639		4A195023 Hs.78628	Hs.46892	Hs.7354		Hs.101862		AA598470 Hs.10022			AA6/91// HS.242/	Hs./004
	HZZ826	N51514	H88540	N24645			T68430	AA625653		H50623		AA156560	AA634482	AA443937	AA418402	AA416795	H11718	W94486		AA195023	N50073	N68327		N49616		AA598470			AA6/91//	H49645
1	21/02	281449	253009	268960			83342	745339		186767		588822	743901	757152	767259	731357	47580	357884		665391	282710	287300		277779		897767		,0000	866694	37539
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1.02254019 1.10135397 1.53682693	-1.0932083	-1.0932083	-1.3017991	1.06893745 -2.2607204 -1.4547576 1.43524787	-1.2711107
1399.912 1399.76 1399.034 1399.18 1397.613	1397.461	1397.461 1397.447	1397.204 1397.009	1396.332 1396.233 1396.038 1395.608 1395.284 1395.155 1394.738 1393.918	1393.082
CTSL C3AR1	ш г	# F &	EIF3S3	sl ZNF43	us ZFP95
cathepsin L complement component 3a receptor 1 ESTs ESTs ESTs ESTs	ESTS, Highly similar to CALCIUM-DEPENDENT GROUP X PHOSPHOLIPASE A2 PRECURSOR [H.sapiens]	ESTS, Highly similar to CALCIUM-DEPENDENT GROUP X PHOSPHOLIPASE A2 PRECURSOR [H.sapiens] ESTS eulkaryolic fransistion initiation	ractor 3, suburnt 3 (garrima, 40kD) ESTs	ESTs, Weakly similar to cytochrome P-450 [H-sapiens] zinc finger protein 43 (HTF6) ESTs ESTs ESTs ESTS ESTS ESTS ESTS ESTS	zinc finger protein homologous to Zfp95 in mouse
Hs.78056 Hs.155935 Hs.194264 Hs.72844 Hs.22929 Hs.24567	Hs.193681	Hs.193681 Hs.188591	Hs.58189 Hs.48805	Hs. 96937 Hs. 74107 Hs. 12692 Hs. 194803 Hs. 56004 Hs. 56004 Hs. 21648 Hs. 27803 Hs. 288702	Hs.110839
W73874 Hs.7826 AA464711 Hs.77328 AA703590 Hs.8416 AA402302 Hs.119189 R43300 Hs.22929 R32939 Hs.24567	T94293 Hs.110613	T94293 Hs.104069 R11316 Hs.113205	Al017703 Hs.58189 N63500 Hs.48805	AA778653 Hs.96937 AA778894 Hs.74107 R43897 Hs.22692 120857 Hs.10657 R39905 Hs.106253 AA28485 Hs.56004 W779167 Hs.21648 AA251137 Hs.87803 R53954 Hs.108455	AA058369 Hs.63426
345538 810242 450284 741962 32541 135203	119914	119914	1636707 278101	1049009 844816 33511 112397 26729 324236 292171 684160	509701
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Ally Docket No. 21726	1.18193763	-1.1391016		-1.44132/							1.38944719					1.42563403				-1.1454306		
Ally	1392.933	1391.325	1390.594	1390.426	1390.387	1389.584		1389.148	1388.848	1388.076	1387.81			1207 601	100:700	1387.378	1387.058			1386.875	1386 844	1
		KDELR1		JMZ3	CITED2	LOC54505	=:				KIAA1042					TRAF3				COX10		
APPENDIX A	ESTs KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein	retention receptor 1 ESTs, Weakly similar to	putative p150 [H.sapiens]	homolog of yeast SPB1 Cbp/p300-interacting transactivator, with Glu/Asp- rich carboxy-terminal domain,	. 2	hypothetical protein	ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!	[H.sapiens]	ESTs	ESTs	KIAA1042 protein	Human DNA from	chromosome 19-specific	cosming report, genomic	sequence TNF receptor-associated	factor 3	ESTs	COX10 (yeast) homolog, cytochrome c oxidase	assembly protein (heme A:	farnesyltransferase) ESTs, Weakly similar to	contains similarity to C2	uomains [C.elegains]
	Hs.42219	Hs.78040	Hs.271739	Hs.23170	Hs.82071	Hs.95665		Hs.241160	Hs.268790	Hs.93605	Hs.6705			10000	/000c.sn	Hs.89676	Hs.105623			Hs.77513	U. 107716	18:10/716
	AA418389 Hs.42219	Hs.78040	Hs.48826	Hs.106582	AA115076 Hs.82071	AA634500 Hs.114623		Hs.101578	Hs.52881	Hs.93605	Hs.6705			100004	AA264106 HS.103064	AA504259 Hs.89676	AA478730 Hs.105623			Hs.77513	0,000,01	US.20042
	AA418389	H27912	W15574	N94524	AA115076	AA634500		N24609	H29303	H09757	N63904			00110044	AA264106	AA504259	AA478730			H21868	010000	687814
k et al.	767287	184175	320254	309676	491565	743925		267293	52618	46561	293804			0,000	324313	825399	753640			160126	40000	130032
Westbrook et al.	GF203	GF200	GF201	GF203	GF201	GF204		GF201	GF201	GF201	GF202			10010	GFZUI	GF200	GF204			GF200	1000	02150

	1.76965052 1.25662309	1.06574403	1.1080938	1.5437901		-1.3640207				-1.2846861			-1.6314993					1.16625145						0100001	0106001.1-		1.35211605
	1386.73 1385.946	1384.823	1384.779	1383.658		1382.008		1381.722		1381.683	1381.619		1380.909		1379.95			1379.588				1379.541		1000	1379.179		1378.916
	KIAA0298										KIAA0667		FYB		NSF			SRF									RI58
ESTs, Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!	gene product		ESTs STS Highly similar to CGL	132 protein [H.sapiens]	Homo sapiens clone 25028	nence	ens cDNA	0,000	ESTs, Weakly similar to !!!!	ENTRY !!!! [H.sapiens]		FYN-binding protein (FYB-		N-ethylmaleimide-sensitive		serum response factor (c-fos	serum response element-	factor)	ens cDNA	ils, clone	OVARCIO00309, weakly	SYNTHASE (EC 4.2.99.2)	ESTs, Weakly similar to	W01A11.2 gene product		retinoic acid- and interferon-	inducible protein (58kD) RI
ESTs, Weakly similar ALU SUBFAMILY SX WARNING ENTRY II	[H.sapiens] KIAA0298 g	EST	ESTs ESTs High	132 protein	Homo sapi	mRNA sequence	Homo sapiens cDNA	ADSE00490	ESTS, Wea	ENTRY IIII	TBP-intera	FYN-bindin	120/130)	N-ethylmal	factor	serum resp	serum resp	binding trar	Homo sapiens cDNA	FLJ10916 fis, clone	CVARCIO	SYNTHAS	ESTs, Wes	Z.TTATOW	[C.elegans] ESTs	retinoic aci	inducible p
	Hs.103009 Hs.21560	Hs.99402	Hs.178071	Hs.180312		Hs.13396		Hs. 7845		Hs.173705	Hs.154740		Hs.58435		Hs.108802			Hs.155321				Hs.9547			Hs.3589		Hs.27610
	N90781 Hs.103009 4A853966 Hs.21560	4A456023 Hs.99402	AA417212 Hs.98210	AA436327 Hs.9288		AA460722 Hs.13396		Hs. 7845		Hs.40997			Hs.58435		Hs.101830			AA487973 Hs.1082				1574914 AA971274 Hs.9547			Hs.90979 Hs.8503		Hs.27610
	- `	_	AA4172	AA4363		AA4607;		H19107		T66154	W70084		N64862		H38086			AA4879				AA9712			T46871		W24246
	303105 1393860	812145	731156	755304		796760		50915	2	22161	344006		293325		190940			840636				1574914			78844		310105
	GF203 GF203	GF203	GF202	GF203		GF202		GF201	; ;	GF203	GF204		GF200		GF201			GF200				GF204		i	GF200		GF200

	1 7059911	1170007:1-		1.28163454			-1.6077252									-1.0411615		2.08013021	1.27178873							1.07704852					1.98089578	1.03179889			
	1070 004	1370.524		1378.086	1376.979		1376.814	1375.97					1375.619			1375.172		1375.107	1374.782	1374.676					1374.367	1373.777	1373.744			1373.593	1373.277	1373.249		1372.928	
	20,400	COMPO					RAB5A	DKFZP566C0424								CYP11B1		KIAA0744	INSIG1							BLVRA									
proteasome (prosome,	macropain) subunit, beta type,	D Homo sanians cDNA	FLJ20311 fis. clone	HEP07319	ESTS	RAB5A, member RAS	oncogene family	DKFZP566C0424 protein	Homo sapiens cDNA	FLJ10754 fis, clone	NT2RP3004544, highly similar	to Homo sapiens mRNA for	KIAA0554 protein	sytochrome P450, subfamily	XIB (steroid 11-beta-	nydroxylase), polypeptide 1	KIAA0744 gene product;	nistone deacetylase 7	nsulin induced gene 1	ESTs	Homo sapiens cDNA	FLJ10296 fis, clone	NT2RM1001044, highly similar	to Homo sapiens HSPC031	mBNA	biliverdin reductase A	ESTs	Homo sapiens mRNA; cDNA	DKFZp4340031 (from clone	DKFZp434O031)	ESTs	ESTs	ESTs, Highly similar to sorting	nexin 9 [H.sapiens]	
_		0808/SH		Hs 18616	_		Hs.73957	Hs.226770	_	_	_	_	Hs.165179 I			Hs.2610		Hs.116753 P		Hs.191952			_	_	Hs.268049	Hs.81029	Hs.193197		_	Hs.47367	Hs.150000	Hs.42640		Hs.7905	
	1	HS./8596		Hs 18616	Hs.27295		RG.46	Hs.108781					Hs.47077			Hs.2610		Hs.102492	Hs.56205	4A702186 Hs.120804					AA987623 Hs.108259	AA192419 Hs.81029	AA700305 Hs.118312			Hs.47367	Hs.39652	Hs.42640		Hs.102940	
	01,000	1460110 AA8644/9 HS./8596		T99312	N22827		R45525	H94739					W33154			AA884709 Hs.2610		N31605	H59620	AA702186					AA987623	AA192419	AA700305			N51917	H74330	N45139		N95433	
	0,100	1460110		199397	265625		35236	256449					321770			1467195		271799	207288	448195					1603408	627542	460580			282201	230180	282980		309932	
	000	GF203		GESON	GF201		GF200	GF201					GF201			GF203		GF203	GF200	GF204					GF204	GF200	GF204			GF201	GF200	GF200		GF201	

	1.18372265	-1.4144/22	1.57799962		1.05422338					-1.2464295			1.39107254			-1.0120935	-1.3789055				1.20904206	2.14000036							-1.1377908	1.05256796			
	1372.497	1372.455	13/2.259	1372.259	1371.802	1371.701			1371.554	1371.013			1370.671	1369.576	1368.938	1368.624	1368.406		1367.851		1367.687	1367.524	1367.417	1367.405			1366.694	1366 565	1366.252	1365.295		1365.039	
	PPGB			KIAA0679	YDD19					RPS2				DARS					S100A8		PPIA		LOC51704					DKEZD564B147	KIAA0483	YDD19			
protective protein for beta- galactosidase	(galactosialidosis)	EST	ESTS	KIAA0679 protein	YDD19 protein	ESTs	Homo sapiens cDNA	FLJ10417 fis, clone	NT2RP1000112	ribosomal protein S2	ESTs, Weakly similar to	reverse transcriptase	[M.musculus]	aspartyl-tRNA synthetase	ESTs	ESTs	ESTs	S100 calcium-binding protein	A8 (calgranulin A)	peptidylprolyl isomerase A	(cyclophilin A)	ESTs	G protein-coupled receptor	ESTs	ESTs, Moderately similar to !!!!	ALU SUBFAMILY SQ	IH saniens]	DKEZDE64B147 protein	KIAA0483 protein	YDD19 protein	Homo sapiens mRNA; cDNA DKFZn564A132 (from clone	DKFZp564A132)	
	Hs.118126	Hs.98096	Hs.222535	Hs.5734	Hs.25615	Hs.268740			Hs.180171	Hs.182426			Hs.59939	Hs.80758	Hs.101270	Hs.26980	Hs.183745		Hs.100000		Hs.182937	Hs.24917	Hs.242407	Hs.269559			He 269634	Uo 151045	Hs 64691	Hs.25615		Hs.17155	
	AA916327 Hs.985	AA412739 Hs.98096	AA701003 Hs.124101	AA497025 Hs.11069	AA282983 Hs.50943	T88939 Hs.13237			N91276 Hs.42367	AA774619 Hs.6045			AA002258 Hs.59939	AA481562 Hs.80758		H53133 Hs.26980	N25234 Hs.113632		AA086471 Hs.100000		H93021 Hs.36561	H39022 Hs.24917	H98742 Hs.62421	AA702118 Hs.124748			AA775108 He 12/1905	A A O 40750 HS 124505	AA040732 HS,100677	AA454632 Hs.123157		AA182001 Hs.17155	
	1473289	730635	397254	897559	713109	22334			305895	399143			427778	815303	25159	202514	267435		562729		241900	192289	261522	447579			908898	000000	9/0214	811874		624811	
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1.4323597 1.16183137	1.15619514 1.84140911 -1.1893589	-1.1381143	1.24986782 -1.3794938	1.51387454	1.13135499	1.15265946 1.32706393 -1.3171693	
1365.034 1364.081	1363.789 1363.759 1363.501 1363.376	1362.998	1362.829 1362.739	1362.509 1362.189	1362.023 1361.979 1361.909	1361.613 1360.368 1360 1359.531	1359.445
	IL13RA1 DKFZP564C1940	GABRP	MTHFD2	IGF2	KHSRP LOC51329	GNE	AKR1B1
ESTs, Highly similar to CGI- 118 protein [H.sapiens] ESTs	interleukin 13 receptor, alpha 1 IL13RA1 ESTs ESTs DKFZP64C1940 protein DKFZP5	gamma-aminobulynic acid (GABA) A receptor, pi methylene tetrahydrofolate dehydrogenase (NAD+ dependent),	cyclohydrolase ESTs insulin-like growth factor 2	(somatomedin A) ESTs KH-type splicing regulatory protein (FUSE-binding protein	ESTs SRp25 nuclear protein UDP-N-acetylglucosamine-2-	epinterase/nv- acetylmannosamine kinase ESTs ESTs ESTs	aldo-keto fedudase family 1, member B1 (aldose reductase) Homo sapiens cDNA FLJ10776 fts, clone
Hs.82389 Hs.26331	Hs.250911 Hs.193415 Hs.104888 Hs.3804	Hs.70725	Hs.154672 Hs.129864	Hs.251664 Hs.58800	Hs.91142 Hs.40095 Hs.103561	Hs.5920 Hs.13308 Hs.59317 Hs.38664	Hs.75313 Hs.34790
Hs.82389 Hs.26331	AA158346 Hs.109656 H91215 Hs.53049 AA521107 Hs.104888 AA455271 Hs.6789	AA102670 Hs.70725	AA480995 Hs.37791 R20798 Hs.129864	Hs.119679	V21621 Hs.93619 H97976 Hs.40095 AA158375 Hs.103561	742695 Hs.13308 AA463461 Hs.59317 NS3376 Hs.38664	435948 AA701963 Hs.114082 1492510 AA879064 Hs.34790
H73313 H05961	AA15834(R91215 AA52110 AA45527	AA1026	AA48099 R20798	N74623 W86185	N21621 H97976 AA1583	T68440 R42695 AA46346 N53376	AA7019 AA8790
232670 44007	591095 195132 826325 810038	563598	814615 130104	296448 416309	266085 251407 591143	83345 32092 811781 284004	435948
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1358.668	1357.81 1357.688	1357.228 1357.074	1357.045	1356.312 1356.036	1355.878 1355.563	1353.482	1353.482 1353.021 1352.423	1351.873	1351.346 1351.313
	PDE6A GSTA3	BNIP3		HKE2 OSMR	EGFL2	TH	Ē	PLEC1	RAD51
ESTS, Weakly similar to putative p150 [H-sapiens] ESS, Modedately similar to IIII ALU SUEFAMILY SQ WARNING ENTRY !!!! Tazabiens] phosphodiosterase 64, cGMP-	Specific, rod, alpha glutathione S-transferase A3 G BCL2/adenovirus E1B 19kD-	Interacting protein 3 ESTs Homo sapiens cDNA FLJ20101 fis, clone	COL04655 HLA class II region expressed		Homo sapiens cDNA FLJ20507 fis, clone KAT09540 EGF-like-domain, multiple 2 E Friend leukemia virus	ntegration 1 Friend leukemia virus	integration 1 F ESTs ESTs	1, intermediate filament g protein, 500kD 1 (S. cerevisiae) og (E coll RecA	
ES' Hs.141358 put ES' ALI WA Hs.270696 [H:4	Hs.182240 spe Hs.102484 gluf BC	Hs.23025 inte Hs.23025 ES Hor	Hs.263925 CO HL	Hs.205736 ger Hs.238648 onc	Hs.202955 FL. Hs.57652 EG		Hs.108043 inte Hs.190349 ES Hs.25425 ES		Hs.23044 hor Hs.221631 ES
N72010 Hs.40481 AA173888 Hs.111088	Hs.63260 Hs.102484	AA446839 RG.67 AA482037 Hs.23025	Hs.15943	W88772 Hs.50546 AA909184 Hs.93476	Hs.8993 Hs.57652	RG.30	N50806 Hs.108043 AA777510 Hs.121945 H05785 Hs 25425	AA448400 Hs.79706	AA873056 Hs.74 AA459858 Hs.98120
N72010 AA173888	W92514 N30096	AA446839 RG.67 AA482037 Hs.230	R87717	W88772 AA909184	H53732 H39187	N50806	N50806 AA777510 H05785	AA448400	AA873056 Hs.74 AA459858 Hs.98
290895	361840 256907	783697 746075	180832	417573 1523225	236129 175103	280882	280882 449144 44030	781362	1476053 795812
GF201 GF202	GF201 GF201	GF200 GF203	GF204	GF201 GF204	GF200 GF200	GF200	GF200 GF203	GF200	GF203 GF201

-1.4713061 1.3455235 1.11598852 1.00853413 1.00853413 1.3394138 -1,7002114 1.7038688 1.7003695 1.3524856	-1.0717527	1.68383268 -1.1673173
1350.828 1350.649 1350.513 1349.636 1349.636 1349.339 1349.065 1349.032 1348.047 1348.647 1346.95 1346.95	1345.963	1345.826 1345.683
BSN EF4B DDB1 SPAG7 ZFD25 CCK CASP6 ANXA1 C7 RPL44	CLPS	KIAA0191
bassoon (presynaptic dyomatix protein) ESTS euksryotic translation initiation factor 4B admage-specific DNA binding protein 1 (127kD) ESTS sperm associated antigen 7 zinc finger protein (147kD) ESTS. Moderately similar to alternatively spliced product using exon 134 H. sapiens) Chollecystokinin caspase 6, apoptosis-related cysteine protease annexin A1 EST complement component 7 richosomal proteins CHA4 ESTS, Moderately similar to semaphorin C IM. musculus) Human stopies cDNA FLJ10290 fis, clone MAMMA1002385, weakly similar to semaphorin C IM. musculus) HBG7D HUMD RADIOLICEOPROTEIN HBG7D	partial cus colipase, pancreatic ESTs	ESTs KIAA0191 protein
Hs. 194684 Hs. 111515 Hs. 122592 Hs. 108327 Hs. 108327 Hs. 108327 Hs. 20429 Hs. 20247 Hs. 3280 Hs. 328	Hs.1340 Hs.269591	Hs.34720 Hs.12413
H18306 Hs.98876 H776507 Hs.39843 AA778885 Hs.122592 N25085 Hs.43817 AA872402 Hs.93379 AA608557 Hs.74623 AA641254 Hs.106021 T57851 Hs.90436 AA278839 Hs.50216 AA57844 Hs.51451 N40841 Hs.80247 H63077 Hs.78225 AA694378 Hs.78225 AA694378 Hs.78285 AA699359 Hs.118857 AA283300 Hs.9598	AA626336 HS.116966 T54662 HS.1340 AA705702 HS.120968	AA456093 Hs.34720 AA448593 Hs.12413
GF203 171664 GF204 259467 GF202 254749 GF202 1472753 GF203 1472753 GF203 703844 GF204 669458 GF204 258790 GF203 208718 GF200 208718 GF200 208718 GF200 208718 GF200 208718 GF200 208718 GF200 208718 GF200 208718		GF203 813513 GF200 785963

	-1.5550152 1.19773857	1.73769132		-1.1489588		1.62847951	11,000/1.	1.26983213
1345.36	1345.347 1345.282	1345.279 1345.277	1344.749	1344.518	1344.121 1343.463	1343.194	1342.641	1342.429 1342.221
	NOS	YDD19	IL13RA1	APM1	АМН	Ė	TYROBP	SOD1 YDD19
ESTS, Weakly similar to 6- PYRUVOX. TETRAHYDBOBIOPTERIN SYNTHASE H. saplens Homo sapiens cDNA FLJUGSS iffs, done RTJUGSS iffs, done NT2RP2001070, weakly similar to PUTATIVE PYRDOXAMINE 5:	1.4.3.5) SON DNA binding protein	ESTS, nignij silnilar to cor- 110 protein [H.sapiens] YDD19 protein	interleukin 13 receptor, alpha 1 IL13RA1 Homo sapiens mRNA, chromosome 1 specific	ranscript NAA0492 adipose most abundant gene transcript 1	anti-Mullerian hormone ESTs ESTs, Weakly similar to	unknown [S.cerevisiae] 3'(2'), 5'-bisphosphate	nucleolidase i TYRO protein tyrosine kinase binding protein	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult)) YDD19 protein
Hs.14204	Hs.267963 Hs.92909	Hs.177861 Hs.25615	Hs.250911	HS.12/338 Hs.80485	Hs.112432 Hs.177466	Hs.261023	Hs.271752 Hs.9963	Hs.75428 Hs.25615
N75842 Hs.14204	AA172372 Hs.20608 AA431848 Hs.92909	N22302 Hs.43136 AA425000 Hs.80075	ဖွ	H0Z1/3 HS.1/945 H45617 HS.80485	AA884397 Hs.125575 AA426516 Hs.67332	W45285 Hs.106057	AA19/334 HS.86112 AA664094 Hs.116936	AA599127 Hs.75428 W88792 Hs.21218
300405	594994 773618	254004 768356	502819	124/42	1461725 768944	328613	645U79 855476	950489 417855
GF201	GF202 GF200	GF202 GF203	GF201	GF201	GF204 GF204	GF202	GF203	GF200 GF201

-1.3612454	1.42560896		1.13130343		1.15979761		-1.1126706						-1.063496	-2.3378134	-1.4210431		-1.3494999			-1.1923838	-1.3003142		-1.6124491	1.19000347			-1.0194559		1.00475693
1342.118	1341.581	1340.801	1340.504	1340.258	1340.156	1339.743	1339.715		1339.166				1339.163	1338.705	1338.521		1338.414		1338.017	1337,995	1337.709		1337.156	1336.409	1336.379	1335.376	1334.045		1333.556
	GSN			YME1L1					MAP4				GNAL				RPS5P1						FVT1				YME1L1		ILF2
Human Chromosome 16 BAC clone CIT987SK-A-635H12 gelsolin (amyloidosis, Finnish	type) ESTs, Weakly similar to	aralar1 [H.sapiens]	ESTs	YME1 (S.cerevisiae)-like 1	ESTs	ESTs	ESTs	microtubule-associated protein	4	guanine nucleotide binding	protein (G protein), alpha	activating activity polypeptide,	olfactory type	EST	ESTs	ribosomal protein S5	pseudogene 1	Homo sapiens clone 23579	mRNA sequence	ESTs	ESTs	follicular lymphoma variant	translocation 1	ESTs	ESTs	ESTs	YME1 (S.cerevisiae)-like 1	interleukin enhancer binding	factor 2, 45kD
Hs.183755	Hs.80562	Hs.99486	Hs.269938	Hs.206521	Hs.54911	Hs.108209	Hs.47189		Hs.239298				Hs.154145	Hs.97999	Hs.18723		Hs.237225		Hs.170226	Hs.72548	Hs.28273		Hs.74050	Hs.269545	Hs.55756	Hs.191415	Hs.206521		Hs.75117
AA021202 Hs.108604	H72027 Hs.80562	AA459651 Hs.99486	AA706834 Hs.119971	N53511 Hs.102686	N93185 Hs.54911	W87801 Hs.108209	N51069 Hs.47189		AA130870 Hs.110969				AA479952 Hs.87365	AA406058 Hs.97999	R97804 Hs.18723		AA463629 Hs.23747		H29566 Hs.7071	AA164301 Hs.72548	R96490 Hs.28273		AA459208 Hs.74050	AA700989 Hs.118865	AA459676 Hs.55756	AA454022 Hs.61282	AA425447 Hs.74553		AA894687 Hs.75117
3 364111	214990	-	4		304841	417059	281936		586839				3 753626	743024	200174		811836		52577	595318	199571		814260	397224	795570	795279	_		1493390
GF203	GF200	GF201	GF203	GF201	GF202	GF201	GF202		GF201				GF203	GF202	GF200		GF203		GF201	GF202	GF200		GF200	GF203	GF201	GF201	GF202		GF203

TORREY BAY TRACT

1.14488012 1.35707487 1.07556784	1.66943908	1.50829358	-1.2510742	-1.3976359	-1.3697441	-1.0442964	1.20033393
1332.604 1332.347 1332.279	1331.679 1330.882	1330.727 1330.497 1330.37	1330.121	1330.08 1330.037 1329.592 1329.57	1329.514	1328,436	1328.319 1328.009
	RRBP1 CSTA	KIAA0671 KIAA0212		CXCR4 DKFZP586N1922		ENSA	TSC22
Homo sapiens cDNA FLJ10330 fis, clone NTZRM200624, weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 4 ESTS	ribosome binding protein 1 (dog 180kD homolog) cystatin A (stefin A) Homo sapiens mRNA for	TL132 KIAA0671 gene product KIAA0212 gene product	EST chemokine (C-X-C motif),	receptor 4 (fusin) DKFZP586N1922 protein ESTs ESTs	ESTs. ESTs, Weakly similar to ORF2 [M.musculus] Homo sapiens cDNA FL.20331 fis, clone	HEP10410 endosulfine alpha transforming growth factor beta-stimulated protein TSC-	22 ESTs, Weakly similar to ORF YKR087c [S.cerevisiae]
Hs. 42362 Hs. 48644 Hs. 105326	Hs.98614 Hs.2621	Hs.234573 Hs.169836 Hs.154332	Hs.44647	Hs.7357 Hs.7757 Hs.97543 Hs.175400	Hs.42376 Hs.28439	Hs.50848 Hs.111680	Hs.114360 Hs.98123 Hs.8108
N71647 Hs.42362 N62825 Hs.48844 AA469958 Hs.105326	AA447804 Hs.104253 W72207 Hs.2621	Hs.100581 Hs.29941 Hs.108897	Hs.44647	Hs.89414 Hs.31760 Hs.97543 Hs.80310	Hs.28439	R41461 Hs.21897 AA046043 Hs.111680	AA664389 Hs.74632 AA412289 Hs.98123 N22924 Hs.8108
N71647 N62825 AA469958	AA447804 W72207	N64391 N90775 N23299	N34892	T62491 H20519 AA460151 N93193	H97475 H87363	R41461 AA046043	AA664389 AA412289 N22924
295140 278540 730386	813859 345957	290235 303112 267808	276689	79629 173145 795875 304858	251910	29258 488751	868630 731476 266747
GF200 GF203 GF203	GF202 GF201	GF203 GF201 GF201	GF202	GF200 GF204 GF201 GF201	GF203	GF203 GF202	GF201 GF202 GF202

1.17058937	-1.0322737	-1.1898041	1.28702763	-1.1850469			1.06422889	1.07763785			-1.4430053													-1.0283304	1.00657727	-1.0588775		-1.9426316	1.00119837	1.21520222
1327.295	1326.745	1326.431	1326.12	1325.664		1325.368	1323.988	1323.724			1323.236		1323.068				1322.934			1322.732	1322.694			1322.045	1321.268	1321.193		1320.465	1319.328	1319.279
		PA2G4				CLAPS2		PLIN					MIR16							DBY				IIIH4	FLJ10667				DKFZP586P2421	
ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H-sapiens]	ESTs proliferation-associated 2G4,	38KD	ESTs	EST	adaptor-related protein	complex 2, sigma 1 subunit	ESTs	perilipin	ESTs, Weakly similar to	alleritatively spiliced product	using exon 13A [H.sapiens]	membrane interacting protein	of RGS16	ESTs, Weakly similar to !!!!	ALU SUBFAMILY SC	WARNING ENTRY !!!!	[H.sapiens]	DEAD/H (Asp-Glu-Ala-	Asp/His) box polypeptide, Y	chromosome	ESTs	inter-alpha (globulin) inhibitor	H4 (plasma Kallikrein-sensitive	glycoprotein)	hypothetical protein	ESTs	Homo sapiens mRNA for	KIAA1397 protein, partial cds	DKFZP586P2421 protein	ESTs
Hs.112200 Hs.59669	Hs.36125	Hs.5181	Hs.38559	Hs.103904		Hs.119591	Hs.177713	Hs.103253			Hs.68751		Hs.107014				Hs.117688			Hs.99120	Hs.6818			HS./6415	Hs.86149	Hs.223756		Hs.102237	Hs.109439	Hs.80890
AA056387 Hs.112200 M92315 Hs.59669		4A488332 Hs.5181	AA701634 Hs.38559	AA156737 Hs.103904		4A421518 Hs.119591	V48345 Hs.100965	T70850 Hs.103253			AA180060 Hs.68751		H19340 Hs.92611				H17321 Hs.117688			4A447588 Hs.99120	H09825 Hs.6818			V7/653 Hs.386/1	753929 Hs.86149	AA135638 Hs.103838		AA187679 Hs.111114	AA219100 Hs.109439	4A180163 Hs.80890
509478 /	_	842973 /	433407	502397		739109 /	279741 N	108330			611953 /		51239 H				20075 H			_	47005 H			247863 P	39814 F	501543 /				609530 /
GF202	GF202	GF202	GF203	GF202		GF201	GF203	GF200			GF202		GF201				GF204			GF201	GF201			GF 200	GF203	GF202		GF202	GF202	GF202

-1.6928237	-1.8262513		1.68097916	1.34737598	1.09035579	-1,4842574		1.02874047		1.2071073	1.63624966	1.75022368
1319.099	1318.551	1318.377	1318.045	1317.991	1317.641	1317.233		1316.981	1316.886	1316.604	1316.458	1316.307 1316.003 1315.875
				PRKCSH					NME2	ATP6A1		SKAP-HOM
EST	Homo sapiens clone 23736 mRNA sequence ESTs Weakly similar to	KIAA0246 [H.sapiens] Homo sapiens mRNA; cDNA DKF7n564E2282 (from clone	DKFZp564E2282) protein kinase C substrate 80K	H ESTs	Homo sapiens mRNA; cDNA DKFZp564E153 (from clone DKFZp564E153)	ESTS	ESTS, Weakly similar to !!!! ALU CLASS F WARNING	ENTRY !!!! [H.sapiens]	non-metastatic cells 2, protein (NM23B) expressed in ATPase, H+ transporting, lysosomal (vacuolar proton	pump), alpha polypeptide, 70kD, isoform 1	Homo sapiens cDNA FLJ10849 fis, clone NT2RP4001414, highly similar to SEPTIN 2 HOMOLOG	ESTs SKAP55 homologue ESTs
Hs.42217	Hs.7888	Hs.18575	Hs.109694	Hs.1432 Hs.34574	Hs.8769	Hs.124778 Hs 98073		Hs.119830	Hs.275163	Hs.5119	Hs.8768	Hs.52644 Hs.84063
H96658 Hs.42217	AA398264 Hs.7888	AA702243 Hs.18575	AA136016 Hs.109694	AA427406 Hs.22909 B92347 Hs.34574				AA704587 Hs.119830	AA496628 Hs.119232	N28391 Hs.5119	AA496944 Hs.8768	AA682502 Hs. 10413 W93127 Hs. 59422 R81177 Hs. 52644 AA682502 Hs. 84063
251827	726703	447510	502546	770993	283398	436782		450598	755750	263040	897527	103 1364 415063 147468 450653
GF202	GF202	GF204	GF202	GF201	GF200	GF204	3	GF203	GF201	GF200	GF202	GF202 GF204 GF203

	1.10895867	1.35975398	1.09634443	2.53770803	-1.6954827	1.84869504 1.74605552	-2.2262449	1.08248771	1.08248771		-1.5494513 1.0067078
	1315.276	1315.234	1315.092	1314.978 1314.403	1313.872 1313.735 1313.52	1313.222 1313.217	1312.933 1312.905 1312.817	1312.21	1312.21	1311.457	1311.286 1311.233 1311.117 1310.875
	RNH		FXR2	SMCY	KIAA0438	CD24	RDHL] PP	PPP1CA	PPP1CA		SCHIP-1
APPENDIX A	ribonuclease/angiogenin inhibitor	Homo sapiens cDNA FLJ11340 fis, clone PLACE1010771, highly similar to M.musculus HCNGP mRNA	fragile X mental retardation, autosomal homolog 2 SMC (mouse) homolog: Y	some	KIAA0438 gene product ESTs ESTs	CD24 antigen (small cell lung carcinoma cluster 4 antigen) ESTs	retinol denydrogenase homolog pyrophosphatase (inorganic) ESTs	protein phosphatase 1, catalytic subunit, alpha isoform PPP1CA	protein phosphatase 1, catalytic subunit, alpha isoform PPP1CA ESTs, Weakly similar to	reverse dansomplasse moments [H.sapiens]	1
	ribonucli	Homo s FLJ113 PLACE to M.mu	fragile) autosor SMC (n	chromosome ESTs	KIAA04 ESTs ESTs	CD24 a carcino	retinol de homolog pyrophos ESTs	protein catalyti	catalytic ESTs, V	[H.sapiens]	ESTs ESTs ESTs ESTs
	Hs.75108	Hs.27299	Hs.52788	Hs.80358 Hs.7788	Hs.21490 Hs.40098 Hs.103165	Hs.278667 Hs.38331	Hs.179608 Hs.184011 Hs.6829	Hs.183994	Hs.183994	Hs.6759	Hs.61490 Hs.61515 Hs.25298 Hs.14619
	Hs.75108	AA457232 Hs.11379	AA489729 Hs.52788	AA465521 Hs.80358 AA453994 Hs.7788	AA142966 Hs.21490 W51909 Hs.40098 AA134111 Hs.103165	Hs.83525 Hs.38331	AA609992 Hs.94547 AA608572 Hs.36454 AA133167 Hs.6829	AA443982 Hs.118229	AA443982 Hs.78092	AA148533 Hs.6759	AA708955 Hs.61490 AA610005 Hs.61515 AA456143 Hs.25298 H98001 Hs.14619
	R88242	AA45723	AA48972	AA46552 AA45399	AA14296 W51909 AA13411	H59915 H64938	AA60999 AA60857 AA13316	AA44398	AA44398	AA14853	AA70895 AA61000 AA45614 H98001
של פו מו.	166195	838662	823663	814942	504657 324513 503334	204335	1031994 950700 490755	756666	756666	491529	506143 1032006 796367 251461
Westoloon et al.	GF200	GF202	GF200	GF203 GF201	GF201 GF203 GF201	GF200 GF200	GF204 GF202 GF201	GF200	GF200	GF204	GF204 GF204 GF202 GF200

1.3330906	1.15318565	-1.2295246 -1.2003774 -1.3671223	-1.1608456	1.44136837		1.09742651	1.33559452	1.33559452	1.088022
1310.782	1310.701 1310.588	1310.35 1310.158 1310.099	1309.495	1309.457 1309.239 1309.027	1308.902 1308.537 1308.184	1307.621	1307.292	1307.292	1306.136 1305.627
ATP6D	VAPA	H3F3B	LOC51321		ABP/ZF	PRKCBP1	YWHAB	YWHAB	KIAA0028 KIAA0512
ATPase, H+ transporting, lysosomal (vacuolar proton pump) 42RD', vacuolar proton ATPase, subunit C; V- ATPase, subunit C; V- ATPase, subunit C membrane protein)-associated	protein A (33kD) ESTs	H3 histone, family 3B (H3.3B) H3F3B ESTs ESTs	hypothetical protein Homo sapiens mRNA; cDNA DKFZp566D1146 (from clone	DKFZp566D1146) ESTs ESTs	Alu-binding protein with zinc finger domain ESTs ESTs	protein kinase C binding protein 1 tyrosine 3-	monoxygenase activation protein protein, beta polypeptide tyrosine 3-monoxygenase/tryptophan 5-monooxygenase/tryptophan 5-	monooxygenase activation protein, beta polypeptide leucyl-tRNA synthetase,	mitochondrial KIAA0512 gene product
Hs.86905	Hs.9006 Hs.117085	Hs.180877 Hs.98244 Hs.92993	Hs.268122	Hs.7358 Hs.124195 Hs.98588	Hs.86185 Hs.59839 Hs.5422	Hs.75871	Hs.182238	Hs.182238	Hs.2450 Hs.48924
Hs.86905	Al005339 Hs.9006 AA779234 Hs.117085	AA608514 Hs.75387 AA416662 Hs.98244 AA004810 Hs.92993	AA449688 Hs.3619	AA432253 Hs.7358 N38791 Hs:124195 AA448171 Hs.98588	W88571 Hs.86185 AA454172 Hs.59839 W15263 Hs.5422	AA480906 Hs.75871	Hs.108250	Hs.5049	H19822 Hs.2450 AA114250 Hs.48924
H05768	A1005339 AA77923	AA60851 AA41666 AA00481	AA44968	AA43225 N38791 AA44817	W88571 AA454172 W15263	AA48090	H62594	H62594	H19822 AA11425
43826	1632221 452671	950574 730992 429123	785766	782306 244011 782771	417424 795315 322537	814595	208161	208161	172495 564158
GF200	GF204 GF203	GF200 GF202 GF202	GF203	GF201 GF202 GF201	GF201 GF201 GF201	GF200	GF200	GF200	GF201 GF202

Homo sapiens mRNA; cDNA APPENDIX A

1.16142914		-1.5048237		-1.0916932		-1.6823489	-1.0542576	-2.1251145												1.16915451		1.29886629	-1.0812468			1.08177551		1.10971236	-1.0270901	-1.1653255	1.02438415
1305.242		1305.229		1305.228		1304.269	1304.057	1303.222			1302.997					1302.415	1302.323			1302.307		1302.294	1301.996			1301.648	1301.447	1301.415	1301.326	1301.315	1301.095
				RAD23B		COX7B					SRM160									DYRK2		FKBP1A				ALDH5A1			SST	COL9A3	
DKFZp434G0972 (from clone DKFZp434G0972)	Homo sapiens cDNA FLJ20092 fis, clone	COL04215	cerevisiae)		cytochrome c oxidase subunit	Allb	ESTs	ESTs	Ser/Arg-related nuclear matrix	protein (plenty of prolines 101-	ike)	ESTs, Weakly similar to	EPIDERMAL GROWTH	-ACTOR RECEPTOR	KINASE SUBSTRATE EPS8	H.sapiens]	ESTs	dual-specificity tyrosine-(Y)-	phosphorylation regulated	kinase 2	FK506-binding protein 1A	(12kD)	ESTs	aldehyde dehydrogenase 5	family, member A1 (succinate-	semialdehyde dehydrogenase) ALDH5A1	ESTs			collagen, type IX, alpha 3	ESTs
D Hs.106148 D	Tι	Hs.23618 C		Hs.178658 h	9.	Hs.75752 V	Hs.4210 E	Hs.121820 E	S	ā	Hs.18192 III	ш	ш	ш	×	Hs.172849	Hs.172717 E	ō	α.	Hs.173135 Ki	ш	Hs.752 (1	Hs.48689 E	e			Hs.81810 E	Hs.106432 E	Hs.12409 s		Hs.98095 E
Hs.106148		AA505134 Hs.23618		AA489678 Hs.75563		4A629999 Hs.75752	Hs.106298				Hs.95322					Hs.39603				AA452376 Hs.8950		AA625981 Hs.752	AA251561 Hs.48689			4A486410 Hs.5299	AA150107 Hs.81810	Hs.106432	Hs.12409	4A017526 Hs.53563	4A421166 Hs.98095
R39582		AA5051		AA4896		AA6299	R38196	N48593			R26536					H73479	R52089			AA4523		AA6259	AA2515			AA4864	AA1501	R52679	R51912	AA0175	AA4211
137602		825805		824352		884511	23774	279269			132395					232887	40402			787861		745496	684813			842879	491504	41739	39593	361204	731098
GF203		GF203		GF200		GF203	GF202	GF202			GF201					GF201	GF201			GF200		GF202	GF203			GF202	GF201	GF202	GF200	GF200	GF202

APPENDIX A	
APPENDIX	
APPEND	×
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	1.98004121									-1.2119116	-1.4632683		1.38975054		-1.2920071				-1.1176394			2.83523652	-1.0148636		-1.600327		1.34503068		
	1300.875	1300.69		1300.417		1299.742	1299.688			1299.391	1298,468	1298.298	1298.104		1297.684	1297.637	1297.11	1296.824	1296.513		000	1296.399	1296.155		1295.459		1294.949	1294.39	1294.209
	EYA2			NR3C2						TCF6L1			NUP54			FLN29		DKFZP434B027	PFKL			LOC51256			ECHS1		NDUFA5		KIAA0454
eves absent (Drosophila)	homolog 2 ESTs	EST	nuclear receptor subfamily 3,	group C, member 2	Homo sapiens mRNA for	cytochrome b5, partial cds	ESTs	transcription factor 6-like 1	(mitochondrial transcription	factor 1-like)	ESTs	ESTs	nucleoporin p54	Human cytochrome P4502C9	(CYP2C9) mRNA, clone 25	FLN29 gene product	ESTs	DKFZP434B027 protein	phosphofructokinase, liver	ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ	WARNING ENTRY !!!!	[H.Sapiens] hypothetical protein	ESTs	enoyl Coenzyme A hydratase,	short chain, 1, mitochondrial	(ubiquinone) 1 alpha	subcomplex, 5 (13kD, B13)	ENIS	KIAA0454 protein
	Hs.29279 Hs.43845	Hs.156972		Hs.1790		Hs.31086	Hs.125475			Hs.75133	Hs.44829	Hs.43481	Hs.9082		Hs.167529	Hs.5148	Hs.146013	Hs.7970	Hs.155455		100000	HS.183997	Hs.182356		Hs.76394		Hs.83916	HS.48372	Hs.129928
	AA402207 Hs.29279 W37418 Hs.43845	AA884666 Hs.125610		AA447079 Hs.1790		W04674 Hs.100692	AA865224 Hs.125475			AA449118 Hs.75133	N59244 Hs.44829	AA620896 Hs.43481	AA733061 Hs.9082			N21170 Hs.5148	AA058713 Hs.59380	10	W72140 Hs.119336		10070 -11-0000	AA136247 HS.67607 N23315 HS.8645	AA165678 Hs.23034		AA626255 Hs.76394		AA608515 Hs.83916	No/9/2 HS.483/2	AA433920 Hs.8167
	741139 322005	1468651		784296		320509	1455242			785845	289505	1055581	399562		195712	264895	488160	731369	346009		100101	267859	593185		745542		950578	230476	//3685
	GF200 GF202	GF204		GF201		GF201	GF204			GF200	GF203	GF204	GF203		GF200	GF201	GF201	GF201	GF203		10010	GF203	GF202		GF203		GF200	10212	GF201

GF200	767069	AA424516	AA424516 Hs.82845	Hs.82845	Human clone 23815 mRNA sequence DEAD/H (Asp-Glu-Ala- Asp,His) hox polymentide 17		1294.141	1.18083676
GF202	843085	AA488628 Hs.6179	Hs.6179	Hs.6179	(72kD) H.sapiens mRNA for	DDX17	1293.574	1.5272982
GF201	884283	AA669750 Hs.6940	Hs.6940	Hs.12028	retrotransposon		1293.406	
GF202	772962	AA476258	4A476258 Hs.44070	Hs.44070	ESTs		1292.668	-1.1305772
GF203	898210	AA598597 Hs.8145	Hs.8145	Hs.174139	chloride channel 3	CLCN3	1292.648	-1.6006005
GF200	194384	R83000	Hs.75924	Hs.101025	basic transcription factor 3	BTF3	1292.147	1.74788634
GF201	795770	AA460319	AA460319 Hs.48469	Hs.48469	LIM domains containing 1	LIMD1	1292.073	
GF203	755474	AA410636	AA410636 Hs.78770	Hs.172801	isoleucine-tRNA synthetase	IARS	1292.021	1.16747621
GF200	141314	R63811	363811 Hs.25580	Hs.113029	ribosomal protein S25	RPS25	1291.773	-1.045467
GF203	454970	AA676625 Hs.9029	Hs.9029	Hs.9029	DKFZP434G032 protein	DKFZP434G032	1291.601	-2.0493659
					major histocompatibility			
GF201	447509	AA702254	AA702254 Hs.72930	Hs.11135	complex, class II, DN alpha	HLA-DNA	1291.547	
GF203	665952	AA193442	AA193442 Hs.65805	Hs.65805	ESTs		1291.472	1.68787524
					ESTs, Weakly similar to			
					phospholipase C-delta4			
GF204	449159	AA777524	AA777524 Hs.121947	Hs.165374	[R.norvegicus]		1291.192	
					growth arrest and DNA-			
GF200	591683	AA147214	AA147214 Hs.80409	Hs.80409	damage-inducible, alpha	GADD45A	1291.044	1.05012787
GF201	52642	H29590	Hs.14822	Hs.14822	ESTs		1290.724	
					Nck, Ash and phospholipase C	0		
GF201	745433	AA625859	AA625859 Hs.104481	Hs.104481	binding protein	NAP4	1290.5	
GF204	866633	AA679150	AA679150 Hs.100739	Hs.7935	KIAA0952 protein	KIAA0952	1290.332	
					Homo sapiens cDNA			
					FLJ10846 fis, clone			
GF201	743263	AA400093	AA400093 Hs.32271	Hs.32271	NT2RP4001373		1290.248	
GF203	435739	AA700783	AA700783 Hs.118369	Hs.186813	ESTs		1290.04	1.066758
					ESTs, Weakly similar to			
					kinase-related protein ros-1			
GF201 GF201	259066 195369	N32832 R89584	Hs.51695 Hs.107815	Hs.271274 Hs.107815	precursor [H.sapiens] ESTs		1289.98 1289.788	
GF203	247050	N53940	Hs.47726	Hs.278554	heterochromatin-like protein 1 HECH	HECH	1289.454	-1.1847003

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	-1.5737246			-1.178433	-1.88356	1.31821614				-1.1471003		-1.1273775	-1.0322181	-1.1362976	-1.6227151	-1.0669797		-1.2553473	-1.0844666
1288.966	1288.491	1288.456 1288.135	1288.071	1287.106 1287.034	1286.135	1285.674			1285.172	1284.491	1283.53	1282.456	1282,446	1282.117	1282.088	1281.828		1281.079	1279.961
		MTP	TEAD4	HSA9761	EIF4B							SULT1C	LOC51022			RBMS2			
ESTs, Weakly similar to DY3.6 [C.elegans]	SRrp129 [H.sapiens] microsomal triglyceride	polypeptide, 88kD) EST	TEA domain family member 4 TEAD4	transferase ESTs	eukaryotic translation initiation factor 4B	EST	ESTs, Weakly similar to	mariner transposase	[H.sapiens]	ESTs	ESTs	SULT1C sulfotransferase	CGI-133 protein	ESTs	EST	RNA binding motif, single stranded interacting protein 2	ESTs, Weakly similar to cDNA EST vk386e10.3 comes from	this gene [C.elegans] ESTs, Weakly similar to coded	for by C. elegans cDNA yk30b3.5 [C.elegans]
Hs.81001	Hs.103521	Hs.195799 Hs.116066	Hs.94865	Hs.125819 Hs.26016	Hs.93379	Hs.105183			Hs.251659	Hs.191593	Hs.70723	Hs.75854	Hs.5054	Hs.266155	Hs.46891	Hs.20938		Hs.19954	Hs.116122
Hs.108298	Hs.103521	4A421278 Hs.2827 4A625671 Hs.116066	Hs.94865	AA418523 Hs.98297 R53940 Hs.26016	W86908 Hs.14977	AA481729 Hs.105183			Hs.15545	AA412047 Hs.122578	AA131663 Hs.70723	AA489314 Hs.75854	AA421273 Hs.5054	Hs.130841	Hs.46891	Hs.1172		AA504824 Hs.19954	Hs.4284
T98785	R88506	AA421278 AA625671	W74602	AA418523 R53940	W86908	AA481729			T89273	AA412047	AA131663	AA489314	AA421273	W72969	N49090	AA708161 Hs.1172		AA504824	H14604
122276	166268	731054 745361	346696	767310 39926	416479	838518			110403	729956	503817	842928	731044	344848	279770	460806		825718	48659
GF201	GF203	GF201 GF204	GF201	GF203 GF201	GF203	GF202			GF204	GF202	GF201	GF200	GF202	GF203	GF202	GF203		GF203	GF202

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1.00615799				1.03374177	1.23892466		1.01593373	1.06167346		1.51027827	-1.1504871		-1.1693998	-1.1138537	-1.9289217	1.06870022	1.3030754	1.17757184
1279.839 1279.816	1279.742	1279.211	1278.003	1277.255	12/6.815	5	1276.665	1276.536		1276.448	1276.106	1275.757	1274.972	1274.794	1274.059	1273.927	1273.785 1273.757	1272.722
TDPX1 RPL7A	DLAT		CDC16				HDGF					KIAA0716		DKFZP586I1023		FPRL1	GTF3A	
thioredoxin-dependent peroxide reductase 1 (thiol-specific antioxidant 1, natural killer-antioxidant b) (killer-antioxida) factor B) (killer-antioxida) factor B) (hosomal protein L'a ditydrolipoamide S-acephtransfarea (EZ	dehydrogenase complex) Human clone 23933 mRNA	sequence CDC16 (cell division cycle 16,	S. cerevisiae, homolog) Homo sapiens BAC clone	RG114B19 from 7q31.1	ESIS	nepatoma-derived growth actor (high-mobility group	protein 1-like)	ESTs	Homo sapiens clone 25071	and 25177 mRNA sequences	ESTs	KIAA0716 gene product	ESTs	OKFZP58611023 protein	ESTs	formyl peptide receptor-like 1	general transcription factor IIIA GTF3A ESTs	Homo sapiens cDNA FLJ20022 fis, clone ADSE01331
Hs.146354 Hs.99858	Hs.115285	eg S	Hs.1592		Hs.50158		Hs.89525			Hs.10590		Hs.118140	Hs.12974	Hs.111515	Hs.161102	Hs.99855	Hs.75113 Hs.47230	Hs.50813
Hs.90298 Hs.99858	Hs.115285	Hs.129673	Hs.1592	Hs.9489	N67334 Hs.50158		AA453831 Hs.89525	AA058597 Hs.23247		4A504825 Hs.10590	Hs.94477	AA668695 Hs.118140	4A404273 Hs.12974	4A463272 Hs.22636	Hs.93801	Hs.251	AA459999 Hs.62145 N51323 Hs.47230	Hs.50813
H68845 H23421	N29901	R39465	AA410604 Hs.1592	AA458938 Hs.9489	N67334		AA453831	AA058597		AA504825	N93853	AA668695	AA404273	AA463272	N35493	R80041	AA459999 N51323	W03754
212165 51981	271006	23933	755385	814417	286446		813673	380890		825697	309224	857312	758319	811751	272192	146605	796461 283114	297212
GF200 GF200	GF201	GF204	GF201	GF203	GF202	5	GF200	GF203		GF203	GF202	GF204	GF202	GF203	GF202	GF200	GF203 GF202	GF200

ESTs, Weakly similar to coded

				-1.0804652			1.24814898			1.00799793	1.72999383	-1.0809299	1.05983495	-1.0595695		1.14918631		1.14918631	-1.0098585	1.21872157	-1.7118261	-1.1273451		-1.2175992	-1.0038723	-1.0588513	1.24297932		1.21394995	-1.4098598
	1272.419	1271.834	1271.479	1271.357	1271.347		1271.107	1270.784		1270.28	1269.864	1269.494	1269.341	1268.694		1268.473		1268.473	1268.294	1267.755	1267.561	1267.505		1265.995	1265.801	1264.645	1264.37		1264.352	1264.27
					DKFZP434A043					KIAA0277			ITGA1			딤		FII		P84	MYO1B					KIAA0970			DDX8	
for by C. elegans cDNA	yk27g3.5 [C.elegans]	ESTs	ESTs	ESTs	DKFZP434A043 protein	Human zinc finger protein	mRNA, complete cds	EST	guanine nucleotide exchange	factor for Rap1	ESTs	ESTs	integrin, alpha 1	EST	Friend leukemia virus	integration 1	Friend leukemia virus	integration 1	ESTs	nuclear matrix protein p84	myosin IB	EST	Homo sapiens mRNA; cDNA DKFZp434G1919 (from clone	DKFZp434G1919); partial cds	EST	KIAA0970 protein	ESTs	DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 8	(RNA helicase)	ESTs
	Hs.10101	Hs.269792	Hs.116153	Hs.54721	Hs.102708		Hs.78765	Hs.116106		Hs.80620	Hs.268916	Hs.24143	Hs.116774	Hs.16019		Hs.108043		Hs.108043	Hs.112972	Hs.1540	Hs.34160	Hs.48803		Hs.7256	Hs.56167	Hs.103329	Hs.180037		Hs.171872	Hs.99250
	AA459905 Hs.10101	N75976 Hs.131858	AA626334 Hs.116153	N91527 Hs.54721	AA454110 Hs.123983		T47229 Hs.78765	AA625907 Hs.116106		AA451891 Hs.80620	H66883 Hs.36728	4A283699 Hs.24143	H68922 Hs.116774	T90871 Hs.16019		N50806 RG.30		V50806 Hs.108043	4A621324 Hs.112972	4A280748 Hs.99930	AA448661 Hs.34160	N63497 Hs.48803		4A520992 Hs.7256		R36431 Hs.103329	4A699495 Hs.117110		AA465387 Hs.77711	AA454005 Hs.99250
	809413	295260	745600	299997	788261		75923	744962		786672	210710	700299	212078 H	112440		280882		280882	1048794	711450	786072	278091		826276	_	_	432480		-	795255
	GF201	GF204	GF204	GF202	GF204		GF200	GF204		GF200	GF200	GF203	GF200	GF200		GF200		GF200	GF202	GF200	GF203	GF202		GF203	GF202	GF200	GF203		GF200	GF202

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					-1.3039267	-1.0691961	-1.0111522		-1.0683011	-2.4788493			1.17543574						-2.0598801	1.10840085					-1.0268638			-1.0491201
1263.345	1263.324		1263.296	1262.877	1262.589	1262.506	1261.853		1261.787	1261.356		1259.645	1259.462		1259.426				1259.207	1259.202		1258.824			1258.777		1257.918	1257.805
PTPRC	PSIP1						KIF3B		ELF3			VAMP8			PRSS12							INHBA						
protein tyrosine phosphatase, receptor type, c polypeptide	PC4 and SFRS1 interacting protein 1	Homo sapiens cDNA FLJ20783 fis, clone	COL03108	EST	ESTs	ESTs	kinesin family member 3B	E74-like factor 3 (ets domain	ranscription factor)	ESTs	vesicle-associated membrane	protein 8 (endobrevin)	ESTs	protease, serine, 12	(neurotrypsin, motopsin)	ESTs, Moderately similar to !!!!	ALU SUBFAMILY SQ	WARNING ENTRY !!!!	[H.sapiens]	ESTs	inhibin, beta A (activin A,	activin AB alpha polypeptide)	putative DNA-directed RNA	polymerase III C11 subunit	H.sapiens]	AIMOs sucioses comon	FLJ20496 fis, clone KAT08729	EST
р Hs.170121 ге	Р Hs.82110 р	TΨ	Hs.246885 C	Hs.114119 E	Hs.167805 E	Hs.131703 E	Hs.168212 ki		Hs.166096 tr	Hs.193777 E	>	Hs.172684 p	Hs.271745 E	ď	Hs.22404 (r	ш •	Κ:			Hs.146074 E		Hs.727 a		٥	Hs.110857	3	Hs.239625 F	
AA455497 Hs.10511	AA626371 Hs.26365		N29800 Hs.102479	4A702420 Hs.114119	717 Hs.109263	399 Hs.131703	375 Hs.16745		AA433851 Hs.77224	AA704538 Hs.119740		963 Hs.7588	353 Hs.9168		783 Hs.22404					457 Hs.93781		159 Hs.93717			AA126951 Hs.110857		AA453275 Hs.108619	138 Hs.43330
809719 AA48	745118 AA62		270786 N298	447556 AA70	243602 N49717	286684 N67899	111006 T90375		770910 AA43	451123 AA70		80715 T62963	120413 T95953		145310 R77783					271110 N34457		269815 N27159			511632 AA12		795375 AA45	
GF201	GF204		GF201	GF204	GF202	GF203	GF200		GF200	GF203		GF204	GF200		GF204				GF202	GF202		GF201			GF202		GF201	GF202

Atty Docket No. 21726 -1.0135636 1.77961317 1.43749017 1.17115457 1.17115457 1.17103878 1.17103878 1.17103878 1.1460883	1252.19 1252.05 1251.873 1251.283	
1256.927 1256.788 1256.327 1255.394 1255.394 1255.394 1254.781 1254.207 1253.365 1253.365 1253.365 1253.365 1253.365 1253.365 1253.365 1253.365 1253.365 1253.365		
FY OKI DINB1 DINB1 ACOX3 IL1RL1 AADAC AADAC KIAA0130		
APPENDIX A Duffy blood group homolog of mouse quaking protein) CKI (KH domain RNA binding protein) Human clone 23773 mRNA sequence argo selection protein (mannose 6 phosphale argo selection protein) MK-ZPS681023 protein DK-ZPS681023 protein MACOX3 Interleukin 1 receptor-like 1 IL1RL1 ESTS ESTS ESTS ESTS Weakly similar to Pro- Pol-dUTPasse polyprotein ESTS EMM-musculus) ESTS EMM-musculus) ESTS EMM-musculus)	ESTS ESTS ESTS ESTS Homo sapiens cDNA FLJ/10347 ffs, clone NTZRMZCO1035, highly similar to CCR4.ASSOCIATED FACTOR 1	
Hs.183 Hs.15020 Hs.29019 Hs.247058 Hs.140452 Hs.111515 Hs.66 Hs.71818 Hs.587 Hs.587 Hs.587 Hs.58875 Hs.233952 Hs.233952 Hs.24106 Hs.233952 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106 Hs.24106	Hs.226318	
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T82477 AA489388 H66603 H43004 AA416787 H88221 AA678622 AA128152 R51494 AA04532 N765311 W92160 AA199666	AA46516 AA77822 R55017 R37165	
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-1.4134333 1.54845792 1.49547164	-1.06645/ 1.27609736 -2.2465717	1.26626851 -2.3895955 -1.4735871	-1.0040012 -1.3445694 1.07823967	-1.9908087
1251.226 1250.809 1250.699 1250.243	1240.14 1247.802 1247.566	1247.28 1247.261 1246.856 1246.503 1246.494 1246.124 1246.124	1245.28 1245.131 1244.694	1244.442 1244.096 1243.914 1243.867 1243.808 1243.808
FAAH	DSP	AK3	GNS ARHGEF1 PLN	ARPC3 SMA3
EST Homo sapiens mRNA; cDNA DKFZp5860021 (from clone DKFZp5860021) fatty acid amide hydrolase ESTs	ES1s desmoplakin (DPI, DPII) ESTS, Moderately similar to PANOREATIC HORMONE PRECURSOR [H.sapiens] PRECURSOR (International call principle of sufficiency similar to	acturio suprindiatoria actualistica actualis	glucosamine (N-acety)-6- sulfatase (Sanfilippo disease IIID) Rho guanine nucleotide exchange factor (GEF) 1 prospholamban	complex, subunit 3 (21 kD) ESTS ESTS ESTS ESTS ESTS SMA3
Hs.55294 Hs.48778 Hs.24781 Hs.112607	Hs.125522 Hs.74316 Hs.43266 Hs.20588	Hs.23133 Hs.274691 Hs.119321 Hs.2268 Hs.48362 Hs.270100 Hs.8330 Hs.47259	Hs.164036 Hs.252280 Hs.85050	Hs.6895 Hs.221504 Hs.8841 Hs.49272 Hs.230618 Hs.251397
	Hs.94066 Hs.39188 Hs.107470 Hs.20588	H18453 Hs.23133 AA489040 Hs.12470 AA703374 Hs.119321 H15408 Hs.2258 N52289 Hs.48362 AA777590 Hs.121951 A44777591 Hs.8330 N51441 Hs.47259	AA035347 Hs.2703 AA481277 Hs.26531 AA427940 Hs.85050	H73961 Hs.108391 AA284267 Hs.102961 T48412 Hs.8841 W87823 Hs.49272 N68993 Hs.49594 H18423 Hs.62036
W04569 AA774648 AA431988 AA60887C	N77006 R91822 N22836 H66312	H18453 AA48904) AA70337, H15408 N59289 AA77759 T40891 N51441	AA03534 AA48127 AA42794	H73961 AA28426 T48412 W87823 N68993 H18423

-1.0435647		-1.1984868	1 13833776				-1.4094269	-1.2742108		-1.0885781	1.12545086			-1.0592515		-1.0461579	1.14050757	-1.1670272	-1.2200262		1.36938/3/	-1.0033343	1.125/0/04
1243.15		1241.818	1241 75) : :	1241.579	1240.968	1240.827	1240.54		1240.532	1240.451		1240.189	1240.036		1239.864	1239.529	1239.472	1239.214		1238.803	1230.401	1238.212
ITGA2	!	XPC	BINX1			RPP14								KIAA0118				LGALS9			CAP-C	(SI)	
integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2		o,	(acute myelold leuxernia 1; amit oncodene)	milar to IIII Y SX RY IIII	[H.sapiens]	clease P (14kD)	ESTs	EST	Homo sapiens mRNA; cDNA DKFZp566C034 (from clone	DKFZp566C034)	ESTs	Homo sapiens mRNA; cDNA DKFZp586J231 (from clone		KIAA0118 protein	Homo sapiens cDNA FLJ20018 fis, clone	ADSE00909	ESTs location coalectoside-binding			associated		n r (leukocystatin)	ESIS
Hs 271986		Hs.320	Hs 129914		Hs.193612	Hs.155150	Hs.15069	Hs.44844		Hs.29464	Hs.97613		Hs.7252	Hs.184627		Hs.44095	Hs.114180	Hs.81337	Hs.246028		Hs.50758	HS.143212	Hs.128200
AA463610 Hs 1142		AA287404 Hs.320	AA425238 He 99914		4A011673 Hs.103319			N36989 . Hs.44844		AA074227 Hs.67614	AA398332 Hs.97613		AA443116 Hs.7252	AA076645 Hs.69748		N29825 Hs.44095	H62839 Hs.114180	AA434102 Hs.81337	W56586 Hs.7254		0		V51268 HS.128200
811740		701112 #	773915 1		429707		_	273635 N		383185 /	726681 /			526184 A		270883 N	208377 H	770192					283014
GF200) j	GF200	GF200	3	GF201	GF201	GF203	GF202		GF203	GF203		GF201	GF200		GF203	GF203	GF200	GF202		GF203	GFZUZ	GF203

1.91258808 1.04989034 1.44469028	1.19631001 -1.1629471 -1.7567715 1.11048617	1.26589158 -1.1900453 -1.541297	-1.1763527	
1238.199 1237.319 1237.869 1237.844 1237.372 1236.832	1236.099 1235.962 1235.146 1234.765 1234.573	1234.454 1233.377 1232.754 1232.653 1232.403	1232.354 1231.969 1231.847 1231.549	1231.483
B3GAT3 KIAA0322	K/AA0595	COL5A1 DIM1 SNAP25	RALY	
beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I) ESTs ESTs KIAA0322 protein ESTs	ESTs, Weakly similar to KIAA0980 protein [H saplens] ESTs, Weakly similar to ZK856,11 (C.elegans] KIAA0595 protein ESTs	Homo sapiens clone 25058 Harly sequence collager, type V, alpha 1 Homo sapiens mRNA; cDNA DKFZp434M0420 (from clone DKFZp434M0420) smillar to S, pombe dim1+ synaptosomal-associated Horofer, 2504 Homo sanians mRNA; cDNA	DKFZp434H1322 (non dione) DKFZp434H1322 (non dione) DKFZp434H1322 (non dione) DKFZp434H1322 (non dione) ESTs, Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	ESTs
Hs.26492 Hs.36823 Hs.30495 Hs.153685 Hs.124278 Hs.36120	Hs.44054 Hs.42129 Hs.746957 Hs.271689 Hs.268855	Hs.179397 Hs.146428 Hs.273369 Hs.5074 Hs.84389	Hs.97277 Hs.74111 Hs.268587 Hs.68301	Hs.180195
Hs.26492 Hs.36823 Hs.30495 Hs.7142 Hs.79969 Hs.36120	N34687 Hs.44054 AA465678 Hs.42129 AA435950 Hs.104929 H58175 Hs.124144 R93394 Hs.59978	R38894 Hs.91555 R75635 Hs.1849 AA443976 Hs.114993 AA603342 Hs.5074 AA663884 Hs.84389	AA504617 Hs.74111 AA504617 Hs.74111 ROE283 Hs.14088 AA083514 Hs.68301	AA883656 Hs.120374
R56054 H53829 H04828 R87212 H08206 R99333	N34687 AA46567 AA43595 H58175 R93394	R38894 R75635 AA44397 AA80634	R35849 AA504611 R05293 AA08351	AA8836E
40880 202612 43966 180885 45601 201990	271357 814865 730559 205582 275950	25058 143523 757205 1350852 969877	136984 825583 125118 549157	1466606
GF201 GF200 GF203 GF200 GF201 GF204	GF201 GF203 GF203 GF203 GF200	GF202 GF200 GF202 GF204 GF201	GF200 GF200 GF201 GF201	GF204

	-1.0935393 1.49826785	1,33962044 1,47922451 -1,0362426 1,01537175		1.1942627
1231,446 1231,246 1231,032 1230,767	1230.612 1230.587 1230.402 1230.344 1230.296	1229,801 1229,801 1229,687 1229,454	1229.342 1229.293 1229.182	1228.725
ADF		BNIP2 LIPG DYRK4	SMPD2 GRO1	ERBB2
ESTs Homo sapiens done 25218 HMNA sequence ESTs destrin (actin depolymerizing factor) Homo sapiens mRNA; cDNA DKRZA34P0735 (from clone	DKFZp434P0735) ESTS ESTS ESTS ESTS ESTS ESTS ESTS	Lozdadowicki serio 1980- interacting protein 2 lipase, endothellal dual-specificity tyrosine-(Y)- phosphoryation regulated kinase 4 ESTs sphingomyelin phosphodisetrase 2, neutral	sphingomyelinase) GRO1 oncogene (melanoma growth stimulating activity, alpha) ESTs, Weakly similar to Durative n 150 H, sapelnsi	ESTs verb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)
Hs.125757 Hs.64001 Hs.7740 Hs.82306	Hs.27192 Hs.22305 Hs.32448 Hs.88253 Hs.103002	Hs.155596 Hs.65370 Hs.17154 Hs.28360	Hs.55235 Hs.789 Hs.114157	Hs.62927
1467936 AA883551 Hs.125757 22135 R42888 Hs.64001 429517 AA011389 Hs.90972 768292 AA424824 Hs.82306	N95764 Hs.27192 R44581 Hs.22305 H96554 Hs.32448 AA464583 Hs.88253 W02753 Hs.55266	N62514 Hs.118967 AA599574 Hs.65370 AA452617 Hs.17154 R67839 Hs.28360	AA680132 Hs.55235 W42723 Hs.789 AA703013 Hs.114157	AA443351 Hs.46254
1467936 32195 429517 768292	308452 33102 250963 812954 327179	288796 1069733 788286 140537	433170	376736
GF204 GF204 GF201 GF201	GF201 GF201 GF203 GF203 GF201	GF203 GF200 GF200 GF203	GF204 GF201	GF202 GF200

1.22214565	1.03243817	1.03243817	1.64184424	1.41505063	-1.5896646 1.29822192	-1.1811764 1.43676296	1.00616523	1.14373399	-1.631009 1.60216908
1227.867	1227.798	1227.474 1227.423	1226.743	1226.599	1226.314 1226.294	1225.907 1225.405	1225.387	1224.659	1224.389 1224.047 1223.763
RARRES2	SLPI PPP1CA	PPP1CA	90018	NDUFA9		VASP	SLC14A1	CPA1	APLP1 EFNB2
retinoic acid receptor responder (tazarotene induced) 2 secretory leukocyte protease	inhibitor (antilieukoproteinase) SLPI protein phosphatase 1, catalytic subunit, ajpha isoform PPP1CA	catalytic subunit, alpha isoform PPP1CA ESTS	ESTS, rightly similar to CGT-84 protein [H.sapiens] S100 calcium-binding protein P	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9 (39KD)	EST ESTs vasodilator-stimulated	phosphoprotein ESTs solute carrier family 14 (urea transporter), member 1 (Kidd	blood group) Homo sapiens cDNA FLJ10196 fis, clone	carboxypeptidase A1 (pancreatic)	anyton bota (1-7) processor like protein 1 ephrin-B2 EST
	Hs.251754 III P Hs.183994 o	P Hs.183994 o Hs.37856 E	Hs.111449 p		- 8	Hs.44183 p	Hs.171731 b		Hs.74565 li Hs.30942 e Hs.105488 E
AA481944 Hs.37682	AA683520 Hs.110329 AA443982 Hs.118229	AA443982 Hs.78092 H60688 Hs.37856	AA283599 Hs.111449 B32952 Hs.2962	4	AA777932 Hs.121997 AA708096 Hs.130348	AA410429 Hs.93183 AA417982 Hs.44183	H82236 Hs.64607	AA845178 Hs.2879	N62866 Hs.74565 AA461108 Hs.94414 AA521017 Hs.105488
	378813 A 756666 A	756666 A 208984 H	713205 A			753418 A 767721 A	240062 H	 m	289645 N 796198 A 826305 A
GF200	GF201 GF200	GF200 GF200	GF203	GF200	GF203 GF203	GF200 GF203	GF200	GF203	GF203 GF200 GF204

APPENDIX A	ribophorin I 1223.72 -1.3219723	adapiot-related protein complex, gamma 2 suburit G2AD 1223.22 -1.3304755 Homo caniare chino 29877		inini, alpria o onin, actin-binding protein,	ZA COHOZA 1ZZZ.Z15	myeloid/lymphoid or mixed- lineage leukemia (trithorax	(figure);	MLL13	KIAA0320	DKFZP564F0923 protein DKFZP564F0923 1220.804			1218.929	EST 1218.714 -1.3567785	1218.574	ESTs 1218.573	EST 1218.51 -1.4024674	in kappa	variable 1D-8 IGKV1D-8 1218.4 -1.3131751	ESTs, Weakly similar to	stearoyl-CoA desaturase	[H.sapiens] 1218.25 -1.1847457	a disintegrin and	metalloproteinase domain 17		converting enzyme) ADAM17 1218.165	1218.097	prominin (mouse)-like 1 PROML1 124794815		alpha polypeptide PDGFA 1217.449	1917 994
	RPN1		2444		COHOS			MLL 13	KIAA03	DKFZP		ARPC3							IGKV1					2		ADAM1		PROMI		PDGFA	
APPENDIX A	ribophorin I	adaptor-related protein complex 1, gamma 2 subur Homo capions clone 23837	mRNA sequence	coronin, actin-binding prote	2A	myeloid/lymphoid or mixed- lineage leukemia (trithorax	(Drosophila) nomolog),	translocated to, 3	KIAA0320 protein	DKFZP564F0923 protein	actin related protein 2/3	complex, subunit 3 (21 kD)	ESTs	EST	EST	ESTs	EST	immunoglobulin kappa	variable 1D-8	ESTs, Weakly similar to	stearoyl-CoA desaturase	[H.sapiens]	a disintegrin and	metalloproteinase domain	(tumor necrosis factor, alph	converting enzyme)	ESTs	prominin (mouse)-like 1	platelet-derived growth fac	alpha polypeptide	i i
	Hs.2280	Hs.8991	Hs.110480	HS.11609	Hs.44396			Hs.404	Hs.150443	Hs.25524		Hs.6895	Hs.3640	Hs.59897	Hs.47809	Hs.25545	Hs.93674		Hs.156110			Hs.247474				Hs.64311	Hs.127066	Hs.112360		Hs.37040	02200
	Hs.113365	Hs.113856	AA291491 Hs.110480	AA459519 HS.11669	AA983765 Hs.44396			4A443284 Hs.404	W86876 Hs.108710	AA883402 Hs.125458		4A915980 Hs.3325	4A600201 Hs.3640	AA001603 Hs 59897	Hs.47809	Hs.25545	Hs.93674		AA488070 Hs.105678			AA457374 Hs.6202				Hs.64311	AA865302 Hs.127066	Hs.112360		AA701502 Hs.37040	OLEGO II GOMENIA
	R36132	H26294	AA29149	AA45951	AA98376			AA44328	W86876	AA88340;		AA915980	AA60020	AA00160	N54387	W37504	N24024		AA488070			AA45737				H28287	AA86530	R40057		AA70150	
k et al.	137189	161763	724895	810891	1580874			783998	416409	1461333		1473922	949947	497797	245125	321945	268795		840677			838155				182177	1455342	27544		435470	
Westbrook et al	GF203	GF203	GF201	GF200	GF204			GF203	GF201	GF204		GF203	GF202	GESOS	GESON	GF204	GF202		GF202			GF202				GF204	GF204	GF202		GF201	
_																															

	2.01618005	1.0376884			-1.2867642	1.05433867	-1.5320277					-1.2170352			1.18666906	1.2229557		-2.7694391	-1.4547952	1.84769351	
	1217.069	1215.909	1215.646 1214.844	1214.749	1214.348 1214.302	1214.081	1213.42		007 0707	1213.132	1212.993	1212.946	000 0101	1212.892	1212./06	1212.454	1212.337	1211.641	1211.31	1211.271	1211.234
		SLC1A5		2 HMOX2	DVL2 PHF1	ARHGDIA							9	I PR3	KIAA0426			SART1			BAK1
Homo sapiens intersectin 2 long isoform (ITSN2) mRNA,	complete cds solute carrier family 1 (neutral amino acid transporter),	member 5 ESTs, Weakly similar to alternatively spliced product	using exon 13A [H.sapiens] ESTs	heme oxygenase (decycling) 2 HMOX2 dishevelled 2 (homologous to	Drosophila dsh) PHD finger protein 1	(GDI) alpha	(GDI) aipina ESTs	ESTs, Weakly similar to	putative progesterone binding	protein [H.sapiens]	ESTs	ESTs	inositol 1,4,5-triphosphate	receptor, type 3	KIAA0426 gene product EST, Weakly similar to ZINC FINGER PROTEIN 117	[H.sapiens]	ESTs squamous cell carcinoma	antigen recognised by T cells	EST	ESTs	BCL2-antagonist/killer 1
	Hs.166184	Hs.183556	Hs.30211 Hs.122231	Hs.63908	Hs.118640 Hs.166204	Us 150161	Hs.50571			Hs.109494	Hs.106289	Hs.108785	:	Hs.77515	Hs.97476	Hs.86356	Hs.268930	Hs 18946	He 45012	Hs.58213	Hs.93213
	AA465719 Hs.16566	T70098 Hs.4059	H52062 Hs.30211 AA629348 Hs.116330	AA626370 Hs.83853	R39405 Hs.25288 AA682855 Hs.95128	A A 450 400 LIP 4745	N74963 Hs.50571				H10387 Hs.13347	AA609454 Hs.108785		AA701976 Hs.77515	AA708279 Hs.97476	AA205432 Hs.86356	H56946 Hs.37384	AA45575 He 18946	N39450 Hs 45012		
	814981	80910	197512 743732	745116	137506 450386	010010	299508			505414	47280	743568		435953	397658	646556	204774	810027	976026	344806	235938
	GF203	GF200	GF201 GF204	GF201	GF200 GF201	000	GF203	3		GF201	GF201	GF202		GF201	GF203	GF203	GF201	CESOS	0000	GF202	GF201

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	1.5833317	-1,2930366		1.83729995			1.44884288		-1,8850026				-1.1104029		1.3867615	1.26301749	-1.1357657	1.33872702	1.45952885	1.52499128	-2.6041815						-2.4691996	-1.1768107		-1 4467384	100.001		
	1210.891	1210.835	1210.072	1209.965	1209.89	1208.883	1208.751	1208.657	1208.393	1208.016	1207.732	1206.996	1206.898	1206.615	1206.575	1206.532	1206.424	1206.248	1206.168	1205.975	1205.9		1205.562	1205.217			1204.708	1204.599		1904 193	1204, 123	1	1203.721
		PCTK3							DKFZP586I1023	KIAA0962			HSPC232		UCP4								ISG20										
Homo sapiens mRNA,	transcript KIAA0495	PCTAIRE protein kinase 3	EST	ESTs	ESTs	ESTs	ESTs	ESTs	DKFZP586I1023 protein	KIAA0962 protein	ESTs	ESTs	hypothetical protein	ESTs	uncoupling protein 4	ESTs	ESTs	ESTs	EST	ESTs	ESTs	interferon stimulated gene	(20kD)	ESTs	Homo sapiens mRNA full	length insert cDNA clone	EUROIMAGE 30103	EST	ESTs, Weakly similar to	microtubule-based motor	[ri.sapiens] Homo sapiens cDNA	FLJ10607 fis, clone	NT2RP2005147
	He 49658	Hs 2994	Hs.116896	Hs.109097	Hs.25328	Hs.268726	Hs.36545	Hs.113099	Hs.111515	Hs.9059	Hs.121912	Hs.175144	Hs.227676	Hs.24128	Hs.40510	Hs.16222	Hs.88523	Hs.260844	Hs.112912	Hs.29088	Hs.112858		Hs.183487	Hs.44433			Hs.21754	Hs.250986		02300	HS:926/9		Hs.27931
	N97761 He 103377	40	AA663317 Hs.116896	AA171784 Hs.109097	H10993 Hs.25328	R20662 Hs.52125	AA489086 Hs.36545	AA699656 Hs.113099	AA464541 Hs.111430	AA894855 Hs.109257	AA777329 Hs.121912	AA491285 Hs.105287	AA677361 Hs.110934	W87281 Hs.24128	N32286 Hs.40510	H94236 Hs.16222	AA278865 Hs.88523	N49261 Hs.21640	AA620828 Hs.112912	AA053035 Hs.95307	AA620343 Hs.112858		AA150500 Hs.103888	N33115 Hs.44433			R15930 Hs.21754	AA432121 Hs.98677		07900 -11 04 504 4 4	AA443140 HS.926/9		N32919 Hs.27931
	255704	725677	853388	594683	47149	26414	824960	436463	810511	1502317	448290	824640	454501	416855	272663	242070	703559	280342	1055564	510088	1030921		491751	273185			53338	781482		00000	/96/23		259905
	0000	GESON	GF204	GF202	GF201	GF201	GF203	GF204	GF202	GF204	GF204	GF204	GF203	GF201	GF203	GF200	GF203	GF203	GF202	GF202	GF202		GF201	GF201			GF203	GF202		0001	GF 202		GF201

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-1.1339614	1.43467865	-1.1259833 -1.9191869 1.52594571 -1.6450904	1.68989505	-1.2367775	-1.1582757
1203.69	1203.406 1203.001	1202.485 1202.194 1201.946 1201.844 1201.799	1201.615 1201.607	1201.151 1201.099 1201.081 1200.836	1200.667 1199.99 1199.423
	CD164			F3	CADPS HYAL2
Homo sapiens mRNA; cDNA DKFZp586H021 (from clone DKFZp586H021) ESTS, Weakly similar to MITOCHONDRIAL.	H.sapiens] CD164 antigen, sialomucin ESTs, Weakly similar to AT	Hourbing racks I H. Sapiens] ESTs ESTs ESTs	SSTS ESTS, Weakly similar to JJ88J8. I H.sapiensj ESTS, Weakly similar to HVDRPHOLIPID HYDROPEROXIDE GLUTATHIONE	PEHOXIDASE [H.sapiens] ESTs L3 pigment ESTs, Moderately similar to !!!! ALU CLASS C WARNING ENTRY !!!! [H.sapiens]	Ca2+-dependent activator protein for secretion ESTs hyaluronoglucosaminidase 2
Hs.173515	Hs.16786 Hs.43910	Hs.109314 Hs.21447 Hs.110092 Hs.59521 Hs.72367	Hs.125256	Hs.44426 Hs.169404 Hs.272674 Hs.259836	Hs.151301 Hs.22856 Hs.76873
Hs.21277	AA448182 Hs.16786 AA598561 Hs.43910	V53492 Hs.109314 H09064 Hs.21447 AA004595 Hs.110092 M94247 Hs.59521 AA161466 Hs.72367	R09498 Hs.20370 AA922722 Hs.125256	AA452145 Hs. 43098 H75435 Hs. 39730 R76554 Hs. 6257 AA773993 Hs. 3347	742894 Hs.74574 110030 Hs.22856 4A453909 Hs.76873
H81010	AA44818 AA59856	N53492 H09064 AA004595 W94247 AA161466		AA452145 H75435 R76554 AA773993	R42894 H10030 AA45390
241003	782794 898198	245444 46051 428236 358699 592497	127710	787851 213157 144801 858447	32304 46931 788190
GF200	GF201 GF200	GF200 GF201 GF202 GF202 GF202	GF200	GF202 GF201 GF201 GF204	GF201 GF201 GF200

ESTs, Weakly similar to

					1.13856957						1.30839118						-1.2181052				1.06045021		-1.3227841	1.20322365		1.14068205		1.11478926	-1.4100662	-1.2563966	-1.1239945
	1199.382		1199.323	1199.248	1199.023		1198.983			1198.855	1198.566	1198.239			1198.062	1197.881	1197.571	1197.255			1196.91		1196.673	1196.464		1196.178	1195.816	1195.735	1195.457	1195.437	1194.827
			IFI27				APOH							_				DKFZP434C091			SLC23A1		SFRS2IP			SFRS2		YDD19			KIAA0202
[Human endogenous retrovirus type C oncovirus	[H.sapiens]	interferon, alpha-inducible	protein 27	ESTs	ESTs	apolipoprotein H (beta-2-	glycoprotein I)	Homo sapiens cDNA	FLJ20109 fis, clone	COL05067	ESTs	ESTs	ESTs, Moderately similar to	probable ligand-binding protein	RYD5 [R.norvegicus]	ESTs	ESTs	DKFZP434C091 protein	solute carrier family 23	(nucleobase transporters),	member 1	splicing factor, arginine/serine-	rich 2, interacting protein	ESTs	splicing factor, arginine/serine-	rich 2	ESTs	YDD19 protein	ESTs	ESTs	KIAA0202 protein
	Hs.113980		Hs.278613	Hs.36563	Hs.129038		Hs.1252			Hs.118194	Hs.169961	Hs.94179			Hs.127059	Hs.25209	Hs.99539	Hs.51692			Hs.82042		Hs.51957	Hs.61648		Hs.73965	Hs.127669	Hs.25615	Hs.114261	Hs.72805	Hs.80712
	Hs.113980		4A157813 Hs.2867	AA404609 Hs.36563	Hs.16039		Hs.1252			Hs.13432	Hs.47049	AA460314 Hs.94179			AA863023 Hs.127059	Hs.25209	AA461119 Hs.99539	Hs.51692			AA461071 Hs.82042		Hs.39860	AA406039 Hs.61648		4A454585 Hs.73965	4A863346 Hs.127669	AA453815 Hs.25465		Hs.72805	AA443347 Hs.80712
	R99560		AA15781	AA404609	T85931		H68848			R67903	N51585	AA46031			AA86302;	R54594	AA461119	H77332			AA46107		H78241	AA40603		AA45458	AA86334	AA45381	H84759	N77877	AA44334
	202051		588915	725143	112541		212188			140267	280466	795757			1455480	40104	796199	233538			795989		234562	743062		809535	1456813	813755	219937	299815	783721
	GF204		GF201	GF204	GF200		GF201			GF201	GF202	GF201			GF204	GF201	GF202	GF204			GF200		GF200	GF202		GF200	GF204	GF202	GF203	GF200	GF200

Atty Docket No. 2172	-1.0199487	1.13926494	1.31481569	1.15916165	1.38316362 -1.8982835	-1.2935801	1.00462178	-1.6386564	
Atty	1194.541 1194.514 1194.391	1194.004	1193.79 1193.76 8	1193.726 1193.69 1193.422	1192,495	1192.208	1192.084 1191.96 1191.823	1191.64	1191.602
		TOPBP1	NET-2 KIAA0937	DGS-A	C110RF11		PI AU	TNFSF9	
TOBO <i>LO</i> '86∠∠6860 APPENDIXA	ESTs ESTs ESTs	topoisomerase (DNA) II binding protein	transmembrane 4 superfamily member (fetraspan NET-2) KIAA0937 protein ESTs, Moderately similar to	alternatively spliced product using exon 13A [H.sapiens] ESTs DiGeorge syndrome gene A	ESTS chromosome 11open reading frame 11 ESTS	Homo sapiens cDNA FLJ1217 fis, clone PLACE1008044, highly similar to NUCLEAR PORE COMPLEX PROTEIN NIP107 Homo sapiens mRNA; cDNA DKFZP434C185 (from clone	DKFZp434C185) ESTs plasminogen activator,	tumor necrosis factor (ligand) superfamily, member 9 ESTs, Weakly similar to	predicted using demender [C.elegans]
	Hs.42302 Hs.16920 Hs.191866	Hs.91417	Hs.16529 Hs.62264	Hs.107082 Hs.125059 Hs.106311	ns.128045 Hs.124275 Hs.23560	Hs.236204	Hs.29809 Hs.23139 Hs 77274	Hs.1524	Hs.132875
	N30308 Hs.42302 AA700041 Hs.16920 AA629990 Hs.118649	R97785 Hs.91417	AA055491 Hs.63190 H54681 Hs.28337	R63714 Hs.107082 H62801 Hs.38108 AA629338 Hs.106311	AA626083 HS.126049 R51382 HS.124275 R32442 HS.23560	N30751 Hs.92395	AA857127 Hs.29809 N32820 Hs.23139 AA284668 Hs 77274	AA778663 Hs.1524	AA404278 Hs.16265
ok et al.	258026 N3 435011 AA 884510 AA	200136 R9	377296 AA 203183 H5		39219 R5		1434940 AA 259033 N3 714106 AA	0	758336 AA
Westbrook et al.	GF201 GF203 GF204	GF200	GF202 GF203	GF202 GF201 GF201	GF203 GF203 GF203	GF203	GF204 GF201	GF203	GF201

-1.1631099	-1.176685 1.41286976		1 0562344	1.0502414	1.12291779 1.25427235 1.35432088	-1.579297		1.16004441	-1.0693739
1191.389	1190.82	1190.496 1190.201	1189.957	99.00	1189.07 1188.831 1188.358	1188.21	1186.151	1185.771	1184.882 1184.609 1184.607
PSMC3	CLAPS3 RABIF	MDM2	PTB	COGBP1	SSR3	S100A9	LLGL2	GLI3	
proteasome (prosome, macropain) 26S subunit, ATPase, 3 ESTs	adaptor-related protein complex 3, sigma 1 subunit RAB interacting factor	mouse double minute 2, human homolog of; p53- binding protein ESTs	polypyrimidine tract binding protein (heterogeneous nuclear ribonucleoprotein I) CUG triplet repeat, RNA-	binding protein 1 signal sequence receptor, gamma (translocon-	associated protein gamma) ESTs ESTs	ESTs S100 calcium-binding protein A9 (calgranulin B)	lethal giant larvae (Drosophila) homolog 2 GLI-Kruppel family member GLI3 (Greig	syndrome) ESTs. Moderately similar to	kinesin-73 [D.melanogaster] ESTs ESTs
Hs.250758 Hs.59805	Hs.80917 Hs.90875	Hs.170027 Hs.31050	Hs.172550	Hs.81248	Hs.28707 Hs.110006 Hs.12308	Hs.193251 Hs.112405	Hs.3123	Hs.72916	Hs.55271 Hs.45117 Hs.22978
AA282230 Hs.75526 W99305 Hs.59805	AA460727 Hs.80917 AA012984 Hs.90875	R80235 Hs.89636 H43101 Hs.31050	17	R15111 Hs.81248	N47682 Hs.28707 W72749 Hs.110006 R15820 Hs.12308	AA699557 Hs.118334 AA864554 Hs.112405	T40541 Hs.3123	AA418036 Hs.72916	AA284305 Hs.89370 N49850 Hs.45117 R92412 Hs.22978
712916	796757		m	25588	280985 346119 53005	433468	60565	767495	327221 282475 198190
GF204 GF202	GF200	GF201 GF204	GF201	GF200	GF203 GF202 GF202	GF203 GF204	GF201	GF203	GF201 GF202 GF200

DSBSZZSB.CZCECI

-1.6457359	-1.4118657	1.16742206		-1.3427144	-1.3326304 1.59293149 -2.7568431 -1.2485876	
1184.549	1184.201 1183.816 1183.557 1183.359	1182.889 1182.743 1182.651	1181.101	1180.804 1180.396 1180.302 1180.057	1178.926 1178.926 1178.693 1177.982	1177.944 1177.924 1177.661
ERCC2	YDD19	TSPAN-5 GS3955	NME4	NOL1	DKFZP586G011	MLSN1
excision repair cross- complementing rodent repair deficiency, complementation group 2 (xeroderma pigmentosum D) ESTs, Weakly similar to hypotherical protein H saniens)	Final Property of the Property	tetraspan 5 GS3955 protein ESTs	ESTs, Weakly similar to KIAA0647 protein [H.sapiens] non-metastatic cells 4, protein expressed in Homo sapiens mRNA; CDNA Homo sapiens mRNA; CDNA Homo spiens mRNA; CDNA fron clone	DKFZp761K2024) nucleolar protein 1 (120kD) ESTs	ESTs ESTs DKFZP586G011 protein ESTs	ESTS melastatin 1 ESTs
Hs.99987 Hs.171802	Hs.27931 Hs.25615 Hs.114138 He 116078	Hs.20709 Hs.155418 Hs.184387	Hs.20047 Hs.9235	Hs.21415 Hs.15243 Hs.269860 Hs.155342	Hs.47196 Hs.14831 Hs.234265 Hs.109909	Hs.55262 Hs.43265 Hs.167554
Н54492 Hs.99987 AAAFRON He 18677	A772728 HS.14760 AA130874 HS.11868 AA702728 HS.114138 AA7027291 HS.114078	AA464601 Hs.20709 AA013260 Hs.46698 AA425543 Hs.39358	Hs.20047 Hs.9235	N63445 Hs.21415 N50854 Hs.15243 AA778045 Hs.124018 H11054 Hs.92501		
R54492	N25262 N25262 AA130874 AA702728	AA46460 AA013260 AA425543	H18440 H54417	N63445 N50854 AA77804	N51121 AA453251 W15521 W49629	W02693 N35472 N70116
39722	267495 586854 383958 744011	812967 360155 768961	51093	277996 280970 379659	282015 282015 795344 320157 325029	327082 272148 296345
GF201	GF201 GF203 GF203	GF202 GF201 GF203	GF201	GF203 GF201 GF204	GF203 GF201 GF202 GF203	GF201 GF204 GF204

	-1.295536 -1.0557773		1.24512303				1.22872789			1.0456229	-1.0160019				-1.7110835		1 1000117	-1.10001147	0.5/091026		-1.6920018	1 22573392	1.10930202	1.03222103	1.15358061	1.70781107	
	1177.562 1176.921	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1176.294	1175.893		1175.484	1175.06	1174.835	1174.571	1174.422	1174.174		1173.958		1173.763		000	11/3.508	11/3.665	1173.283	1172.752	1179 733	1172.469	1172.344	1171.677	510:1/11	
	CPD		GAA				HNRPH1		NPHP1				PK1.3				L	UXS1253E		VIPR1							
APPENDIX A	carboxypeptidase D ESTs	glucosidase, alpha; acid (Pompe disease, glycogen	storage disease type II) ESTs	ESTs	ESTs, Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!	[H.sapiens]	neterogeneous nuclear	ESTs	nephronophthisis 1 (juvenile)	ESTs	ESTs	gene from NF2/meningioma	region of 22q12	Homo sapiens culva FLJ11036 fis, clone	PLACE1004289	DNA segment on	chromosome X (unique) 1253	expressed sednence	EST	receptor 1	ESTs	Homo sapiens cDNA	ESTs	ESTs	ESTs	ESTs	
	Hs.5057 Hs.31746	!	Hs.1437 Hs.124944	Hs.12364		Hs.22883	He 945710	Hs.269558	Hs.75474	Hs.114687	Hs.118118		Hs.75361		Hs.16740			Hs.278482	Hs.49235	Hs.198726	Hs.98330	10000 TI	Hs.30724	Hs.114055	Hs.62722	Hs.210568	
	AA418397 Hs.79656 H92533 Hs.31746		AA444009 Hs.1437 R40663 Hs.124944			R44835 Hs.22883	040101 DE 101060	AA702012 Hs.114087	4A400187 Hs.75474	W86826 Hs.114687	475737 Hs.118118		AA700048 Hs.75361		R22632 Hs.16740			91	N66627 Hs.49235	473241 Hs.1139	7	10000	N52530 HS.30634 N62701 HS.30724		#	372661 Hs.29275	
K et al.	767272 AA 221584 H9		756549 AA 28436 R4			33852 R4	440000			_	233174 H7		435024 AA		130243 R2			-	278906 N6	215000 H7		•	26/6/3 NZ 288948 N6	_		156270 R7	
Westbrook et al.	GF203 GF203		GF201 GF203	GF201		GF204	00010	GF203	GF201	GF203	GF202		GF201		GF200	3		GF200	GF202	GF201	GF202	i	GF203	GF200	GF202	GF200	

1.24214812		-1.4297293 1.01065661 1.09221313 -2.776386	1.28510386	-1.7770318 -1.0348272 -1.2004803 1.30861344 -1.586568	2.62177364
1171.137 1170.766 1170.42 1169.155	1169.14 1169.024 1168.764 1168.63	1168.63 1168.268 1167.971 1167.959	1167.856	1167.025 1166.934 1166.733 1166.239 1165.883 1165.828	1165.685
расн	TFAP2A KIAA0571 NCOA4	PDPK1 BIN1 ZWINT	GFPT1 TCTE1L	POED4	SMARCD3 SH3BP5
dachshund (Drosophila) homolog ESTs ESTs ESTS ESTS ESTS (Autrascription factor AP-2 alpha (activating enhancer-AP-Indring	protein 2 alpha) ESTs Grb2-associated binder 2 nuclear receptor coactivator 4	o-phosphonositoe dependent protein kinase-1 bridging integrator 1 ZW10 interactor ESTs	guarmine nococo- phosphate transaminase 1 t-complex-associated-testis- expressed 1-like 6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of handrowine nirchar factor 1	on inspancy en nucean factor in inspancy en nucean factor in programmed cell death 4 ESTs ESTs ESTs ESTs ESTs SWI/SNF related, matrix associated, actin dependent	regulator of chromain, subfarnily d, member 3 SH3-domain binding protein 5 (BTK-associated)
Hs.63931 Hs.185918 Hs.271667 Hs.9887	Hs.18387 Hs.16443 Hs.30687 Hs.99908	Hs.154729 Hs.193163 Hs.42650 Hs.109391	Hs.75307	Hs.3192 Hs.100407 Hs.159225 Hs.38867 Hs.222414 Hs.7168 Hs.117907	Hs.77069 Hs.109150
AA677921 Hs.63831 AA705015 Hs.119862 AA677215 Hs.107832 R58970 Hs.9887	AA481755 Hs.18387 AA464975 Hs.16443 AA865573 Hs.30687 AA133212 Hs.75418	N22904 Hs.42462 AA453175 Hs.6619 AA706968 Hs.42650 N62434 Hs.109391	AA478571 Hs.1674 AA399285 Hs.75307	A4459609 Hs.3192 R26827 Hs.70197 W43000 Hs.58871 N75365 Hs.118175 AA127395 Hs.125085 AA025794 Hs.7168 AA679428 Hs.117907	AA035796 Hs.77069 AA188661 Hs.109150
431003 462665 454150 41132	810781 810097 1470151 490805	266720 788107 451907 292122	753157 726637	809421 132690 323274 298862 564567 365423 432199	360047
GF203 GF204 GF203 GF201	GF201 GF201 GF204 GF201	GF203 GF200 GF203 GF202	GF203	GF203 GF200 GF202 GF203 GF201 GF201	GF200 GF202

1.02632571	1 37298409	1.42243904	-1.1463032	1.84363711	-1.3486778	1.13716219 -1.1753476 1.23882673
1164.736 1164.646 1164.312	1163.922	1163.04	1162.954 1162.688 1162.019 1161.825	1161.576 1161.553	1161.403	1161.332 1161.296 1161.116
CHES1	TNFRSF8	rarz RGS10	BUB1 DKFZP586I1023	TIM17		KIAA0929 KIAA0461 KPNB1
checkpoint suppressor 1 Homo sapiens cDNA FLJ10229 fis, clone HEMBS1001242, highly similar to Homo sapiens topoisomerase-related function protein mRNA ESTs	tumor necrosis factor receptor superfamily, member 8 fibroblast growth factor 2	(basic) regulator of G-protein signalling 10 budding uninhibited by	benzimidazoles 1 (yeast homolog) ESTs ESTs ESTs DKFZP58611023 protein translocase of inner	mitochondrial membrane 17 (yeast) homolog A ESTs Homo saniens mRNA for	KIAA1306 protein, partial cds KIAA0929 protein Msx2 interacting nuclear target	(MINT) homolog KIAA0461 protein karyopherin (importin) beta 1
Hs.25534 Hs.23703	Hs.1314	Hs.56066 Hs.82280	Hs.98658 Hs.190338 Hs.24360 Hs.6557 Hs.111515	Hs.20716 Hs.193833	Hs.181077	Hs.184245 Hs.107088 Hs.180446
H84982 Hs.111597 H05635 Hs.106561 AA165629 Hs.273703	AA147594 Hs.85034	H38539 Hs.56066 AA709036 Hs.82280	AA446462 Hs.98658 AA699369 Hs.117091 N51604 Hs.24360 T63988 Hs.101138 AA421270 Hs.5670	AA708446 Hs.20716 N36994 Hs.53798	AA410469 Hs,22592	H74133 Hs.3340 AA775828 Hs.107088 AA251527 Hs.81690
H84982 H05635 AA16562	AA14759	R38539 AA70903	AA44646 AA69936 N51604 T63988 AA42127	AA708446 N36994	AA41046	H74133 AA775828 AA251527
221846 43329 593431	505538	23073	781047 432557 281580 79782 731031	506032 273652	753764	214906 878496 684634
GF200 GF203 GF203	GF201	GF200 GF203	GF201 GF203 GF203 GF201 GF201	GF203 GF201	GF202	GF200 GF203 GF200

APPENDIX A	ESTs, Highly similar to	homolog of the Aspergillus

	-1.9740137		:	1.0114718	-1.5104173		2.26333528			-1.7213576							-2.0458127		-1.9166608	-1.7433678			-1.098204	1.06402355		-1.1637156		1.32500007	-1.7762666	-2.1088061		
		1160.791			1160.613			1159.795		1159.337		1159.098	1158.601	1158.516				1158.399		1158.327			· ~					•	1156.982	1156 874		
				TP53			EDIL3			PTD010		ARHGAP8					BPHL											ANXA8	HSPBP1	IGSE4	5	
nidulans sudD gene product	H.sapiens]	ESTs	umor protein p53 (Li-	-raumeni syndrome)	ESTs	EGF-like repeats and discoidin	-like domains 3	ESTs	ESTs	PTD010 protein	Rho GTPase activating protein		ESTs	ESTs	biphenylhydrolase-like (serine	hydrolase; breast epithelial	nucin-associated antigen)	ESTs	ESTs	EST	Homo sapiens mRNA; cDNA	OKFZp564B222 (from clone	DKFZp564B222)	ESTs	ESTs	ESTs	ESTs	annexin A8	Hsp70 binding protein	mmunoglobulin supertamily,	elilizei +	2018
Ē	Hs.105168 [H	Hs.42993 Et	_	Hs.1846 Fr	Hs.98708 E	ũ	Hs.129764		Hs.42373 E:	_	œ.	"	Hs.30939 E		Ē	Ξ	Hs.184552 m	Hs.34924 E	_	_	Ι	٥	Hs.100261 D	Hs.98321 E	Hs.193804 E	Hs.103364 E	Hs.16450 E	Hs.87268 a	Hs.53066 H	E 70006-11		HS.23935
	AA481406 Hs.105168	N24786 Hs.42993		339356 Hs.1846	AA431184 Hs.98708		W01171 Hs.50436	N50904 Hs.38282	_	Ξ		AA037410 Hs.103428	H09664 Hs.30939				N46098 Hs.119666	00	398008 Hs.104010				4A447504 Hs.100261	AA456082 Hs.98321	AA011308 Hs.14104	AA479155 Hs.103364	AI002071 Hs.16450	AA252968 Hs.87268	AA401391 Hs.53066	000000 -11 100000	Ω	H52786 Hs.23935
	746347 AA			24415 R3	782152 AA		296793 W0		261571 H9	_		321271 AA	46438 H0				277749 N4						784285 AA				C		743114 AA		'n	41850 R5
	GF203	GF201		GF200	GF202		GF200	GF201	GF201	GF200		GF201	GF201	GF204			GF203	GF204	GF200	GF202	į		GF202	GF203	GF201	GF203	GF204	GF200	GF202	Č	GF202	GF201

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	-1.4909378	1.20552613	1.19986824	-1.0022633			-1.5141322				1.00838857 1.0593029		-1.1386557
1155.645	1155.401	1155.297 1155.276	1154.734	1154.275		1154.173	1153.68	1153.205	1153.019		1153.005 1152.909		1152.817 1152.693 1152.681
TDPX1		EIF4B	KCNH2	SORL1		TGM2		FNTA					GALNT1
thioredoxin-dependent peroxide reductase 1 (thiol- specific antioxidant 1, natural killer-enhancing factor B) Homo sanians clone 2.4850	mRNA sequence eukaryotic translation initiation	factor 4B EST potassium voltage-gated	related), member 2	sortilin-related receptor, L(DLR class) A repeats-containing	transglutaminase 2 (C polypeptide, protein-glutamine-	gamma-glutamyltransferase)	ESTs	famesyltransferase, CAAX	ESTs	ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	[H.sapiens] ESTs	UDP-N-acetyl-alpha-D- galactosamine:polypeptide N- acetylgalactosaminyltransferas	e 1 (GaINAc-T1) EST ESTs
Hs.146354	Hs.13544	Hs.93379 Hs.18377	Hs.188021	Hs.278571		Hs.8265	Hs.11443/ Hs.21965	Hc 138381	Hs.264606		Hs.260287 Hs.28274		Hs.80120 Hs.31964 Hs.42846
AA457115 Hs.89984	R38938 Hs.13544	AA057371 Hs.18113 T98484 Hs.18377	AA427490 Hs.19944	T51689 Hs.79624			N54157 Hs.1082/2 AA398290 Hs.21965	AA11210E De 78630	AA464518 Hs.99616		AA488646 Hs.52510 N99253 Hs.28274		AA029851 Hs.80120 H23232 Hs.31964 N32502 Hs.42846
810446	24850	472163 122126	770012	72391		590692	247462 726767	030002	810205		843251		470187 52092 270889
GF201	GF202	GF203 GF200	GF200	GF200		GF201	GF201 GF203	10010	GF201		GF202	} 5	GF204 GF202 GF201

1.52237309	1.64154079	1.33140325	1.08505928	1.12200286	1.69259916	-1.1597573
1152.569 1152.484 1152.081 1151.318	1151.211	1150.613 1149.895 1148.845	1148.592 1148.537 1148.238	1147.874	1147.449 1147.306	1147.303
RAB4	EIF3S6 SCYB14	SMARCA5 PLA2G5	UBE2H TNRC3	DKFZP586I1023	TAF2A	MMP3
Homo sapiens mRNA for KIAA1197 protein, partial cds ESTS ESTS RAB4, member RAS oncogene family	nitiation (D) s s), ix	regulator or chromatin, subfamily a, member 5 bbs. ESTs phospholipase A2, group V ubiquitin-conjugating enzyme	BC8) ESTs Homo sapiens clone 25059 mRNA sequence	DKFZP58611023 protein ESTs, Moderately similar to pig-c protein [H.sapiens] TATA box binding protein	polymerase II, A, 250kD ESTs	96
Hs.6982 K Hs.184544 E Hs.44979 E Hs.119007 o	Hs.106673 ft	Hs.9456 s Hs.114750 E Hs.290 F	Hs.28505 E Hs.85986 E Hs.7181 r		Hs.1179 Hs.102399	Hs.83326
AA634430 Hs.6982 AA169159 Hs.5316 N39581 Hs.44979 AA478440 Hs.119007	AA669674 Hs.90344 W72294 Hs.103176	AA416971 Hs.129749 AA702689 Hs.114750 R32409 Hs.290	AA520978 Hs.28505 AA233901 Hs.85986 R43595 Hs.22948	<u>></u>	AA677306 Hs.1179 N21015 Hs.102399	794 Hs.83326
743866 AA6344; 609980 AA1691; 277056 N39581 786220 AA4784	856961 AA66	730037 AA41697 448073 AA70268 135692 R32409		19936/ R95691 796665 AA461487 246144 N55492	454440 AA67730 264747 N21015	324492 W51794
GF204 GF202 GF201 GF202	GF202 GF201	GF203 GF204 GF200	GF200 GF203 GF201	GF202 GF202 GF200	GF201 GF203	GF203

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1.16756441	1.04883568	1.26540759	1.84719562	1.84719562	-1.6108449	1.33532741	1.40297048			-1.2603314	1.82859897	1.71153632				1.155575	1.08541429						1.2206816	
1147.098	1146.848 1146.079	1145.615	1145.44	1145.44	1144.599	1144.382	1144.373			1144.33	1143.706	1143.414	1143.408	1143.105		1141.974	1141.858	1141.805		1140.908	1140.535	1140.398	1140.383 1139.96	
GCN2	IMAGE145052	TAF2F	RAB6	RAB6	0GI-96						FBX5			GARS		PCNA						CREBBP		
GCN2 eIF2alpha kinase Homo saniens clone 25023	mRNA sequence small acidic protein TATA box binding protein (TBP)-associated factor, RNA	polymerase II, F, 55kD BAB6, member BAS	oncogene family RAB6, member RAS	oncogene family	ESTS CGI-96 protein	ESTS	ESTs	ESTs, Weakly similar to	DIPEPTIDYL PEPTIDASE IV	LIKE PROTEIN [H.sapiens]	F-box protein Fbx5	ESTs	ESTs	glycyl-tRNA synthetase	proliferating cell nuclear	antigen	ESTs	ESTs	ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!	[H.sapiens]	ESTs Corre bioding protoin	(Rubinstein-Taybi syndrome)	Homo sapiens clone 23551 mRNA sequence FSTs	
Hs.261587	Hs.90858 Hs.78050	Hs.155188	Hs.5636	Hs.5636	Hs.190592 Hs 239937	Hs.44436	Hs.89072			Hs.91625	Hs.111452	Hs.42050	Hs.124070	Hs.75280		Hs.78996	Hs.83313	Hs.187578		Hs.17448	Hs.23728	Hs.23598	Hs.184019 He.196459	13.130455
Hs.42457	Hs.90858 Hs.78050	Hs.77298	Hs.107563	RG.8	4A609661 Hs.111945	Hs.44436	4A282971 Hs.89072			Hs.91625	AA283003 Hs.111452	Hs.42050	Hs.102856	AA629909 Hs.75280		4A450265 Hs.78996	Hs.83313	AA055052 Hs.103481		AA429367 Hs 17448	Hs.23728	Hs.59189	Hs.28109	18.00040
AA419603 Hs.42457	R56893 Hs.90858 AA490390 Hs.78050	AA036649 Hs.77298	H20138	H20138	AA609661	N48788	AA282971			N62508	AA283003	H95239	N80054	AA629909		AA450265	N62122	AA055052		AA429367	R54558	W89077	H23210	741666
752636	41108 823819	365930	172440	172440	1031810	279443	713078			288775	713115	234320	299943	884655		789182	287569	377363		770954	39770	417694	51772	95776
GF202	GF204 GF200	GF200	GF200	GF200	GF204	GF200	GF203			GF203	GF203	GF200	GF201	GF201		GF200	GF203	GF201	; ;	GE201	GF201	GF201	GF201	GFZUZ

Westbrook et al.	k et al.			APPENDIX A		Atty	Atty Docket No. 2172
GF204	1504457	1504457 AA904806 Hs.130100	Hs.131945	KIAA0940 protein sulfotransferase, estrogen-	KIAA0940	1139.778	
GF200	785595	AA449459 Hs.54576	Hs.54576	preferring	STE	1139.77	-1.1757131
GF202 GF200	/95612 563574	AA460005 HS.38375 AA113339 HS.90553	HS.203772	FSHD region gene 1	FRG1	1139.43	1.17454956
				Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3'			
				part of a gene for a novel KIAA0279 LIKE EGF-like			
				domain containing protein (similar to mouse Celsr1, rat			
				MEGF2), a novel gene for a protein similar to C. elegans			
GF203	785897	AA449474 Hs.122552 AA489782 Hs.105296	Hs.122552 Hs.105296	B0035.16 a EST		1139.252 1138.83	1.20782897 1.22135834
				interferon gamma receptor 2 (interferon gamma transducer			
GF200	785575	AA448929 Hs.7478	Hs.177559	, ,	IFNGR2	1138.493	1.39614192
GF200	135673	B31591 Hs.24219	Hs.226031	ESTs, Highly similar to KIAA0535 protein [H.sapiens]		1138.196	-1.1173779
5				ARP3 (actin-related protein 3,			
GF201	271568		Hs.5321	yeast) homolog	ACTR3	1138.19	
GF201	416390	_	Hs.58927	nuclear VCP-like	NVL	1137.697	1000010
GF203	196435	R91517 Hs.34455	Hs.34455	ESTS Homo conjene clone 93097		113/.1/	1.31963337
GF202	44156	H06157 Hs.12473	Hs.12473	mRNA sequence		1136.706	-1.6084652
GF200	489079	AA057156 Hs.75596	Hs.75596	interleukin 2 receptor, beta FSTs. Weakly similar to !!!!	IL2RB	1136.519	1.06808217
				ALU SUBFAMILY J WARNING ENTRY !!!!			
GF201 GF203	429685 785585	AA011598 Hs.36409 AA44944 Hs.98969	Hs.36409 Hs.98969	[H.sapiens] ESTs		1135.797 1135.34	-2.0631124

A 71011	LENDIA A	
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-1.6010816	1.006444	-1.3655738 1.22045769	-1.825487	1.10293741 -2.1226437	1.18137811	
1134.85 1134.376 1134.245	1134.202 1133.739 1133.647	1133.243 1133.24	1132.935 1132.85 1132.49	1132.334	1131.751	
KLRB1	ARHE	MLLT4	ADAM10 DCTD	PRPSAP1		
KAT03874 eceptor	ILJ.1037 fis, clone NT2RM2001221, weakly similar to KALIRIN ESTs ras homolog gene family, member E myeloid/ymphol or mixed- myeloid/ymphol or mixed- innanch entkemia frithorax	(Drosophia) homolog); (Translocated to, 4 ESTs	metalloprotease domain 10 dCMP deaminase ESTs phosphoribosyl pyrophosphate	synthelase-associated protein 1 ESTs ESTs, Moderately similar to !!!! ALU SUBFAMILY SP ANARNING FATTRY !!!	H.sapiens) Homo sapiens cDNA Homo sapiens cDNA 172 170505 fis, clone NT2 PP2000510 ESTs, Moderately similar to N- copine [H.sapiens]	
Hs.46624 Hs.268881 Hs.169824	Hs.22451 Hs.268573 Hs.6838	Hs.100469 Hs.268695	Hs.172028 Hs.76894 Hs.116034	Hs.77498 Hs.112748	Hs.34579 Hs.16677 Hs.7130	
N49967 Hs.46624 R98492 Hs.35956 AA976691 Hs.94962	Hs.22451 Hs.125123 Hs.114554	AA453304 Hs.9874 R36095 Hs.124254	AA043347 Hs.62629 AA448207 Hs.76894 AA628257 Hs.116034	R44822 Hs.77498 AA609684 Hs.112748	Al024769 Hs.34579 AA134743 Hs.16677 H29500 Hs.7130	
N49967 R98492 AA976691	R34205 T97312 W86282	AA453304 R36095	AA043347 AA448207 AA628257	R44822 AA609684		
282737 201173 1585517	136449 121804 415851	788155 136830	487773 784777 1055861	33949 1031838	1631466 502530 52730	
GF201 GF200 GF204	GF200 GF204 GF201	GF203 GF203	GF201 GF200 GF204	GF200 GF202	GF204 GF203 GF201	

1.01114711 -1.764024 -1.059891	-1.1723664	-1.0997151 1.31123657	-1.0883186	-1.5096475 1.11735241 -1.310569 -2.8064723	1.12028058	1.33425776
1131.055 1130.604 1130.013 1129.436	1128,417 1128,615 1128,375	1128.149 1127.896	1127.653 1127.634 1127.487 1127.211	1126.821 1126.768 1126.344 1126.281 1126.066	1125.78	1125.317 1125.27
AF1Q KIAA0909 CL683 MEOX1	нмвү	RTN3	YDD19	HAX1 HNRPR	PSG5 MN1	DGCR6
ALL1-fused gene from chromosome 1 KIAA0909 protein hypothetical protein mesenchyme homeo box 1 high-mobility group fromkitenne chromosomal)	protein isoforms I and Y ESTs ESTs. Weakly similar to CAMP-DEPENDENT PROTEIN KINASE INHIPITOR MIJSCI-EBRAIN	FORM [H.sapiens] reticulon 3 Homo sapiens clone 23556	mRNA sequence ESTs ESTs YDD19 protein ESTs, Weakly similar to 5'-TG	H. sapiens HS1 binding protein heterogeneous nuclear ribonucleoprotein R FSTs	pregnancy specific beta-1-glycoprotein 5 meningioma (disrupted in balanced translocation) 1 DiGentre syndrome critical	region 6 ESTs
Hs.75823 Hs.107362 Hs.43728 Hs.438	Hs.139800 Hs.16773 Hs.30343	Hs.106106 Hs.252831	Hs.106300 Hs.12420 Hs.79191 Hs.25615	Hs.112148 Hs.15318 Hs.15265 Hs.8832 Hs.72069	Hs.268515	Hs.153910 Hs.37751
AA456008 Hs.75823 N51651 Hs.6798 AA418750 Hs.43728 AA426311 Hs.438	AA448261 Hs.64605 W37782 Hs.109020 R63085 Hs.107596	H04769 Hs.106106 AA430035 Hs.95363	R43869 Hs.106300 R94659 Hs.27786 H08734 Hs.83490 AA044296 Hs.25282	AA460136 Hs.119382 R76263 Hs.15318 AA779191 Hs.122584 AA453619 Hs.8832	W51985 Hs.118289 R59212 Hs.79085	AA033564 Hs.77118 AA436174 Hs.37751
812105 280527 768007 769028	782811 322194 137984	152289 781097	33500 198451 45318 486340	795864 144777 453790 795439		471266 754379
GF200 GF201 GF202 GF200	GF200 GF203 GF201	GF203 GF200	GF201 GF200 GF201 GF204	GF202 GF200 GF203 GF201	GF201	GF200 GF202

1.16726997	1.14186722 1.17103121 -1.8275724 -1.6857314	1.59982438 -1.2587897	-1.2807051	-1.7154858 1.23238656 -1.4030622	1.02980478	-1.7728406 -1.7728406 1.49320102
1124.713 1124.647 1124.544	1124.455 1124.219 1123.921 1123.321 1122.7	1122.292	1120.881	1120.104 1119.842 1119.837	1119.733	1119.518
DKFZP727C091	SPP1		KIAA0606	BCAR1	DSCR2	New York
ESTs ESTs DKFZP727C091 protein secreted phosphoprotein 1 (osteopornin: none sileoprotein learly T-lymphoxyle activation	1) ESTS ESTS ESTS ESTS ESTS ESTS	Homo sapiens mRNA for KIAA1219 protein, partial cds ESTs KIAA0606 protein; SCN Circadian Oscillatory Protein	(SCOP) Homo sapiens cDNA FLJ20216 fis, clone COLF3242	ESTS ESTS breast cancer anti-estrogen resistance 1 ESTS ESTS	Down syndrome critical region gene 2 cofactor required for Sp1 transcriptional activation,	subunit z (190kb.) STS ESTs, Weakly similar to predicted using Genefinder [C.elegans]
Hs.89303 Hs.142722 Hs.43141	Hs.313 Hs.120790 Hs.268699 Hs.20996 Hs.107561 Hs.122925	Hs.25431 Hs.114052	Hs.38176 Hs.20082	Hs.22467 Hs.273219 Hs.106289 Hs.193540	Hs.5198	Hs.239500
AA284031 Hs.89303 H63959 Hs.18870 AA447476 Hs.43141	AA775616 Hs.313 AA707013 Hs.120790 R45579 Hs.12408 R49102 Hs.20996 H45289 Hs.107561 Alou3706 Hs.122925	AA024902 Hs.102223 AA701297 Hs.114052	W86822 Hs.38176 AA702978 Hs.20082	AA478474 IS.24181 H29265 Hs.32467 AA626335 Hs.4894 H16709 Hs.106289 AA121518 Hs.70834	AA488445 Hs.5198	AA282594 Hs.87508 AA504120 Hs.99743 AA398922 Hs.110759
700646 209199 784272	378461 451363 35265 38588 176554 392111	3 6 5231 435651	416434	786612 49839 745604 49382 489931	843224	727164
GF203 GF201 GF202	GF203 GF203 GF202 GF204 GF204	GF202 GF203	GF203 GF204	GF201 GF201 GF203 GF202 GF202	GF202	GF203 GF203 GF203

EST, Weakly similar to

-1.6701431		-1.5424077 -2.5665371	1.0953264		1.38780043 -1.6072254	-1.2254305	-1.0650274	1.8978635	1.15897731
1111,757 1111,432 1111,143	1111.119 1110.641 1110.555	1109.941 1109.23	1109.124 1108.866	1108.206	1107.69	1107.614 1107.483	1107.205 1106.946 1106.872	1106.24 1106.24	1106.136
	NUDT1	CDK10	HPX42B PON1		NAIP	MKNK1 KIAA1035		KIAA1289	MSL3L1
connector enhancer of KSR- like protein CNK1 [H.sapiens] ESTs ESTs	nudix (nucleoside diphosphate linked moiety X)-type motif 1 ESTs ESTs	cyclin-dependent kinase (CDC2-like) 10 ESTs haemopoietic progenitor	homeobox paraoxonase 1 ESTs, Weakly similar to IIII ALU CLASS C WARNING	ENTRY !!!! [H.sapiens] neuronal apoptosis inhibitory	protein ESTs MAP kinase-interacting	serine/fhreonine kinase 1 KIAA1035 protein Homo sapiens mRNA; cDNA DKFZp434D2426 (from clone	DKFZp434D2426); partial cds EST ESTs	KIAA1289 protein ESTs male-specific lethal-3	(Drosophila)-like 1
Hs.121920 Hs.173202 Hs.124087 Hs.88121	Hs.388 Hs.269736 Hs.268843	Hs.77313 Hs.173134	Hs.125231 Hs.1898	Hs.271756	Hs.79019 Hs.165364	Hs.5591 Hs.21542	Hs.20000 Hs.238914 Hs.112196	Hs.207577 Hs.103280	Hs.88764
AA777429 Hs.121920 N62379 Hs.33215 AA609640 Hs.124087 AA256163 Hs.88121	AA443998 Hs.388 AA663920 Hs.128629 R92011 Hs.34547	AA789328 Hs.77313 H09241 Hs.101211	AA872096 Hs.125231 R09781 Hs.1898		H21071 Hs.79019 AA479969 Hs.105624	AA431885 Hs.5591 R37357 Hs.21350	AA703117 Hs.20000 AA884717 Hs.125671 AA420967 Hs.112196	AA677406 Hs.42913 AA004648 Hs.103280	AA418900 Hs.88764
449371 290567 1031790 681879	756502 855683 195274	1391682 46195	1476309 128143	292697	51463 753979	773637 28270	434828 1467244 731231	454914 428737	768050
GF204 GF203 GF204 GF203	GF201 GF204 GF201	GF203 GF202	GF204 GF200	GF201	GF200 GF203	GF201 GF203	GF203 GF204 GF202	GF203 GF201	GF203

-2.2583264	1.03990164	-1 4919691		1.2907796							-1.4477048		-1.4726357		1.15029365	1.15029365	1.05244693		1.5458576		1.09146371	-2.4468405	-2.417521	1.17156255	-1.1362785		-1.3561002		000000000	1.3/694663	
1105.934	1105.783	1105 567		1105.045			1104.816	1104.774			1104.699		1104.689	1104.268	1104.053	1104.053	1103.645		1103.577		1103.555	1103.509	1103.323	1102.442	1102.226	1102.182	1102.177		1101.711	1101.636	
PMSCL1	DDR1			SRP72									HUNK		FKBP5	FKBP5			ME3		KCNQ2								ASM3A	KPNB2	
		proline-rich protein MP4	intrillasculus) signal recognition particle	-	Homo sapiens cDNA	=LJ10931 fis, clone	OVARC1000564	(0	Homo sapiens cDNA	FLJ10029 fis, clone	HEMBA1000817	normonally upregulated neu	umor-associated kinase HL		FK506-binding protein 5 FK			malic enzyme 3, NADP(+)-	dependent, mitochondrial MI	potassium voltage-gated channel, KQT-like subfamily,	member 2 KC	ø	s	Ø	· so	ø	s	acid sphingomyelinase-like		karyopherin (importin) beta 2 KF	
polyr Hs.91728 auto:	disoc Hs.75562 famil		ns.zadao mining	Hs.237825 72kD	Hom	FLT.	Hs.13794 OVA	Hs.24286 ESTs	Hom	E.	Hs.173259 HEM	horn	Hs.109437 tumo	Hs.187934 ESTs	Hs.7557 FK5(32	_	Hs.2838 depe		Hs.4975 men	Hs.127831 ESTs					Hs.21711 ESTs	acid	_	Hs.168075 kary	
AA459213 Hs.74285	AA487526 Hs.75562	-	AA463215 HS.29896	W32523 Hs.110852			AA625856 Hs.13794	AA779356 Hs.24286			AA678306 Hs.101366		N66354 Hs.109437		W86653 Hs.41737				AA779401 Hs.2838		451461 Hs.4975		22	A 205389 Hs 41145	A460463 Hs.13872	4A447542 Hs.99113	316146 Hs.21711		AA676836 Hs.42945	AA481067 Hs.82925	
814270 Av	841384 Av		/96921 A	321510 W			745423 A.	454953 A.			430927 A.		285367 N					•	896921 A		179534 H	_	. ~	. ~	. ~	. ~	_		460106 A	814696 A	
GF200	GF200		GF 202	GF202			GF204	GF204			GF203		GF202	GF204	GF200	GF200	GE203	3	GF203	}	GE200	GE202	GF202	GF203	GF203	GF201	GF203		GF201	GF200	

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-1.0462292	-1.0462292		1.02551362	-1.260946	1.006453	-1.3763646			1.00461525	-1.236242	1.20162402	1.17170958		-1.40556		1.12014953	-1.8702653		1.56162902		-1.633197	2.05132296	1.65966206	-1.0679711		-1.1597328				1.58476207
1101.359	1101.359		1100.432	1100.356	1099.923	1099.75		1099.739	1099.651	1098.85	1098.419	1097.775	1096.636	1096.484		1096.317	1095.578		1094.55	1094.353	1094.244	1094.129	1094.024	1093.562		1093.182	1093.018			1092.973
TRIP6	TRIP6		GNS						GATA4	BGN	KIAA0560	KIAA0905							SF3B3			STHM	BM-005			МУНЭ				
thyroid hormone receptor interactor 6	thyroid hormone receptor interactor 6	glucosamine (N-acetyl)-6- sulfatase (Sanfilippo disease	IIID)	ESTs	ESTs	ESTs	Homo sapiens cDNA Fl.120167 fis. clone	COL09512	GATA-binding protein 4	biglycan	KIAA0560 gene product	yeast Sec31p homolog	ESTs	ESTs	Homo sapiens mRNA for	KIAA1192 protein, partial cds	ESTs	splicing factor 3b, subunit 3,	130kD	ESTs	ESTs	sialyltransferase	hypothetical protein	ESTs	myosin, heavy polypeptide 9,	non-muscle	EST	ESTs, Moderately similar to !!!!	WARNING ENTRY !!!!	[H.sapiens]
Hs.119498	Hs.119498		Hs.164036	Hs.50139	Hs.214428	Hs.63131		Hs.10248	Hs.243987	Hs.821	Hs.129952	Hs.70266	Hs.182258	Hs.112968		Hs.7579	Hs.58350		Hs.195614	Hs.47343	Hs.98226	Hs.107573	Hs.173001	Hs.268135		Hs.146550	Hs.121931			Hs.202989
AA485677 Hs.78614	AA485677 Hs.119498		N32895 Hs.37432	N67268 Hs.50139	R19399 Hs.20858	N53352 Hs.47627		N52971 Hs.47590	Ξ.	R77226 Hs.114529		AA488663 Hs.70266	W86162 Hs.38947	AA621310 Hs.112968		AA775865 Hs.7579	AA199881 Hs.58350		R52789 Hs.75300	W93592 Hs.47343	AA417356 Hs.98226	AA454682 Hs.107573	AA159179 Hs.50854	H20670 Hs.31766		T69926 Hs.44782	AA777875 Hs.121931			R70361 Hs.52580
0 811108	0 811108		3 259859	2 286381				1 283741		_	٠,	2 843265		2 744627		3 878550	3 645259		0 41541	1 357278	2 731193	~	2 592928			0 81129	449403			155201
GF200	GF200		GF203	GF202	GF200	GF202		GF201	GF200	GF200	GF202	GF202	GF204	GF202		GF203	GF203		GF200	GF201	GF202	GF202	GF202	GF203		GF200	GF204			GF200

1.04214043 -1.1012381 1.03145745	-1.1121016	-1.199121 1.21299574 1.40556258	2.55008484	-2.231079 1.28055028 1.28055028		1.28091721
1092.875 1092.736 1092.709 1092.667	1092.482 1092.44 1092.254	1092.158 1091.968 1091.903 1091.779	1091.777 1091.464 1091.446	1091.313 1090.792 1090.792	1090.648	1090.064 1089.763 1089.41
PCI KIAA0784	_	HSPC210 ZNF6	USP8	KNS2 KNS2	AKR7A2	KIAA0273
protein C inhibitor (plasminogen activator inhibitor III) KIAA0784 protein EST	ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) ESTs EST	hypothetical protein zinc finger protein 6 (CMPX1) EST ESTs	ubiquitin specific protease 8 ESTs Homo sapiens unknown mRNA	ESTs, Highly similar to nicolinic acetylcholine receptor alpha-7 chain precursor, neurona [H.saplens] kinesin 2 (60-70kD) kinesin 2 (60-70kD)	ESTs, Highly similar to QA79 membrane protein [H.sapiens] aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase)	KIAA0273 gene product ESTs ESTs
Hs.76353 Hs.3657 Hs.46850 Hs.184993	Hs.77578 Hs.125470 Hs.105012	Hs.4104 Hs.75839 Hs.47288 Hs.36152	Hs.152818 Hs.12594 Hs.7540	Hs.167418 Hs.117977 Hs.117977	Hs.8890 Hs.6980	Hs.75899 Hs.190332 Hs.188634
R10382 Hs.113201 AA495802 Hs.3657 N48294 Hs.46850 AA131530 Hs.25893	AA426237 Hs.77578 AA883523 Hs.125470 AA478476 Hs.105012	AA233790 Hs.4104 AA669341 Hs.75839 NS1536 Hs.47288 R89595 Hs.36152	AA399952 Hs.42329 T72596 Hs.12594 N52205 Hs.7540	N71634 Hs.2540 AA410207 Hs.114587 AA410207 Hs.80494	AA400508 Hs.8890 T62865 Hs.6980	AA405628 Hs.75899 AA677024 Hs.131782 AA677924 Hs.114733
129032 768377 279592 503725	760231 1467409 786616	666254 884822 281508 201348	743154 22154 284306	295116 754436 754436	743331	772481 454545 431009
GF203 GF203 GF202 GF201	GF200 GF204 GF203	GF203 GF202 GF202 GF204	GF201 GF201 GF203	GF203 GF200 GF200	GF201 GF201	GF200 GF204 GF203

APPENDIX A Homo sapiens mRNA for

1.28674054	-1.0397812	2.04792938 1.20325102 1.08215808 -1.0628759	-1.2147857	-1.5954932 1.36499053	1.40815835	1.04600556	1.13487511 1.07552492 -1.4189068	-1.330606	1.10718915
1087.926 1087.684 1087.58	1087.525 1087.515	1086.284 1086.236 1086.059 1085.739 1085.329	1085.128 1084.926	1084.899 1084.69	1084.149	1084.147 1083.958	1083.384 1083.334	1082.939	1082.829
KIAA0353		РТРВА	DKFZP586J0917	YDD19	MAT2A		KIAA0332	KATNA1	
Horno sapieris miniva ior HELG protein KIAA0353 protein ESTs Waaklv similar to	d.79C4.1.2 [H.sapiens] ESTs protein tyrosine phosphatase,	polypeptide PSTs ESTs ESTs ESTs	DKFZP586J0917 protein ESTs Homo sapiens cDNA FLJ10659 fis, clone	NT2RP2006071 YDD19 protein methionine	adenosyltransferase II, alpha ESTs, Weakly similar to similar to S. cerevisiae longevity-assurance protein 1	[C.elegans] ESTs	ESTs KIAA0332 protein ESTs katanin p60 (ATPase-	containing) subunit A 1 ESTs, Weakly similar to R12C12.6 [C.elegans]	ESTs
Hs.5814 Hs.10587 Hs.27524	Hs.28937 Hs.268797	Hs.26045 Hs.103173 Hs.270106 Hs.102248 Hs.15574	O.	Hs.107882 Hs.25615	Hs.77502	Hs.118338 Hs.134901	Hs.13854 Hs.7976 Hs.23651	Hs.180859 Hs.121619	Hs.44933 Hs.23392
AA864226 Hs.5814 AA877815 Hs.10587 H24347 Hs.27524	R69179 Hs.28937 R85261 Hs.32912	H82419 Hs.26045 N72834 Hs.103173 AA676537 Hs.131487 AA489681 Hs.102248 197475 Hs.15574		H23532 Hs.5580 AA495812 Hs.105364	T59286 Hs.77502	R45550 Hs.23882 W67134 Hs.6811	AA521311 Hs.88061 AA460510 Hs.7976 AA130351 Hs.23651	2 = 2	v390/4 Hs.44933 v24046 Hs.43507
1470365 AA8 1161564 AA8 52066 H24	141589 R69 180314 R85	240099 H82 344802 W7: 433053 AA6 824358 AA4		52013 H23 768400 AA	79502 T59	35147 R45 343073 W6	827204 AA6 795805 AA4 587398 AA		276484 N38 269303 N24
GF203 GF203 GF201	GF200 GF203	GF200 GF202 GF204 GF203	GF200	GF202 GF203	GF200	GF203 GF201	GF203 GF200 GF202	GF202 GF204	GF202 GF202

DDBG//98.D/DEDI

-1.872741	1,49239632 2.04617284 1.08243949 1.82915897 -1.0346597	1.0924836	-1.5948125 -1.0072262 1.56930543	-1.1656052	2.18041109
1082.576 1081.519	1081.121 1081.086 1080.0359 1080.002 1079.738 1079.505	1079.019 1078.871 1078.567	1077.799 1077.774 1077.465 1077.37	1077.129 1076.775 1076.761	1076.743
	J.	10		_ 8	7
RPS14	RPL23L	SLC6A10	PDK2	GAS41 PKM2 VPS45B	IGFBP7
Homo sapiens cDNA FLJ11088 fis, clone PLGET00287, waakly similar to INNER CENTROMERE PROTEIN Inspormal grotein S14 EST, Hidhy Similar to	unknown [H.sapiens] ESTs ESTs ribosomal protein L23-like ESTs ESTs ESTS	Homo sapiens mRNA for KIAA121 protein, partial cds solute carrier family 6 (neurotransmitter transporter, creatine), member 10 ESTS ESTS	ESTs EST pyruvate dehydrogenase kinase, isoenzyme 2 ESTs	glioma-amplified sequence-41 GAS41 pyruvate kinase, muscle vacuolar protein sorting 45B (yeast homolog)	Homo sapiens mRNA; cDNA DKFZp434B1620 (from clone DKFZp434B1620) insulin-like growth factor binding protein 7
Hs.49282 Hs.3491	Hs.229745 Hs.44526 Hs.206974 Hs.3254 Hs.98153 Hs.25248	Hs.205293 Hs.275732 Hs.187247 Hs.23804	Hs.118820 Hs.45027 Hs.92261 Hs.18128	Hs.4029 Hs.198281 Hs.6650	Hs.43112 Hs.119206
AA621335 Hs.112975 H73727 Hs.117871	AA780270 Hs.122153 V33620 Hs.44526 AA700553 Hs.113159 AA453015 Hs.3254 AA487051 Hs.2848 AA412495 Hs.98153 NRA738 Hs.95248	N35889 Hs.42919 AA707453 Hs.120012 AA437124 Hs.98932 AA453997 Hs.23804	AA426066 Hs.118820 N39577 Hs.45027 H29474 Hs.92261 AA707125 Hs.18128	T62072 Hs.4029 AA446865 Hs.14018 AA885433 Hs.57738	AA024449 Hs.43112 T53298 Hs.119206
	AA780270 N33620 AA700553 AA453015 AA487054 AA412495 N89738	N35889 N35889 AA707453 AA437124 AA453997	AA426066 N39577 H29474 AA707125	T62072 AA446865 AA885433	AA024449 T53298
1048795 214565	1035588 243524 432668 788334 841176 730507	272531 272531 1291956 757365 795262	757236 277039 49860 452068	85670 784214 1466844	365245
GF202 GF200	GF204 GF200 GF200 GF200 GF202 GF202	GF201 GF204 GF202 GF202	GF204 GF202 GF200 GF203	GF201 GF202 GF203	GF201 GF202

Atty Docket No. 2172	1.38090219	1.64328989	-2.0452686	-2.6311049	-1.0106173	-1.6559244	1.08518226	
Atty	1076.129 1075.699 1075.451 1074.623	1074.615 1074.576 1074.571 1074.214 1073.839	1073.559 1073.416 1073.387	10/3.019 1072.977	1072.041 1071.98 1071.753	1071.301	1070.847	1070.496
South Name about their man half Name having	G.	RS1	YDD19 KIAA0427		GPR69A	STK17A	PSMA4	7
APPENDIX A	ESTs SYT interacting protein ESTs ESTs ESTs Hono sapiens mRNA; cDNA DK72265412163 (from clone	DKFZp64N2163) insulin receptor substrate 1 ESTs ESTs ESTS ESTS ESTS EGTs, Weakly similar to RNA POLYMERASE II	ELONGATION FACTOR ELLZ [H.saplens] YDD19 protein KIAA0427 gene product ESTs	ESTs ESTs	G protein-coupled receptor 69A ESTs ESTs	sentrevirreorinte Mirase 17a (apoptosis-inducing) Homo sapiens mRNA for KIAA1341 protein, partial cds	ESTs proteasome (prosome, macropain) subunit, alpha type, 4	Homo sapiens cDNA FLJ20450 fis, clone KAT05607
	Hs.44949 Hs.11170 Hs.83071 Hs.38200	Hs.117920 Hs.96063 Hs.99367 Hs.60451 Hs.112198	Hs.108815 Hs.25615 Hs.64096 Hs.20468	Hs.18920 Hs.99253	Hs.13351 Hs.228052 Hs.107410	Hs.9075 Hs.44268	Hs.98780 Hs.251531	Hs.14220
	AA460420 Hs.44949 AA417283 Hs.11170 R45335 Hs.33071 AA463993 Hs.38200	H24313 Hs.117920 AA460841 Hs.96063 AA454562 Hs.99367 AA011281 Hs.60451 AA481057 Hs.112198	AA464143 Hs.12866 H51122 Hs.26913 U55962 Hs.64096 AA025930 Hs.20468	AA002064 Hs.18920 AA451859 Hs.99253	R59621 Hs.13351 W86464 Hs.58836 AA282263 Hs.107410	AA453754 Hs.9075 H96671 Hs.42222	AA432061 Hs.98780 AA206497 Hs.96282	AA443105 Hs.14220
retal.	796478 731136 34142 810689	51947 796284 809503 359837 814675	810328 179631 41430 365642	428045 786298	42123 416614 713044	813689	784122	809467
Westbrook et al.	GF203 GF202 GF204 GF201	GF204 GF201 GF202 GF202 GF204	GF201 GF203 GF201 GF201	GF204 GF203	GF202 GF202 GF204	GF202 GF200	GF202 GF204	GF201

1.35095285		1.10731742	-1.3842699	-1.9202397	-1.1945313	-1.1274867	-1.3342989	-2.0244578	1.60873555	1.39928888	-1.0750517	1.34033849	-1.1182676
1070.083		1069.755	1069.324	1069.084	1068.594	1068,429	1068.35 1068.14	1067.553	1067.464 1067.017 1066.601	1066.527	1066.498 1066.129	1066.111	1065.034 1065.02
UBE2V2		PPFIA3	ILT7		MBD2	DKFZP564M182		DKFZP434F162	SOI	L13RA1			NF2 PRKCZ
ubiquitin-conjugating enzyme E2 variant 2	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein	(liprin), alpha 3 immunoalobulin-like transcript	EST, Moderately similar to Pro-	Forecont assignment [M.musculus]	protein 2	DKFZP564M182 protein ESTs. Weakly similar to	CORNIFIN A [H.sapiens]	DKFZP434F162 protein iduronate 2-sulfatase (Hunter	syndrome) ESTs ESTs	interleukin 13 receptor, alpha 1 IL13RA1 Human insulin-like growth factor binding protein 5	(IGFBP5) mRNA ESTS Homo sapiens cDNA	COLF6543	acoustic neuroma) protein kinase C, zeta
Hs.79300		Hs.109299	Hs.48647	Hs.106634	Hs.25674	Hs.20760	Hs.58348 Hs 22646	Hs.7987	Hs.172458 Hs.12381 Hs.269711	Hs.250911	Hs.103391 Hs.43691	Hs.57672	Hs.902 Hs.78793
AA448676 Hs.79300		Hs.109299	Hs.48647	Hs.106634	4A428341 Hs.25674	Hs.94903	Hs.58348 Hs 22646	Hs.7987	N20482 Hs.93410 AA454552 Hs.12381 N33012 Hs.126676	AA781508 Hs.23191	Hs.103391 Hs.43691	AA283603 Hs.104046) Hs.902 Hs.106094
AA448676		W72861	N62837	R44519	AA428341	W673608 H73608	W94063	H11661	N20482 AA454552 N33012	AA781508	H08560 N35259	AA283603	AA428960 Hs.902 R24258 Hs.1060
786083		344942	289610	33350	769673	235055	357544	48286	264166 809504 272879	855177	45542 271935	713214	769716 131239
GF200		GF202	GF202	GF202	GF203	GF200	GF201	GF202	GF201 GF201 GF203	GF203	GF200 GF201	GF203	GF201 GF200

1.21952835	1.03241239 1.40789905 -1.0048179	-1.5957696		-1.6629473	-1.0816446		-1.02518
1064.966	1064.735 1064.26 1064.248 1064.029 1063.773	1063.036	1063.033	1063.006	1062.838 1062.701 1062.219	1061.876	1061.419 1061.36 1061.231
NDUFA7	KIT KIAA0890		PITPNM	STGGALNACIV	BSMAP		НОХ11
NADH dehydrogenase (ubiquinne) 1 alpha subcomplex, 7 (14.5kD, B14.5a) v-kit Hardy-Zuokerman 4 feline sarrosma viral oncogene	homolog ESTs ESTs KIAA0890 protein ESTs	EST ESTs, Weakly similar to ZC155.4 [C.elegans]	phosphatidylinositol transfer protein, membrane-associated PITPNM NeuAc-alpha-2,3-Gal-beta-1,3-Gal-Ac-alpha-2, 6-Gal-Mo-alpha-2, 6-Gal-Mo-	statytiransterase alphaz,o- sialytiransferase brain-specific membrane-	anchored protein ESTs ESTs EST, Highly similar to CYCLIC- AMP-DEPENDENT TRANSCRIPTION FACTOR	ATF-4 [H.sapiens] EST Human D9 splice variant B	mRNA, complete cds homeo box 11 (T-cell lymphoma 3-associated breakpoint) ESTs
Hs.19561	Hs.81665 Hs.269315 Hs.189014 Hs.6141 Hs.235883	Hs.125417 Hs.107755	Hs.93837	Hs.3972	Hs.5012 Hs.108795 Hs.104741	Hs.228728 Hs.122136	Hs.37616 Hs.89583 Hs.117955
AA022627 Hs.19561	N20798 Hs.81665 AA279070 Hs.87668 AA700452 Hs.120027 AA630000 Hs.6141 W45453 Hs.110079	AA879404 Hs.125417 AA460363 Hs.107755	N40945 Hs.93837	AA449321 Hs.32411	H46527 Hs.5012 H97215 Hs.108795 AA476576 Hs.104994	AA777917 Hs.121988 AA780027 Hs.122136	AA453832 Hs.37616 AA007444 Hs.89583 AA858394 Hs.117955
364469	265060 703960 460628 884513 328889	1505650	277186	785694	178098 260757 785368	449329 462003	813675 429368 1475195
GF200	GF200 GF204 GF204 GF203 GF203	GF204 GF202	GF201	GF202	GF204 GF201 GF203	GF204 GF204	GF200 GF201 GF204

Att. Deplement	Atty Docket No. 217	1061.18	1060.977	1060.635 -1.5467291	060.592	060.416		1059.881 -1.5407672		1059 043	1058.974 1.2950787		1058.95		1.38911735	058.586	1058.387	1058.233				1058.138 1.32749204							1056.961 1.07638194	1056.672	1056.567 -1.8254903	1056.556	
		1061	1060	1060	106(1060	106(1058		1056	1058		105	1058	105	105	105	105				105						50.	105	105	105	105	
					T1A-2	CD14		YDD19					DCAMKL1		KIAA0801														BGN			SPIN	
	APPENDIX A	ESTs	ESTs Homo sapiens cDNA FLJ20363 fis, clone	HEP17001 lung type-I cell membrane-	associated glycoprotein	CD14 antigen	ESTs	YDD19 protein	ESTs, Moderately similar to	DECTEIN [H capions]	FROI EIN [III:3apiei13]	doublecortin and CaM kinase-	like 1	ESTs	KIAA0801 gene product	EST	ESTs	ESTS	ESTs, Weakly similar to ORF2	contains a reverse	transcriptase domain	[H.sapiens]	Homo sapiens cDNA	FLJ11011 fis, clone	PLACE1003174, moderately	similar to UBIQUITIN-	CONJUGATING ENZYME EZ-	18 KD (EC 6.3.2.19)	biglycan	EBCC5 protein [H.sapiens]	EST	spindlin	
		Hs.31864	Hs.269426	Hs.15839	Hs.135150	Hs.75627	Hs.122244	Hs.25615		110 4 00750	Hs. 190736	13:10:45	Hs.21355	Hs.98757	Hs.17585	Hs.116865	Hs.42522	Hs.125510				Hs.25276						Hs.21275	Hs.821	He 14671	Hs.42371	Hs.271871	
		Hs.31864	Hs.38542	Hs.121584	AA149827 Hs.26666	AA701476 Hs.75627	AA781491 Hs.122244	AA677300 Hs.64906		110 404707	AA400165 HS.104/0/	13.32740	Hs.21355	4A431778 Hs.98757	Hs.17585	AA635183 Hs.116865	Hs.42522	4A883822 Hs.125510				Hs.25276						AA620611 Hs.5375	Hs.821	4 4703057 Hs 14671	Hs 42371	4A428181 Hs.98543	
		H51425	H66708	H03955	AA149827	AA701476	AA781491	AA677300		704004	AA400163	AA330013	N34513	AA431778	H89698	AA635183	N26663	AA883822				R38239						AA620611	N51018	A A 703057	H97385	AA428181	
	et al.	179556	211870	151597	505076	435434	855157	454795		1000	142/61	607060	277423	782526	250519	1031003	269288	1461635				137417						1048702	244147	436550	251195	773554	
	Nestbrook et al.	GF201	GF201	GF203	GF201	GF201	GF204	GF203		200	10215	50215	GF201	GF202	GF200	GF204	GE201	GF204	3			GF200						GF202	GF200	70030	GE202	GF201	

Atty Docket No. 21726	1.00727364		-1.1506241	2.26864309		2.22708131	-1.086654	-1.1226105	-1.8456771	1.38300454
Atty Do	1056.554	1056.325	1055.837	1055.824 1055.76	1055.615	1055.603 1055.389	1054.537 1054.527	1054.453	1053.975 1053.894 1053.808	1053.538 1053.471 1052.892
			COX6C			NPAS2 CSDA		CCND1 SOX4		KIAA0666
APPENDIXA	ESTs ESTs, Weakly similar to Similar to obvtoene	desaturase [C.elegans]	Vic Homo sapiens mRNA; cDNA	DNFZp586C1817) ESTS, Moderately similar to !!!!	WARNING ENTRY !!!! [H.sapiens] peuronal PAS domain protein	2 cold shock domain protein A Homo sapiens cDNA FLJ10615 fls, clone	NT2RP2005441 ESTs	adenomatosis 1) SRY (sex determining region Y)-box 4	ESTs, Weakly similar to cDNA EST yk415c12.5 comes from this gene [C.elegans] ESTs	ESTs, Weakly similar to mucin [H.sapiens] Homo sapiens clone LCHN mRNA sequence KIAA0666 protein
	Hs.180284 ES	Hs.97031 de	Hs.74649 Vic	Hs.42458 DK Hs.40098 ES	W, Hs.91052 [H.	Hs.106705 2 Hs.1139 col	Hs.238928 NT Hs.179182 ES		Hs.111314 ES ES Hs.108824 thi Hs.44146 ES	ES Hs.109047 [H Hs.12461 ml Hs.197751 Kl
	Hs.19606	AA404246 Hs.97031	AA456931 Hs.74649	AA035147 Hs.42458 W48852 Hs.56021	Hs.100509	H26182 Hs.106705 AA465019 Hs.89491	AA464962 Hs.5209 R15934 Hs.91375	AA487700 Hs.82932 AA453420 Hs.83484	W72333 Hs.106222 H97880 Hs.108824 N30080 Hs.44146	W91980 Hs,29615 H98619 Hs,12461 AA487243 Hs,90371
	H22173	AA404246	AA456931	AA035147 W48852	R38547	H26182 AA465019	AA464962 R15934	AA487700 AA453420	W72333 H97880 N30080	W91980 H98619 AA487243
retal.	160488	758314	838568	471863 324951	22866	161998 810057	810083 53341	841641	345196 251330 258693	415305 261492 841475
Westbrook et al.	GF200	GF201	GF200	GF203 GF201	GF204	GF201 GF200	GF201 GF200	GF200 GF202	GF201 GF202 GF203	GF201 GF203 GF202

-1.4743954	-1.6570151	1.40379606			1.33033632						1.11509525					-1.6591605	1.12733052	-2.3303815		-1.1982081	1.17459461		1.11982718		1.08514162			-1.0748482
1052.039	1051.867	1051.089	1050.891	1050.844	1050.533			1049.866		1049.631	1049.485	1049.339				1049.076	1049.074	1049.069		1049.026	1048.866		1048.52	1048.444	1048.269	1048.22	1047.768	1047.586
DKFZP586P1422	VTV	YDD19	FBW2	APOA1				TLE3		AES	DKFZP434D1335									PRC1				DKFZP566D143	KIAA0941	KIAA0411		
DKFZP586P1422 protein vitronectin (serum spreading factor, somatomedin B.	complement S-protein)	YDD19 protein	F-box protein Fbw2	apolipoprotein A-I	ESTs	transducin-like enhancer of	split 3, homolog of Drosophila	E(sp1)	amino-terminal enhancer of	split	DKFZP434D1335 protein	ESTs	ESTs, Moderately similar to !!!!	ALU SUBFAMILY SO	WARNING ENTRY !!!!	[H.sapiens]	ESTs	ESTs	protein regulator of cytokinesis	. —	ESTs	Homo sapiens cDNA	FLJ20678 fis, clone KAIA4163	DKFZP566D143 protein	KIAA0941 protein	KIAA0411 gene product	ESTs	ESTs
Hs.108924	Hs.2257	Hs.25615	Hs.13755	Hs.93194	Hs.271634			Hs.31305		Hs.244	Hs.8258	Hs.84560				Hs.23388	Hs.268918	Hs.30411		Hs,5101	Hs.163859		Hs.143601	Hs.224137	Hs.173656	Hs.7977	Hs.34950	Hs.171857
AA459944 Hs.108924		W84774 HS:17643 N68012 HS:40917	99	R97710 Hs.93194				W32778 Hs.83268		AA485742 Hs.244	H25229 Hs.16724	AA459693 Hs.21654				AA432292 Hs.23388	N99553 Hs.53300			AA449336 Hs.5101	AA476257 Hs.104858		AA410608 Hs.91041	AA629804 Hs.85960	R52658 Hs.25938		N64464 Hs.34950	AA465193 Hs.56028
796406	247546	290555	488886	200263	195784			321574		811145	161195	795590				781468	294995	280825		785707	772960		755389	884539	40120	52926	290280	815087
GF202	GF200	GF201	GF201	GF201	GF200			GF201		GF201	GF200	GF201	i			GF202	GF200	GF203		GF202	GF202		GF203	GF201	GF202	GF201	GF201	GF203

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Υ	PPENDIX A		
	PPEND	▽	

	-1.269163	-1.2948094				-1.1261549	-1.7054051	1.04990685	1.15313169			1.03893502		-1.5673521	-1.3608455	-1.1330047				1.31567519		-1.1193717	-1.0703263	-2.3689459	
	1047.555	1047.48	1047.393	1047.321		1046.697	1046.617	1046.28	1045.642		1045.255	1044.953	1044.722	1044.681	1044.555	1043.335	1042.755		1042.36	1042.2	1042.187	1042.077	1041.896	1041.78	1041.471 1041.213 1041.194
		E2IG4	YDD19			PAK2					ALP						KIAA0610		UQCRC2		rpd52L1	NDRG1	(IAA0367		
ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!	H.sapiens]		YDD19 protein	ESTs	p21 (CDKN1A)-activated	kinase 2	ESTs	ESTs	ESTs	alpha-actinin-2-associated LIM	_	ESTs	ESTs	ESTs	ESTs		KIAA0610 protein		ase core protein II	ESTs	tumor protein D52-like 1	lated	KIAA0367 protein	ESTs	Hugo672 fis, clone KAIA4492, Flugo672 fis, clone KAIA4492, inghiv similar to M85549 Homo sepiens sodium/glucose cotransporter-like protein ESTs
ES AL	Hs.192949 [H.:	Hs.8361 ind	Hs.25615 YD	Hs.120573 ES	.Zd	Hs.30692 kin		Hs.97708 ES	Hs.193657 ES	alp	Hs.135281 pro	Hs.70953 ES	Hs.268650 ES	Hs.271377 ES	Hs.173051 ES	Hs.260592 ES	Hs.118087 KIA	_	_	Hs.123065 ES	Hs.16611 tun	_	Hs.23311 KIA	Hs.271609 ES	Ho. 19003 cot Hs.108155 ES
	Hs.125200	Hs.8361		AA884337 Hs.120573		AA505056 Hs.30692	AA398329 Hs.97611	AA412049 Hs.97708	AA251152 Hs.71019		AA972352 Hs.129916	AA126803 Hs.70953	Hs.18381	AA461084 Hs.104959	AA504262 Hs.54835		Hs.28693		AA663058 Hs.118856	Hs.80067	AI014441 Hs.16611	AA489261 Hs.75789	AA447773 Hs.23311	Hs.31822	AA599007 Hs.9003 H67712 Hs.108155 AA285149 Hs.111392
	98060H	R36989	9 R06706										3 T98491	_		5 R12708	5 N38860			2 N24703				3 H21394	, _ ,
	46375	27098	126449	1466911		825660	726675	729953	684240		1584628	490551	122138	796166	825408	129375	279905		852520	269182	1607229	842863	813828	174396	897745 210820 700568
	GF202	GF202	GF201	GF204		GF203	GF203	GF202	GF203		GF204	GF202	GF204	GF202	GF203	GF203	GF201		GF201	GF202	GF204	GF200	GF200	GF203	GF204 GF201 GF204

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843094 788213 112497 472095 132217 121239 50732 327228 785535 129345 140354			APPENDIX A		אייר	Ally Dochet 110, 21720
788213 112497 121239 50732 327228 785535 129345 140354 813249	AA488626 Hs.81424	Hs.81424	ubiquitin-like 1 (sentrin) ESTs, Weakly similar to	UBL1	1041.129	1.04261457
112497 472095 132217 121239 50732 327228 785535 129345 140354 813249	AA453435 Hs.61164	Hs.61164	unknown [D.melanogaster] ESTs, Weakly similar to alternatively spliced product		1041.085	-1.3579424
472095 138217 121239 50732 227228 785535 129345 140354	T91048 Hs.16029	Hs.16029	using exon 13A [H.sapiens] potassium inwardly-rectifying channel, subfamily J, member		1041.024	
121239 50732 327228 785535 826622 246765 129345 140354	AA036956 Hs.102308 R32751 Hs.24552	Hs.102308 Hs.203365	8 ESTs p21 (CDKN1A)-activated	KCNJ8	1040.913 1040.894	1.14576999
121239 267232 327228 785535 826622 246765 129345 140354	26396 Hs.106128	Hs.152663	kinase 3 ESTs, Weakly similar to SmD	PAK3	1040.596	
327228 785535 826622 246765 129345 140354 813249	96708 Hs.17846 17543 Hs.92580	Hs.145061 Hs.92580	homolog, liver [M.musculus] ESTs		1040.283 1040.246	-1.104262
826622 246765 129345 140354 813249	AA284304 Hs.107479 AA450351 Hs.9176	Hs.107479 Hs.9176	KIAA0738 gene product ESTs	KIAA0738	1039.989 1039.915	-1.7400826
129345 140354 813249	AA521490 Hs.30909 N53169 Hs.73849	Hs.30909 Hs.73849	Human Chromosome 16 BAC clone CIT987SK-A-362G6 apolipoprotein C-III Homo sapiens cDNA FLJ10486 fis, clone	APOC3	1039.387 1038.258	1.19269213 1.4411462
140354	112694 Hs.11807	Hs.173946	NT2RP2000205 ESTs, Weakly similar to II!! ALU SUBFAMILY SQ WARNING ENTRY I!!!		1038.24	-1.7900139
813249	85622 Hs.92177	Hs.270876	[H.sapiens] SEC22, vesicle trafficking		1037.912	-1.2250017
	AA455917 Hs.50785	Hs.50785	protein (S. cerevisiae)-like 1 solute carrier family 17 (sodium phosphate), member	SEC22L1	1037.905	-1.4112838
GF203 416401 W86874	W86874 Hs.128827	Hs.128827	4	SLC17A4	1037.712	-2.178762

PENDIX A
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	-1.4014503	1,22217143	1.09999957		1.28043076		1.42231236		-1.2215609	-1.2804493	1.51905491	-1.2961868					000070007	1.09848628			-1.2771674			-1.0010552			
	1037.669	1037.277	1037.193		1037.013	1030.302	1036.345		1036.268	1036.248	1036.217	1036.103				1035.904		1035.651	1035.037		1034.707		1034.592	1034.567	1034.298	1034.198	
	SMPD1						EEF2			ODF2						YWHAB							UBE2L3			C220RF3	
sphingomyelin phosphodiesterase 1, acid lysosomal (acid	sphingomyelinase) ESTs	ESTs	ESTs	Homo sapiens mRNA for	KIAA1281 protein, partial cds	eukarvotic translation	elongation factor 2	Homo sapiens cDNA	FLJ20562 fis, clone KAT11992 outer dense fibre of sperm	tails 2	ESTs	ESTs	tyrosine 3-	monooxygenase/tryptophan 5-	monooxygenase activation	protein, beta polypeptide	Homo sapiens clone 24749	and 24750 mMNA sequences ESTs Weakly similar to NY-	REN-45 antigen [H.sapiens]	Homo sapiens cDNA	PLACE1008002	ubiquitin-conjugating enzyme	E2L 3	ESTs	ESTs chromosome 22 onen reading	frame 3	
	Hs.77813 Hs.72865	Hs.45245	Hs.267706		Hs.42796	HS.122371	Hs.75309		Hs.107444	Hs.129055	Hs.278877	Hs.179635				Hs.182238		Hs.30057	Hs.26506		Hs.28780		Hs.108104	Hs.103185	Hs.125844	Hs.106730	
	AA416890 Hs.77813 AA169379 Hs.72865	AA598822 Hs.45245	AA055766 Hs.103485		AA446881 Hs.42796	AA/8889/ HS.1223/1	R20379 Hs.75309		H09790 Hs.107444	AA400408 Hs.97793	R53258 Hs.106443	T92782 Hs.91074				AA962407 Hs.129934		R95929 Hs.121941	AA457723 Hs.26506		B66820 Hs 28780		AA669526 Hs.108104		W70255 Hs.125844	AA775576 Hs.61743	
	729964	898300	510563			6160201	34849		46667	743278	40449	119004				1569989		199355	810737		140304		823388	344115	344032	378420	
	GF201	GF203	GF202		GF202	GF204	GF200		GF202	GF202	GF202	GF202				GF204		GF202	GF201		GESOO	3	GF201	GF202	GF204	GF204	

1.29710253	-1.3436859	-1.7540913	-2.2749283 1.48870323	-1.0182759 -1.3878583 1.19478147 -1.7533132	-2.2945133	1.26256723 1.08516941 -1.8316364 -1.431653	1.01266192
1034.172 1034.096 1033.965	1033.737 1033.64 1033.503	1032.907 1032.865 1032.71	1032.68 1032.678	1031.625 1031.057 1030.464 1030.306 1029.98	1029.899 1029.25 1028.96	1028.655 1028.408 1027.811 1027.55	1027.36
P130 PIPPIN		DAXX	LEPR	SEC24D CALU ANK2 TBX3-iso	ACP5	PRKCN CA14	TP53BP1
nucleolar phosphoprotein p130 P130 ESTs ortholog of rat pippin PIPPI Homo sapiens mFNA5, cDNA	DKFZp434B0425) ESTs ESTS Homo sapiens mRNA for	KIAA1135 protein, partial cds ESTs death-associated protein 6 Homo sapiens cDNA FLJ10305 fls, clone	NT2RM2000239 leptin receptor SEC24 (S. cerevisiae) related	gene family, member D ESTS calumenin ankyrin 2, neuronal TBX3-iso protein ESTs, Weakly similar to reverse transcriptase related	protein [H.sapiens] ESTs acid phosphatase 5, tartrate resistant	protein kinase C, nu ESTs carbonic anhydrase XIV ESTs	ESTS tumor protein 53-binding protein, 1
Hs.75337 Hs.126900 Hs.106635	Hs.103305 Hs.92096 Hs.112545	Hs.16758 Hs.30875 Hs.180224	Hs.5894 Hs.226627	Hs. 19822 Hs. 19165 Hs. 7753 Hs. 117970 Hs. 267182	Hs.25218 Hs.203402 Hs.1211	Hs.143460 Hs.53631 Hs.235168 Hs 167903	Hs.22979
AA488526 Hs.75337 W68559 Hs.102953 H19246 Hs.106635	AA010188 Hs.103305 R39179 Hs.106326 AA872372 Hs.112545	AA975354 Hs.16758 AA460422 Hs.30875 AA487370 Hs.74522	W84585 Hs.5894 N78902 Hs.94346	AA449107 Hs.19822 R01361 Hs.19165 AA055992 Hs.26067 AA782337 Hs.117970 AA701075 Hs.112371	AA416775 Hs.92314 AA427522 Hs.100829 B08816 Hs.1211		m
843016 342522 51221	430186 23116 1472724	1588700 796480 841498	415795 300015	785840 124143 377641 857603 397488	731338 771060	- 12 40 4 6	
GF200 GF201 GF201	GF201 GF202 GF204	GF204 GF203 GF200	GF203 GF202	GF202 GF200 GF201 GF203 GF203	GF202 GF201	GF202 GF202 GF203 GF203	GF202 GF203 GF203

20022007	-1.094/32/	-1.2253366		-1.0151061		-2.203573	-1.142265	-1.3259251	1.47908822	-1.0768603		-2.0215141			1.52607137			1.11374018										1.56563671			-1.0152223		1.20/252/8
7001	1026.473	1026.429		1026.206	1025.338	1025.173	1025.129	1024.895	1024.839	1023.578		1023.118		1022.61	1022.55			1022.538		1022.49		1022.407	1022.236	1022.038	1021.513			1021.226			1021.01		1020.488
	HOAT			PSMA6					D1S155E	HDAC3				RGS13				SLC20A1					MSH5		KIAA0143						SLC35A1		PLAGL1
trophinin associated protein	(tastin) ESTs	ESTs	proteasome (prosome, macropain) subunit, alpha	type, 6	ESTs	ESTs	EST	ESTs	NRAS-related gene	histone deacetylase 3	ESTs, Highly similar to CGI-	115 protein [H.sapiens]	regulator of G-protein	signalling 13	ESTs	solute carrier family 20	(phosphate transporter),	member 1	ESTs, Weakly similar to FB19	protein [H.sapiens]	Homo sapiens clone 24504	mRNA sequence	mutS (E. coli) homolog 5	ESTs	KIAA0143 protein	Homo sapiens cDNA	FLJ20172 fis, clone	COL09807	solute carrier family 35 (CMP-	sialic acid transporter),	member 1	pleomorphic adenoma gene-	ike 1
	Hs.171955 Hs.100265	Hs.119825		Hs.74077	Hs.268957	Hs.179641	Hs.49143	Hs.12720	Hs.69855	Hs.6975		Hs.56043		Hs.17165	Hs.124538			Hs.78452		Hs.42390		Hs.51649	Hs.112193	Hs.266299	Hs.84087			Hs.255660			Hs.82921		Hs.75825
	194949 Hs.81910 193247 Hs.100265	16		4A047338 Hs.74077	465988 Hs.108271	AA609953 Hs.112792	V66201 Hs.49143	AA707312 Hs.12720	N36232 Hs.43752	479778 Hs.6975		AA479913 Hs.56043		470047 Hs.17165	199945 Hs.124538			W47073 Hs.78452		N67832 Hs.42390		R43867 Hs.51649	AA459915 Hs.71561	4A625804 Hs.116082	4A112057 Hs.84087			AA447764 Hs.12372			AA460679 Hs.82921		AA463297 Hs.75825
	308746 N			509495 A	210906 H	1031176 A	278625 N	451473 A	272748 N	_		772918 A		239446 H	263271 H			325062 W		291690 N		33496 R	795640 A.		530310 A			813661 A			796680 A		796904 A
	GF200 GF201	GF203		GF200	GF201	GF202	GF202	GF203	GF203	GF200		GF202		GF201	GF203			GF200		GF201		GF201	GF201	GF204	GF201			GF202			GF200		GF200

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1.26163461 -2.7864043 -1.3178567	-1.7284522 -1.2701119 1.34719728	-1.0196809	-1.5365655 1.77886915 -1.280562 6	-1.7481581	1.48328288
1020.321 1020.306 1020.235	1020.187 1020.174 1020.098 1019.75	1019.487 1019.342	1019.263 1018.662 1018.393 1018.281 1018.211	1018.185	1017.128 1016.909 1016.878 1016.692 1016.554
	ВРН.	RPS6KA2	SLC6A2 SSI-3 ASPH	SGPL1	PCDH1
ESTs, Weakly similar to hypothetical protein [H.sapiens] ESTs ESTs	biphenylhydrolase-like (serine hydrolase, breast epithelial mucin-associated antigen) ESTs ESTs	ribosomal protein S6 kinase, 90kD, polypeptide 2 ESTs solute carrier family 6	noradrenalin), member 2 ESTS STAT induced STAT inhibitor 3 ESTS aspartate beta-hydroxylase Homo sapiens mRNA; cDNA	DKFZp434C184 (from clone DKFZp434C184) sphingosine-1-phosphate lyase 1 protocadherin 1 (cadherin-like protocadherin 1 (cadherin-like	procedures in the process of the pro
Hs.163203 Hs.30011 Hs.112627	Hs.184552 Hs.269474 Hs.7626 Hs.35976	Hs.211596 Hs.3593	Hs.78036 Hs.269079 Hs.107055 Hs.194225 Hs.121576	Hs.268024 Hs.186613	Hs.79769 Hs.40583 Hs.76325 Hs.191190 Hs.129837 Hs.63131
AA481135 Hs.105154 AA460961 Hs.30011 AA609004 Hs.112627	R54850 Hs.20343 AA609047 Hs.112634 AA489660 Hs.7626 R98442 Hs.35976		R62384 Hs.78036 AA004719 Hs.47482 T72915 Hs.107055 N39325 Hs.14893 R10973 Hs.107941	N93865 Hs.108599 AA435998 Hs.21029	R77512 Hs.113714 AA431986 Hs.40583 T70057 Hs.76325 R00835 Hs.113037 AA778570 Hs.129837 AA054585 Hs.63131
815164 AA4 796117 AA4 1030779 AA6	154465 R54 1031266 AAC 823719 AAA		139840 R62 429011 AAC 84211 T72 243770 N39 129112 R10	309246 N93 730739 AA4	145491 R77 782209 AA-8 80948 T70 123585 R0C 1048915 AA7 487959 AA(
GF203 GF202 GF202	GF200 GF204 GF203 GF200	GF200	GF201 GF201 GF202 GF200 GF200	GF201 GF202	GF204 GF201 GF200 GF202 GF204 GF204

	1.06152669	1.37640878				-1.2291969	1.84204858	-2.232097		-1.2010219								1.21209295							1.19987846
	1016.159	1016.117		1015.77		1015.365	1015.169	1014.802	1014.677	1014.653	1014.341		1014.018		1013.888		1013.866	1013.808	1013.563		1013.451	1013.21	1012.959		1012.929
		PMP24		PGA5				RPL24			DUSP6		DOC-1R		PLA2G7							RANBP7	ZNF187		RALB
ESTs, Weakly similar to III! ALU SUBFAMILY J WARNING ENTRY IIII	[H.sapiens] 24 kDa intrinsic membrane	protein	pepsinogen 5, group l	(pepsinogen A) ESTs, Moderately similar to	hypothetical protein	[H.sapiens]	ESTs	ribosomal protein L24	ESTs	ESTs	dual specificity phosphatase 6 DUSP6	tumor suppressor deleted in	oral cancer-related 1	phospholipase A2, group VII (platelet-activating factor	acetylhydrolase, plasma)	ESTs, Weakly similar to	KIAA0635 protein [H.sapiens]	ESTs	ESTs	ESTs, Weakly similar to testicular tektin B1-like protein	[H.sapiens]	RAN binding protein 7	zinc finger protein 187	v-ral simian leukemia viral oncogene homolog B (ras	related; GTP binding protein)
	Hs.114434	Hs.241205 Hs 86815		Hs.75558		Hs.263858	Hs.126555	Hs.184582	Hs.108003	Hs.43388	Hs.180383		Hs.25664		Hs.93304		Hs.116116	Hs.44841	Hs.187840		Hs.103441	Hs.5151	Hs.237786		Hs.250811
	Hs.114434	R37108 Hs.20528		Hs.75558		4A195276 Hs.55549	Hs.126555	AA633768 Hs.118779	Hs.108003	Hs.43388	AA630374 Hs.79323		AA457108 Hs.25664		Hs.93304		4A625993 Hs.116116	4A454660 Hs.44841	4A699762 Hs.121942		AA626939 Hs.116185	AA126755 Hs.106779	Hs.9219		RG.39
	N53394	R37108	7.75	R72097		AA195276	N64366	AA633768	R07887	N23400	AA630374		AA457108		He5030		AA625993	AA454660	AA699762		AA626939	AA126755	AA001376 Hs.9219		W15297
	284042	25838	100000	155768		665261	290194	857681	127070	268385	854899		810429		238821		745499	811926	461235		1048769	490612	361899		322617
	GF203	GF201	202	GF201		GF202	GF203	GF203	GF201	GF203	GF201		GF201		GF201		GF204	GF203	GF204		GF204	GF201	GF201		GF200

1.51958602	1.07382935 -1.2041555 1.32864829 -1.1691196	1.13778695 1.4022276	-1,0087774
1012.748	1012.476 1012.356 1012.222 1011.339 1011.246	1010.998 1010.597	1010.53 1010.207 1010.129 1009.867
SLC7A8 PMS2L12	TAGLN2 TBX2	СЕВРВ	PSIMB3
solute carrier family 7 (cationic amino acid transporter, y+ system), member 8 postmentic segregation increased 2-like 12 hono sapiems mRNA; DNA DKRZA55A4132 (from clone	DKTZp5644132) transgelin 2 H.saplens mRNA for retrotransposon ESTs T-box 2	CCAAT/enhancer binding protein (C/EBP), beta ESTs	Human DNA sequence from chorne RP11.3951.14 on chromosome 22q13.32-13.33. Contains spend of 91 yr 52x-13.35. Contains (part of) up to six novel genes or pseudogenes, the gene for a rovel in smilar to FOXD4 (forkhead box D4, FREACS), the gene for a rovel phosphoglucomutase like ESTs. Weakly similar to p60 katanin H. sapiens] proteasome (prosome, macropain) subunit, beta type, 3 ESTs, Highly similar to homer-to like ESTs, Highly similar to homer-to-like ESTs.
Hs.22891 Hs.91299	Hs.75725 Hs.75725 Hs.12028 Hs.87089 Hs.168357	Hs.99029 Hs.108631	Hs.7536 Hs.175444 Hs.100861 Hs.82793
W84701 Hs.42653 AA437126 Hs.83644	AA521384 Hs.16726 H08564 Hs.75725 W03926 Hs.12028 AA465398 Hs.87089 N99243 Hs.32931	H26183 Hs.99029 AA463189 Hs.108631	H38991 Hs.110559 N26906 Hs.108603 H09719 Hs.100861 AA620580 Hs.82793 W84663 Hs.108068
W84701 AA437126	AA521384 H08564 W03926 AA465398 N99243	H26183 AA463189	H38991 N26906 H09719 AA62058(
415670	826995 45544 297102 814135 309161	161993 796878	175168 257248 45452 951233
GF201 GF202	GF203 GF200 GF200 GF204 GF200	GF200 GF202	GF204 GF201 GF204 GF200 GF200

-1.256328 1.35406594

1.31912851

-1.12779

-1.1394811

ŧ	Ally	1009.732 1009.638 1009.276	1008.672 1008.385	1007.887 1007.502	1007.485	1007.474 1007.403	1007.216 1006.961 1006.726	1006.498 1006.052 1005.163	1005.132	1004.995	1004.99 1004.792 1004.593	1004.465 1004.384
09897798		DKFZP586I1023			CHD4	C4ST	BMP4 JMJ	GABARAP			S100A12	TFRC
	APPENDIX A	EST ESTs DKFZP586I1023 protein Homo saplens mRNA,	transcript KIAA0495 ESTs Homo sapiens clone 24706	mRNA sequence ESTs chromodomain helicase DNA	binding protein 4	Homo sapiens cDNA FLJ20693 fis, clone KAIA2667 chondroitin 4-sulfotransferase		GABA(A) receptor-associated protein ESTs	ES1, Highly similar to densin- 180 [R.norvegicus]	ATPase type IV, phospholipid- transporting (P-type),(putative) S100 calcium-binding protein	A12 (calgranulin C) ESTs ESTs	transferrin receptor (p90, CD71) ESTs
		Hs.102780 Hs.23296 Hs.111515	Hs.49658 Hs.35088	Hs.151903 Hs.183232	Hs.74441	Hs.197877 Hs.240443	Hs.68879 Hs.40154 Hs.122045	Hs.7719 Hs.49759 Hs.269829	Hs.112670	Hs.70604	Hs.19413 Hs.25819 Hs.82920	Hs.77356 Hs.118368
		N68578 Hs.102780 AA521300 Hs.23296 AA181600 Hs.62741	t Hs.49658 Hs.35088	H55907 Hs.20201 AA454008 Hs.35653	Hs.113736	M49633 Hs.111375 AA989515 Hs.10012	AA463225 Hs.68879 N73555 Hs.40154 AA778610 Hs.122045	AA457725 Hs.7719 N69850 Hs.49759 N54416 Hs.47820	AA609242 Hs.112670	AA436260 Hs.70604	AA700005 Hs.19413 H48096 Hs.25819 AA704519 Hs.82920	AA488721 Hs.77356 AA702517 Hs.118368
		N68578 AA52130 AA18160	W70114 H21520	H55907 AA4540	H02839			AA45772 N69850 N54416		AA4362	AA7000 H48096 AA7045	AA4887 AA7026
	¥ et аl.	292637 827171 613303	344290 159935	204111 795263	151492	324844 1606275	797048 295992 1048963	810741 297638 244806	1031510	754625	436029 193381 451095	841703 447088
	Westbrook et al.	GF202 GF203 GF202	GF201 GF200	GF200 GF201	GF204	GF202 GF204	GF201 GF200 GF204	GF201 GF201 GF200	GF202	GF203	GF201 GF200 GF203	GF200

1.01233548

-2.4798089

-1.2586411

-1.0578119

-1.0374242

1.44638137

-1.5062911 1.2528627

Four-septence CDNA	-1.2733274 -1.2733274 1.4276367 -1.788872	-1.9424476	-1.518272	-1.3038553		1.09095991 1.0113919	1.29140781	1.42569181	1.02565338	1.12157283
56744 AA127861 Hs.29493 Hs.29493 COL07365 56344 AA112860 Hs.22289 Hs.155591 forkhead box F1 1031767 AA60922 Hs.17288 Hs.155591 forkhead box F1 268347 AA415703 Hs.12736 ESTS 268347 AA41578 Hs.110917 Hs.244956 ESTS 268347 AA41578 Hs.110917 Hs.244956 ESTS 268347 AA41578 Hs.118513 Hs.118513 FTS, Weakly similar to AA132070 Hs.61601 Hs.219618 FSTS, Weakly similar to 504179 AA132070 Hs.61601 Hs.221516 ESTS, Weakly similar to 45922 H09541 Hs.107437 Hs.11307 [C.elegans] 840150 AA485265 Hs.25613 Hs.55613 preny protein to please RCET 840150 AA485265 Hs.2017 Hs.241257 (c.elegans) 256950 N32587 Hs.18645 Hs.85146 Hs.85145 COS (C.elegans) 260303 H9823 Hs.85146 Hs.85146 SSTS, Weakly similar to partial 260303 H9823 Hs.85146 Hs.85146 SSTS, Weakly similar to partial 260303 H9823 Hs.85146 Hs.85146 COS (C.elegans) 675 C.elegans of the partial protein 1 Ls.104747 Hs.11307 C.elegans of the partial protein 1 Ls.104747 Hs.83448 Hs.8348 trone epithopsia isomerae 1 67960 T44713 Hs.8348 Hs.83848 Hs.83869 chromosome 5q31-33 region	1004.209 1003.981 1003.89 1003.793	1003.712	1003.56	1003.555	1003.383	1003.154 1002.962	1002.927	1002.856 1002.849	1002.32 1002.10 1002.101	1001.983
56344 AA127861 Hs.29493 Hs.29493 563444 AA112860 Hs.22289 Hs.155591 563444 AA112860 Hs.22289 Hs.155591 1031767 AA009628 Hs.112736 Hs.112736 Hs.12737 Hs.244985 1268347 N26740 Hs.42777 731343 AA416785 Hs.110917 Hs.249495 1295650 N68657 Hs.14808 Hs.14808 Hs.14808 1504179 AA132070 Hs.61601 Hs.221516 795685 AA459936 Hs.27833 Hs.241257 1259950 N32587 Hs.18645 Hs.85613 Hs.55613 Hs.55613 Hs.85613 Hs.8599 Hs.8599 Hs.85999	FOXF1 FOXF1	HNRPA1				RCE1	LTBP1		ETS2 TPI1 DKFZP5640092	
501731 AA127861 Hs.29493 56344 AA11260 Hs.22269 56344 AA11260 Hs.22268 265347 Nz8740 Hs.42771 731343 AA416785 Hs.110917 295650 N66857 Hs.14808 504179 AA132070 Hs.61601 795685 AA459936 Hs.2788 45922 H09541 Hs.107437 840150 AA485265 Hs.2017 256950 N32587 Hs.18645 731353 AA416793 Hs.8645 731353 AA416793 Hs.8645 8395749 AA663983 Hs.8848 67867 AA663983 Hs.8948	Homo saptiens cDNA FLJ20142 fis, clone COL07365 forkhead box F1 forkhead box F1 ESTs	reterogeneous nuclear ribonucleoprotein A1 ESTs, Weakly similar to PROBABLE G PROTEIN- COUPLED RECEPTOR HTA	[R.norvegicus] ESTs, Weakly similar to !!!! ALU CLASS C WARNING	ENTRY !!!! [H.sapiens] ESTs, Weakly similar to	uroplakin 1b [H.sapiens] ESTs ESTs, Weakly similar to similar to Glutaredoxin, Zinc fineer, C3HC4 type	[C.elegans] prenyl protein protease RCE1	factor beta binding protein 1 ESTs, Weakly similar to partial	CDS [C.elegans] ESTs v-ets avian erythroblastosis virus E26 oncogene homolog	triosephosphate isomerase 1 DKFZP564O092 protein Homo saniens mRNA from	chromosome 5q31-33 region
56344 AA112660 56344 AA112660 1031767 AA609628 266347 NXB740 731343 AA416785 504179 AA132070 795685 AA459836 839594 AA504656 839594 AA504656 259950 NX2587 731353 AA416793 675749 AA663983 675749 AA663983 675749 AA663983 675749 AA663983	Hs.29493 Hs.155591 Hs.155591 Hs.112736 Hs.42771	Hs.249495	Hs.118513	Hs.14808	Hs.221516 Hs.37883	Hs.11307 Hs.55613	Hs.241257	Hs.18645 Hs.85999	Hs.85146 Hs.83848 Hs.9043	Hs.18593
	AA127861 Hs.29493 AA112660 Hs.23269 AA112660 Hs.77288 AA609628 Hs.112736	AA416785 Hs.110917			AA132070 Hs.61601 AA459936 Hs.37883	H09541 Hs.107437 AA485265 Hs.55613	AA504656 Hs.2017	N32587 Hs.18645 AA416793 Hs.85999	82	
	GF201 501731 GF200 563444 GF200 563444 GF202 1031767		GF203 324543	GF203 295650	GF201 504179 GF201 795685	GF202 45922 GF202 840150	GF200 839594	GF203 259950 GF204 731353	GF200 260303 GF201 855749 GF201 67960	GF200 123331

-1.2105953 1.4324532 1.39886276	1.07202754 -1.070346 -1.4083452	1,45012228 1,13735984 -1,5478607	-2.771956	-2.3597694
1001.897 1001.877 1001.666 1001.614 1001.415 1001	1000.818 1000.519 1000.013 999.1714 999.1493	998.9786 998.9208 998.7156 998.4099	998.1212	997.7996 997.6902 997.6813
DKFZP586I1023	CASP4	CSNK1E	EFS2	KIAA0876
ESTs ESTs DKFZP58611023 protein ESTs ESTs ESTs	caspase 4, apoptosis-related caspase 4, apoptosis-related cysteine professas et insulin-like growth (actor 1 (somatomedin C) ESTs ESTs	ESTS. SESTS, Highly similar to RAS- RELATED PROTEIN RAB-1A [M.musculus] Cassen kinase 1, epsilon ESTS ESTS, Weakly similar to LPP H. Rapilens) Learn container of the	Intrin sequents count in announce and intrins sequents count in the International inte	TPX-1 PRECURSOR [H.sapiens] KIAA0876 protein ESTs
Hs.179262 Hs.34372 Hs.111515 Hs.7790 Hs.47111 Hs.269055 Hs.48389	Hs.74122 Hs.85112 Hs.109434 Hs.13207 Hs.109999	Hs.178603 Hs.5566 Hs.79658 Hs.269087 Hs.10645	Hs.260150 Hs.24587	Hs.7745 Hs.24174 Hs.98754
Hs.23580 Hs.34372 Hs.107112 7 Hs.7790 Hs.47111 Hs.101459 Hs.48389	145000 Hs.74122 4A456321 Hs.85112 465982 Hs.109434 FB2459 Hs.13207 4A134809 Hs.58117	AA404352 Hs.54541 R59359 Hs.26648 W94106 Hs.110165 N71259 Hs.109330 AA444053 Hs.10845	AA454626 Hs.111754 AA460282 Hs.24587	AA634164 Hs.7745 AA454753 Hs.62246 AA431761 Hs.98754
R23727 N55342 N39240 AA045257 N50740 N30006	H45000 AA45632: N65982 T82459 AA134809	AA40435 R59359 W94106 N71259 AA44405	AA45462 AA46028	AA63416 AA45475 AA43176
131599 245866 276975 376652 283744 268258 284586	183194 813179 293811 22374 502462	758347 37820 358675 294611 756599	811851	868396 809806 782479
GF201 GF203 GF201 GF201 GF202 GF202	GF200 GF200 GF202 GF201 GF201	GF201 GF200 GF202 GF202 GF203	GF202 GF201	GF203 GF201 GF202

1.05560888	-1.3093908	1.04105154	1.90327311 2.06027646	1.07778805	1.26253852		1.20791007	-2.1939561	1.15624894	
997.6758 997.3371	996.7933	996.6422 996.5597	996.2896 996.0245 995.7961	995.4292	995.09	994.8269	994.4209	993.8559 993.8223	993.8214 993.6069 993.4395	993.2401
VRK2 KIAA0601	П		KIAA0480 ZNF146			CAMP		MOCS2	HSD11B1 DKFZP566E2346	=
vaccinia related kinase 2 KIAA0601 protein	professe initional 1 (arist elastase), alpha-1-antitrypsin Homo sapiens mRNA; cDNA DKFZn564G022 (from clone	DKFZp564G022) ESTs Homo sapiens clone 25071	and 25177 mRNA sequences KIAA0480 gene product zino finger protein 146 Homo sapiens CDNA FLI20042 fis, clone	COL00424 ESTs, Highly similar to LYMPHOTOXIN-BETA RECEPTOR PRECURSOR	[H.sapiens]	peptide ESTs, Moderately similar to !!!! ALU SUBFAMILY SO WARNING ENTRY !!!!	[H.sapiens] molybdenum cofactor	synthesis 2 EST hvdroxysteroid (11-beta)	dehydrogenase 1 ESTs DKFZP566E2346 protein	ESI's, Moderately similar to iii: ALU SUBFAMILY SP WARNING ENTRY IIII [H.sapiens]
Hs.82771 Hs.174174	Hs.75621	Hs.107127 Hs.6786	Hs.10590 Hs.92200 Hs.75471	Hs.183861	Hs.185680	Hs.51120	Hs.192926	Hs.70565 Hs.98254	Hs.275215 Hs.269317 Hs.64595	Hs.210706
AA490617 Hs.82771 W80376 Hs.19152	AA167328 Hs.28378	N62924 Hs.107127 AA404269 Hs.6786	R38967 Hs.113392 R26542 Hs.26247 AA504351 Hs.75471	AA598402 Hs.112380	R02558 Hs.121055	AA609759 Hs.51120	AA394066 Hs.129939	AA043466 Hs.70565 AA416760 Hs.98254	AA150918 Hs.37012 N70366 Hs.49847 AA757659 Hs.64585	N95217 Hs.55121
824117 415527	595620	278687 758309	25071 132418 825478	950098	124034	1031940	725978	486641 731310	505059 295432 396045	307314
GF200 GF201	GF202	GF201 GF202	GF204 GF200 GF200	GF202	GF202	GF201	GF203	GF204 GF202	GF200 GF204 GF203	GF201

	1.07659176	-1.0630987	-1.1520753	-1.8437079		-1.1410332	1.12109431	35050305.T
	993.2135	993.1602 992.4723	991.9534	991.9146	991.7543	991.5916 991.1146	990, 7972 990, 6843 990, 6481 990, 454 990, 295	990.1434
	KIAA0681		KIAA0174		DKFZP586M1824	CRIP2	KIAA1010 GTF2H3 NK4 EPHB3 CHL1	
lethal (3) malignant brain tumor I(3)mbt protein	(Drosophila) homolog Homo sapiens mRNA; cDNA DKFZp762E115 (from clone	DKFZp762E115); partial cds ESTs	KIAA0174 gene product	ESTs	DKFZP586M1824 protein	cysteine-rich protein 2 ESTs	Human DNA sequence from clone 967N21 on chromosome 20p12.3-13. Contains the CHGB gene for chromogranin B (secretogranin 1. SCG1), a pseudogene similar to part of KIAAD172, the gene for a novel protein similar to predicted worm, yeast and plant proteins. KIAA1010 protein general transcription factor IIII+ polypeptide 3 (34kD subunit) ESTs natural killer cell transcript 4 EphB3 killer cell transcript 4 EphB3 viole cell transcript 4 EphB3 viole cell adhesion molecule with homologue of L1)	ESTs
	Hs.22237	Hs.109778 Hs.222581	Hs.75824	Hs.108873 Hs.7864	Hs.25882	Hs.70327 Hs.102650	Hs. 88959 Hs. 23860 Hs. 23860 Hs. 125509 Hs. 2913 Hs. 210863	Hs.7171
	Hs.94044	Hs.108297 Hs.40689	Hs.75824	N72286 Hs.42626 AA233552 Hs.7864	Hs.31030	4A485427 Hs.70327 N50517 Hs.102650	W94690 Hs.59564 AA453501 Hs.29860 AA460838 Hs.90304 AA463820 Hs.2913 AA455591 Hs.2913 AA455591 Hs.2913	Hs.7171
	R61289	N64681 H85107	T63171	N72286 AA233552	H50130	AA485427 N50517	W94680 Hs.5956 A4453501 Hs.2386 A4460838 Hs.3003 A4488982 Hs.125 A445899 Hs.2913 A4455591 Hs.2913	N50428
	43090	290072	79710	291394 666138	179199	811046 280683	358052 795379 1461629 813520 27787	280640
	GF203	GF203 GF204	GF200	GF201 GF203	GF204	GF201 GF202	GF202 GF201 GF201 GF204 GF206 GF200 GF200	GF203

-1.1267586	-1.4365818		-1.6006355		-1.0132957	1 1/611705	1,43325023	-1.8556392	1.33866128			1.02/1624	-1.0323043	-1.0421857	-1.0449022		
990.0834	990.0282	989.3245 989.3043	989.0259 988.9362 988.8284	988.6504	988.4298	000 0504	987.713	987.6268	987,0038			986.9797	986.5237	986.3467	986.2922	986.0656	985.9077
PTP4A1	4DAM11	CAMKK2 GAK			ARF3			HDAC3	o ICSMd					IFNAR2		OR7E12P	ALOX5AP
hosphatase	a disintegrin and metalloproteinase domain 11 ADAM11	calcium/calmodulin-dependent protein kinase kinase 2, beta C cvolin G associated kinase	ESTS ESTS ESTS		3 lar to IIII	WARNING ENLY !!!!	[n.sapiens] ESTs		postmeiotic segregation		NT2RP2000153, weakly	similar to GAR2 PROTEIN	EST interferon (alpha, beta and	t) receptor 2	ESTs olfactory receptor, family 7, subfamily E. member 12	lase-	activating protein
Hs.227777	Hs.6088	Hs.108708 Hs.153227	Hs.58471 Hs.121925	Hs.121724	Hs.119177	70,00	HS.72047	Hs.6975	Le 970569	2000		Hs.4997	Hs.93779	Hs.86958	Hs.191184	Hs.120017	Hs.100194
Hs.11937	Hs.6088	AA181179 Hs.108708 AA428959 Hs 9569	W81117 Hs.58471 AA77747 Hs.121925	AA703516 Hs.121724	AA670422 Hs.119177		N78301 HS.48401 AA152312 Hs.72047	Hs.27250		90 190		Hs.124941	Hs.93779	တ္ထ	Hs.113188	AA707468 Hs.120017	Hs.77359
R61674	H43854	AA18117 AA42895	W81117 AA777474	AA70351	AA67042		N78301 AA15231	W46769	9445020	AA43820		R42182	N34418	AA48542	R08296		T49652
42739	184240	624271	448323	306032 450103	878815		248688	324386	044400	0 14403		30580	277339	811044	127246	1291972	62/29
GF200	GF200	GF204	GF202 GF204	GF204	GF203		GF200	GF203	000	00215		GF203	GF202	GF200	GF203	GF204	GF201

-2.203723 -1.1057244 1.18757599		-1.0786292	-1.0964761	1.11908439	-1.0014701 1.05936508
985.5396 985.4669 985.4308 985.1458	984.8716	984.4761 984.3553 984.0721	963.9001	983.7496 983.4711 983.1382 983.0215 982.9915	982.5469 982.4084
ATP5I DKFZP434A014	IMP-2	CYLC2 HRIHFB2122 KIAA0715	EWSR1		CSNK1G3
ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e Homo sapiens clone 23703 mRNA sequence DKFZP434A014 protein ESTS ESTS Homo sapiens cDNA	FLJ1188 fis, clone PLACE1007544 IGF-II mRNA-binding protein 2 IMP-2	cylicin, basic protein of sperm head cytoskeleton 2 putative nuclear protein KIAA0715 protein Ewing sarcoma breakpoint	region 1 Human DNA sequence from clone 34B21 on chromsome 6p12.1-21.1. Contains part of a gene for a novel protein with ZUS domain similar to part of Tight Junction Protein ZO1 (TJP1) and UNC5 Homologs, the gene for a novel BZPP foreirharal hearzodiazanine	recepto ESTs ESTs ESTs ESTs	casein kinase 1, gamma 3 ESTs
Hs.85539 Hs.12532 Hs.178098 Hs.43871 Hs.187850	Hs.27410 Hs.30299	Hs.3232 Hs.40342 Hs.109358	Hs.129953	Hs.183056 Hs.43322 Hs.121593 Hs.41862 Hs.19523	Hs.129206 Hs.139907
AA431433 Hs.85539 AA676234 Hs.12532 AA416585 Hs.97573 N28899 Hs.43871 AA704460 Hs.119822	AA625924 Hs.27410 AA634300 Hs.30299	AA705796 Hs.119918 AA676612 Hs.129908 N57535 Hs.109358	R32756 Hs.99969	AA405625 Hs.72003 N23112 Hs.43322 W86291 Hs.103221 AA776438 Hs.4 862 AA779176 Hs.19523	AA398116 Hs.104667 AA621615 Hs.113000
782439 431526 730971 257206 450713	744983	1292142 882588 279936	135449	772477 266777 415876 453753 453030	726558 1034860
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-1.2342232 -1.5429457 -1.9949174	1.00168883 1.48563558 -1.3534044	1.04166961	-1.4031357 1.77970065 1.20622813	-1.5775646	-1.840955
982.3389 982.2365 981.4733 981.1499	980.7996 980.77996 980.1711	980.0873 980.0611 979.504 979.3691 979.363	979.2385 979.2341 978.9645 978.927	978.8981 978.8937 978.6086 978.5092 978.2125	978.2079 978.1561 978.022 977.971
HSU91641	PGPL	RDGBB	SNX3	PRIMZA SIL	SNRPN
Homo sapiens germline mRNA sequence ESTs alpha2,8-sialyltransferase ESTs, Weakly similar to	putative p150 [H.sapiens] ESTs Pseudoautosomal GTP- binding protein-like	retinal degeneration B beta ESTs ESTs ESTs	ESTS ESTS ESTS sorting nexin 3 Homo sapiens mRNA for	KIAA1151 protein, partial cds ESTs primase, polypeptide 2A (58kD) TAL1 (SCL) interrupting locus ESTs mail nuclear ribonucleoporein polypeptide	N ESTs ESTs ESTs, Weakly similar to Y40B1B.7 [C.elegans] ESTs
Hs.12840 Hs.117964 Hs.22985 Hs.172156	Hs.19085 Hs.104910 Hs.101033 Hs.108029	Hs.109219 Hs.133998 Hs.116119 Hs.22573 Hs.189046	Hs.117331 Hs.190075 Hs.21509 Hs.12102	Hs.6298 Hs.112916 Hs.74519 Hs.99836 Hs.1975 Hs.40173	Hs.250727 Hs.26882 Hs.113999 Hs.122555 Hs.61532
H16573 Hs.12840 N20913 Hs.117964 R43753 Hs.22985 A4490999 Hs.99649	R92216 Hs.19085 AA432268 Hs.104910 AA495949 Hs.101033 AA495972 Hs.101033		AA426027 Hs.117331 R16484 Hs.21500 AA447486 Hs.21509 AA426027 Hs.115106	AA043878 Hs.43559 AA620873 Hs.112916 R61796 Hs.106735 AA490486 Hs.99836 AA704809 Hs.11002 N25738 Hs.40173	T55092 Hs.48375 H18471 Hs.26882 H50654 Hs.113999 AA777656 Hs.122555 AA029063 Hs.61532
49260 H- 265287 N; 34837 R4 824610 Av	195875 Ri 782331 Av 768464 Av			486984 Av 1049335 Av 42325 Br 823887 Av 452818 Av 268476 Ni	74119 51216 194314 448535 470067
GF200 GF204 GF202 GF203	GF200 GF202 GF202	GF201 GF202 GF204 GF204 GF204	GF203 GF200 GF202 GF204	GF204 GF204 GF202 GF203 GF204 GF204	GF200 GF201 GF202 GF204 GF204

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1.98710671 1.38869456 -1.0615864 -1.1080144 1.05409962	1.36618885	-1.1404817 1.5105218 -2.7111498	1.16410911 -1.3851478 -1.085497		-1.4611143
974.0197 973.9126 973.8165 973.7355 973.6062	973.6023 973.6 973.6	973.5017 973.4742 973.4202	973.4136 973.2741 973.0996 973.0318	972.8568	972.6967 972.3209 972.186 971.989
ART4 RERE	ZFP103 SDF2 SDF2	HPS TRA1 TMOD3	INSR INSR PIGK	SRP14	
ESTs EST EST Weakly similar to IIII ALU SUBFAMILY SC WARNING ENTRY !!!! [H. kapiens] ADP-ribosyltransferase 4 arginine guldamic acid dipeptide RE repeats	zinc finger protein homologous to Zip103 in mouse stromal cell-derived factor 2 stromal cell-derived factor 2	Hermansky-Pudlak syndrome tumor rejection antigen (gp96) 1 tropomodulin 3 (ubiquitous) confrontin releasing	hormone insulin receptor ESTs, Highly similar to dJ22E13.1a.1 [H.sapiens] phosphatidylinositol glycan, class K	signal recognition particle 14kD (homologous Alu RNA- binding protein) ESTS, Weakly similar to ORF2 contains a reverse transcriptase domain	[H.sapiens] ESTs ESTs ESTs
Hs.101660 Hs.144162 Hs.11712 Hs.13776 Hs.194369	Hs.155968 Hs.118684 Hs.118684	Hs.83951 Hs.82689 Hs.22826	Hs.75294 Hs.89695 Hs.151584 Hs.62187	Hs.180394	Hs.252673 Hs.15387 Hs.271771 Hs.6688
AA609439 Hs.101660 R98107 Hs.38822 157082 Hs.11712 N70349 Hs.13776 AA021188 Hs.26316	19 Hs.4856 14 Hs.21719 14 Hs.118684	W80375 Hs.103208 AA598758 Hs.82689 AA777400 Hs.22826	R45054 Hs.75294 AA001614 Hs.89695 AA779609 Hs.122651 W05406 Hs.62187	AA988798 Hs.1718	25 Hs.62480 7201 Hs.15387 60 Hs.107954 04 Hs.6688
206849 R98107 206849 R98107 81229 T57082 286998 N70349 364108 AA02111	26505 R20639 35191 R24974 35191 R24974	415525 W80375 897690 AA598756 449044 AA777400	34671 R4505 427812 AA001 1033232 AA779 299154 W0540	•	301068 N81025 454702 AA677201 418328 W90760 38676 R51504
GF202 745 GF200 200 GF202 815 GF203 364	GF201 26E GF200 351 GF200 351	GF202 418 GF200 897 GF203 448	GF200 346 GF200 427 GF204 103		GF202 30 GF204 45 GF201 418 GF202 386

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1.67557502 1.04779511 1.04698136 1.32471724	1.110995 -1.155747 1.17241042 -1.6287345 1.12653115	1.24664741 -1.4055242 1.0677535 -1.9836039 1.23738346	-1.6894286
971.9477 971.8615 971.7662 971.6487 971.3927	971.088 970.929 970.929 970.307 970.0166 969.4953 969.1376	969.0212 968.2416 968.2416 967.8847 967.8848 967.8134 967.6025 967.5025 967.3266	966.9917 966.6259 966.4836 966.3984 966.3556 966.3057
KIAA0782 BNIP3		E1B-AP5 PCP4 GTPBP1 GA17 YDD19	SDC1 CRYGA
ESTs KIAA0782 protein ESTs BCL2/adenovirus E1B 19kD- interacting protein 3 ESTs	G protein-coupled receptor f protein-coupled receptor ESTS ESTS ESTS ESTS ESTS ESTS ESTS EST	ESTs, Weakly similar to zinc finger protein [H. sapiens] Purkinje cell protein 4 GTP binding protein 1 ESTs dendritic cell protein EST YDD19 protein EST	leukocyte immunoglobulin-iike receptor, subtarniiy B (with TM and I'IM domains), member 2 LILRB2 ESTS ESTS ESTS syndecan 1 SDC1 crystallin, gamma A CRYGA
Hs.98675 Hs.21264 Hs.268771 Hs.79428 Hs.35152	Hs.35135 Hs.34526 Hs.9908 Hs.50151 Hs.173958 Hs.27596 Hs.27596 Hs.15403	Hs.155218 Hs.71243 Hs.80296 Hs.227576 Hs.128629 Hs.69469 Hs.207246 Hs.207246	Hs.22405 Hs.244417 Hs.270962 Hs.12923 Hs.13254 Hs.82109
AA432295 Hs. 98675 AA043131 Hs. 21264 H08541 Hs. 21480 AA063521 Hs. 79428 R90288 Hs. 33152	8 8 8	AA464198 Hs.88245 AA132281 Hs.59637 AA422966 Hs.80296 AA022413 Hs.47140 M74247 Hs.118168 R53063 Hs.25991 AA101348 Hs.68469 NGA024 Hs.448913 NG7041 Hs.44918	H54023 Hs.22405 H68977 Hs.108815 H67660 Hs.10044 1160310 Hs.12923 H418065 Hs.13254 AAQ74511 Hs.82109 AA780079 Hs.122566
781474 486171 45531 359982 201207	201207 196115 73531 321834 219847 361379 154138 613173 428697	810395 502199 788566 366484 296889 40228 563634 293975 296010	202897 41133 211227 22194 50541 525926 1033708
GF202 GF203 GF201 GF200	GF200 GF200 GF201 GF203 GF203 GF200 GF200	GF201 GF204 GF200 GF201 GF202 GF202 GF202 GF200	GF201 GF204 GF201 GF204 GF204 GF201 GF201

-2.0163861	-1.2989571	1.16384317	1.18119405		1.0334025	1 1000110	1.12204414				002300	-1.303099	-1.8309639	,	0882880-1-	
960.1844 960.1243	959.8997	959.387	959.2706		959.2072	959.0765	908.0171			0	958.7996	930.4943	958.3198	0007:000	808.127.5	957.9975
TNFSF13B	GADD45B	SIGMA1B			9	H INZ									DKFZP564B0769	
tumor necrosis factor (ligand) superfamily, member 13b ESTs	growth arrest and DNA- damage-inducible, beta	adaptor-related protein complex 1, sigma 2 subunit	ESTs	Homo sapiens chromosome X map Vp1 1.23 L-type calcium channel alpha-1 subunit (CACNAT F) gene, complete cds: HSP27 pseudogene, complete sequence; and JM1 protein, JM2 protein, and	Hb2E genes, complete cds	reticulon 2	ESTS Homo sapiens cDNA	FLJ11211 fis, clone PLACE1007955, highly similar	to Homo sapiens cyclin-D	binding Myb-like protein	mRNA	ESIS	ESTS	5018	DKF.ZP564B0.769 protein ESTs, Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII	[H.sapiens]
Hs.270737 Hs.118947	Hs.278579	Hs.40368	Hs.29467		Hs.227583	Hs.3803	Hs.48996				Hs.5671	Hs.80624	Hs.24122	US.190513	Hs.18368	Hs.143805
AA166695 Hs.72622 R38099 Hs.118947	AA404666 Hs.110280	AA112149 HS.17625 AA449832 Hs.125154	AA479060 Hs.29467		AA018437 Hs.108602	H06249 Hs.3803	AA489061 Hs.48996				W48838 Hs.74934	0	R26859 Hs.24122	Ŋ	T49635 Hs.109755	N32155 Hs.100513
593690 23427	725109	530403	754040		362378	44287	824769				325015	784162	133358	884660	67741	272063
GF202 GF204	GF203	GF203	GF203		GF203	GF202	GF203				GF201	GF202	GF203	GF204	GF202	GF201

COSSITION, CONCENT

APPENDIX A

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Contradiction of the contract of the management of the contract of the contrac

-1,6371584	1.09571873	-1.5203678	1.10560457	-1.0527335	-1.6319651		1.30282249
957.8447	957,4924	957.2621	956.8489	956.1443 956.0256 955.9553 955.9549	955.8019 955.6402 955.4178	955.2696	955.2052
GPA33				8 JM5 DNASE1L1	g COPEB		B3GAL14 CDC14A
ESTS, Highly similar to FH1/FH2 domain-containing protein FH0S [H,sapiens] glycoprotein A33 (transmembrane) Homo sapiens cDNA	FLJ10700 fis, clone NT2RP3000665 Homo sapiens cDNA FLJ20128 fis, clone COL06181	ESTs Homo sapiens cDNA FLJ1181 fis, clone PLACE1007460	ESTs ESTs Homo sapiens cDNA	FLJ20444 fis, clone KAT05128 JM5 protein deoxyribonuclease I-like 1 FST	core promoter element binding protein ESTs	myeloperoxidase UDP-Gal:betaGlcNAc beta 1,3- galactosyltransferase,	polypeptide 4 CDC14 (cell division cycle 14, S. cerevisiae) homolog A
E F Hs.95231 p Hs.143131 (t	F Hs.186571 N H F Hs.6649 C	# N		Hs.273433 F Hs.21753 J Hs.77091 d	e	,	Hs.21495 p
R86847 Hs. 95231 AA055862 Hs. 63225	AA434161 Hs.111713 R10823 Hs.6649	AA481492 Hs.33074 R64048 Hs.28472		W89071 Hs.90914 AA644215 Hs.21753 R77919 Hs.77091 R37377 Hs. 21358	46	AA703058 Hs.1817	AA987754 Hs.21495 AA283949 Hs.65993
165828 R86 510542 AAC	770595 AA ⁴		_ `	417561 W8 845496 AA(145383 R77	(0 m m		1601661 AAS
GF203 GF200	GF201	GF203 GF200	GF202 GF204	GF201 GF203 GF201	GF201 GF202	GF201	GF204 GF203

1.23720696	-1.1470694 -1.0108864 1.00923255	1.2787771	1.36833124 1.81795751 -1.343356 -1.0459055	1.23614434 1.46513098 1.00476287	-2.112634 -1.5656016 1.32955398	-1.423482 1.51060882 1.51060882
954.9617 954.947	953.3264 952.9761 952.8165	952.7789 952.6804 952.5549 952.0255	951.7038 950.8245 950.799 950.7783	950.4673 949.9628 949.772	949.0683 948.9122 948.7075	948.6537 948.3896 948.3896
	LOC51629	KIAA0781 CBS KIAA0824		GOLGA4 FPN1	RABL2B	CANX
ESTs, Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens] ESTs	ESTs, Highly similar to HGC- 32 [R.norvegicus] CGI-69 protein ESTs	ESTs, Highly similar to LECT2 precursor [H.sapiens] KIAA0781 protein cystathionine-beta-synthase KIAA0824 protein	ESTS ESTS ESTS ESTS ESTS	golgi autoantigen, golgin subfamily a, 4 ESTs ferroportin 1; iron regulated gene 1	ESIS, weakly similar to iii. ALU CLASS B WARNING ENTRY III! [H.sapiens] RAB, member of RAS oncogene family-like 2B	ESTs, Weakly similar to 110 KD CELL MEMBRANE GLYCOPROTEIN [H.sapiens] calnexin calnexin
Hs.106845 Hs.26039	Hs.76640 Hs.237924 Hs.14148	Hs.186809 Hs.42676 Hs.84152 Hs.123654	Hs.99308 Hs.177228 Hs.65300 Hs.99248	Hs.183773 Hs.9961 Hs.5944	Hs.37858 Hs.145409 Hs.46941	Hs.55289 Hs.155560 Hs.155560
AA074079 Hs.106845 R53446 Hs.26039	AA192553 Hs.101337 AA485441 Hs.7842 R99773 Hs.14148	~ ~ ~	AA453256 Hs. 99308 R31107 Hs. 24383 AA707171 Hs. 114154 AA453990 Hs. 99248	AA460981 Hs.77335 N91588 Hs.9961 AA011593 Hs.60532	H60696 Hs.37858 AA428182 Hs.100478 N49392 Hs.46941	AA781027 Hs.55289 AA126356 Hs.79933 AA126356 Hs.75076
531459 40038	628529 811062 200934	433544 417566 769857 1584243	795339 134256 451397 795248	796137 303068 429678	208985 773556 277634	1240561 511521 511521
GF202 GF201	GF200 GF203 GF200	GF203 GF201 GF201	GF202 GF200 GF203 GF203	GF200 GF203 GF202	GF203 GF202 GF202	GF203 GF200 GF200

Westbrook et al.	k et al.			Frith the table star that the Australian of Appleadix A	danis Band den und ber den begen begen ber den	Atty	Atty Docket No. 2172
GF204 GF202 GF201	898089 262763 196579	AA598799 Hs.71109 H99490 Hs.42696 R91689 Hs.101911	Hs.71109 Hs.42696 Hs.107845	Homo sapiens mRNA for KIAA1229 protein, partial cds ESTs ESTs		948.3673 948.269 948.1371	1,2801176
GF200	771206	9	Hs.74598	polymerase (DNA directed), delta 2, regulatory subunit (50kD)	POLD2	947.8011	1.24837677
GF201 GF201 GF203	357892 276515 811738	W99328 Hs.110945 N39099 Hs.44944 AA463256 Hs.99588	Hs.110945 Hs.44944 Hs.165538	ESTs Weakly similar to notch4 [H.sapiens] ESTs		947.7194 947.6268 947.3577	1.13364492
GF203 GF201	814702	66	Hs.237825 Hs.46580	signal recognition particle 72kD ESTs	SRP72	947.2816	-1.8379762
GF202 GF202 GF204	48454 53122 1049147	H15040 Hs.21286 R15891 Hs.12581 AA620987 Hs.120872	Hs.12581 Hs.12581 Hs.190268	ES1s Human (clone CTG-A4) mRNA sequence ESTs		947.1924 947.0093 946.961	-1.365/394
GF202 GF200 GF200	1031748 210575 45999	AA609599 Hs.112730 H65066 Hs.2288 H09317 Hs.30917	Hs.178749 Hs.2288 Hs.30917	synovial sarooma, X breakpoint 3 visinin-like 1 EST	SSX3 VSNL1	946.9065 946.7362 946.5275	-1.2452887 1.08928737 -1.3982919
GF202 GF202 GF200	730872 418356 360079	92 98	Hs.59368 Hs.76228	ESTS ESTS amplified in osteosarcoma ESTs, Weakly similar to YCR024c, len.492	6·SO	946.4222 946.351 945.9356	1.21497865 1.1047017 1.16861668
GF204 GF204 GF200	378516 1505294 183337	AA775685 Hs.15502 AA905838 Hs.112629 H42679 Hs.77522	Hs.15502 Hs.8154 Hs.77522	[S.cerevisiae] ESTs major histocompatibility complex, class II, DM alpha	HLA-DMA	945.2659 945.2659 945.0752	1.0565445
GF202 GF204	365348 1461651	AA025166 Hs.61256 AA885316 Hs.125637	Hs.99969 Hs.156992	fusion, derived from t(12;16) malignant liposarcoma ESTs retinoblastoma-binding protein	FUS	944.7559 944.3226	1.13749485
GF200	795888	AA460756 Hs.76272	Hs.76272	2	RBBP2	944.0655	1.19692865

-1.3002591 1.47545565 1.16531707 1.16733752 1.0113984	-1.0083277	1.14771117		-1.3829416 -2.1144999		1.06942092
943.7964 943.7921 943.735 943.631 943.6165	943.5456 943.5132 943.3623	942.7206	942.7011	942.4845	942.4026	942.3303
C2ORF3 NDN	CDSL	TBXAS1	ATP5G2	САСУВР	ATP5G1	
chromosome 2 open reading frame 3 ESTs ESTs ESTs ESTs	F 0	(platelet, cytocrirothe F430, subfamily V) ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9),		_	[M.musculus] ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide	ESTs, Highly similar to hypothetical protein SBBI31 [H.sapiens]
Hs.184175 Hs.227752 Hs.271924 Hs.117815 Hs.50130	Hs.52002 Hs.169829	Hs.2001	Hs.53929	Hs.27258 Hs.40608	Hs.13692 Hs.155433	Hs.184668
AA428242 Hs.98545 N76133 Hs.50708 AA486277 Hs.104034 H38572 Hs.117815 B5158 Hs.61730	.¥ ₹	R76436 Hs.2001	AA455126 Hs.89399		AA412217 Hs.13692	AA191479 Hs.69564
773579 299459 842840 191950	289919 454333 795499	143443	809876	298098 298098 219711	731433	627248
GF202 GF202 GF203 GF203	GF201 GF203 GF201	GF200	GF201	GF203	GF201	GF202

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1.28056451	1.51486227	1.06650946	-1.1924508	1.38823369	1001001	2.21426786
942.258 941.8475	941.5737 941.5695	941.425 940.849	940.7374	940.306	940.2767	940.1917 940.1871
		TRAP95 TPM1 LSM1		HPRP4P CSNK1A1	i	DEK KIAA0414
Human DNA sequence from clone RP3-460.8 on chromosome 2041.12.11.23 Contains part of a gene similar to NDRG1 (N-myc downstream regulated), ESTs, STSs and GSSs. ESTs. Human DNA sequence from clone 718.27 on chromosome 2040.33.1-13.33. Contains part of a gene for a novel protein, the PCK1 gene for a novel protein, the PCK1 gene for soluble phosphoenolopytruxte.	S1S, GSSs and a putative CpG island ESTs thyroid hormone receptor-	tropomyosin 1 (alpha) Lsm1 protein ESTs, Weakly similar to	[H.saplens] ESTs	PRP4/STK/WD splicing factor HPRP4P casein kinase 1, alpha 1 CSNK1A Homo sapiens cDNA FLJ20062 fis, clone	COL01508	DEK oncogene (DNA binding) DEK KIAA0414 protein KIAA
Hs. 240615 Hs. 182299	Hs.83883 Hs.18140	Hs.31659 Hs.77899 Hs.111783	Hs.126265 Hs.126754	Hs.8551 Hs.144477	Hs.257486	Hs.110713 Hs.127649
AA207127 Hs. 4815 AA045673 Hs. 107631	AA487031 Hs.70732 T97809 Hs.18140	AA431181 Hs.24441 AA490210 Hs.23271 AA628430 Hs.111783	R10885 Hs.126265 AA126456 Hs.126754	AA703250 Hs.8551 AA625758 Hs.52195	T59668 Hs.10613	R25377 Hs.84874 AA465708 Hs.127649
648011 AA. 489476 AA.	841141 AA 121543 T9		129128 R1 565025 AA	436155 AA 745402 AA	76196 TS	133136 R2 814976 AA
GF203 GF201	GF202 GF200	GF201 GF203 GF201	GF203 GF202	GF203 GF201	GF201	GF202 GF203

Atty Docket No. 21 /26/		-2.4450559				1.04677309		-1.1433949		1.17272156	-2.0482623	-1.8954187			-1.2450377			1.28898503	-1.3608938	1.29309516			-1.151342	1.88088742		-1.5976185	-2.4468316	4 00601303	20091302	1.16729483	
Atty D	940.1333	939.6873	7000	939.3237		939.1745	939.1094	938.7606		938.7245	938.5656	938.1075			938.0054			937.979	937.8267	937.7689			937.7164	937.7057	937.6871	937.4497	937.2911	007 0440	8112.108	937.0004	936.899
						SOX3									FACTP140															DKFZP434A0225	
APPENDIX A	STS	ESTs	EST, Weakly similar to	butative prod [n.sapleris] ESTs	SRY (sex determining region		ESTs	ESTs	Homo sapiens clone 23904	mRNA sequence	EST	ESTs	chromatin-specific	ranscription elongation factor,	40 kDa subunit	ESTs, Weakly similar to cAMP	nducible 2 protein	M.musculus]	ESTs	ESTs	ESTs, Weakly similar to	Similarity to B.subtilis YQJC	protein [C.elegans]	ESTs	ESTs	ESTs	ESTs	Homo sapiens mRNA for	NAA 1226 protein, partial cus	nypothetical protein ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	H.sapiens]
	Hs.15386 E			Hs 46473 F		Hs.157429 Y	Hs.269479 E	Hs.69662 E	_	Hs.250175 nr	Hs.186573 E	Hs.221597 E	O	4	Hs.14963	ш	_	Hs.21893		Hs.180037 E	ш			_		Hs.126485 E				Hs.83293 h E E A	Hs.201589
	H18472 Hs.15386	AA609594 Hs.112729	000	AA481536 HS.105180 N62952 Hs 46473		4A775423 Hs.124906	Hs.47063	AA461307 Hs.69662		Hs.124277	Hs.47425	AA707858 Hs.120982			AA488340 Hs.115764			AA460258 Hs.21893	W56582 Hs.25144	AA682558 Hs.117265				, Hs.47558	4A115575 Hs.114914	AA143070 Hs.71749	AA486440 Hs.77207		7971C'SH	AA463263 Hs.83293	Hs.97346
	H18472			AA48150 N62952		AA7754	N50454	AA4613		H02231	N52189	AA7078			AA4883			AA4602	W5658	AA6825			N54296	N52857	AA115	AA1430	AA4864	0000	HZZ340	AA4632	H16595
k et al.	51218	1031736	000	815263		878129	280671	796303		151055	284269	413047			842992			796527	340745	431276			244684	283590	491447	588960	842915	0	130916	811729	49266
Westbrook et al.	GF201	GF202	10010	GF204	; ;	GF203	GF201	GF202		GF203	GF202	GF203			GF202			GF202	GF200	GF203			GF200	GF202	GF204	GF202	GF202	C	GFZ00	GF203	GF204

	1.08884381 -1.0873434	1.29785028	-2.2645665	-1.566638 -1.1727449 1.30212371	
936.7129	936.6866 936.6625	936.4274 936.4987	936.4344 936.3155	936.0497 935.9977 935.8969 935.8881 935.8494	
GARP	TOR1B	МАОА			
glycoprotein A repetitions predominant torsin family 1, member B	•	A to the t	replication factors, p ESTs CCAAT transcription binding	[H.saplens] ESTs ESTs, Weakly similar to serfolin [R.norvegicus] ESTs ESTs	
Hs.151641	Hs.252682 Hs.48642	Hs.103816 Hs.183109	Hs.101742 Hs.46826	Hs.269111 Hs.91192 Hs.32425 Hs.269293	
AA122287 Hs.32864	AA040879 Hs.5091 AA412429 Hs.48642	AA011096 Hs.1782 AA011096 Hs.1782	H18934 Hs.101742 N59226 Hs.46826	AA400317 Hs.19980 N63490 Hs.48791 H60691 Hs.108210 AA48889 Hs.32425 AA206915 Hs.86316	
490819	486076 731423	359661 359661	51604 289437	743353 278075 208986 824886 648025	
GF201	GF203	GF202 GF201	GF202 GF201	GF202 GF204 GF201 GF203 GF203	,

1.04178115	1.66728899 1.06821004	-2.3836006 -1.2268635 1.99497994	-1.258011	-1.1160697	-1.0575541	1.36759281	-1.6407943
935.6011 935.5958 935.391	935.3683 935.1719	934.8628 934.8353 934.3566 934.3305	934.249 934.1305	933.9692	933.9025 933.5516 933.5164	933.4861 933.3127 933.2221	933.0991
	ZNF131	SPARC KIAA0386 STAG1	SHM300		WARS MSE55	SRP9	AKAP2
Homo sapiens mRNA; cDNA DKFZp434P0235 (from clone DKFZp434P0235) ESTs	bhZ-10) ESTs secreted protein, acidic,	n) rrto is]	protein Htf9C [M.musculus] RNA binding protein Homo sapiens cDNA	FLJ10835 ffs, clone NT2RP4001210 Homo sapiens cDNA FLJ20104 ffs, clone	COL04806 tryptophanyl-tRNA synthetase serum constituent protein	article 9kD	FLJ I 1004 lis, cione PLACE1002941 A kinase (PRKA) anchor protein 2
Hs.34348 (18.26135 Hs.44976	Hs.78743 p	Hs.111779 (Hs.268112 (Hs.101359 Hs.25037	Hs.63609 F		Hs.172572 (Hs.82030 t Hs.148101	Hs.75975 Hs.243662 Hs.193580	Hs.125139 Hs.42322
AA16944 Hs.42595 H17785 Hs.26135 N39233 Hs.44976	AA449429 Hs.111379 R08938 Hs.112313	H95960 Hs.111779 AA758257 Hs.121599 H57941 Hs.101359 R36160 Hs.25037	R96880 Hs.63609 AA776677 Hs.124737	N51083 Hs.27021	AA416684 Hs.57770 AA133278 Hs.12112 H15910 Hs.64098	R43360 Hs.75975 N63953 Hs.31991 AA782380 Hs.130762	AA437219 Hs.125139 H99415 Hs.42322
594031 50037 276972	785572 127931	250654 396857 205090 137245	200302 970532	281960	731270 502198 159462	32257 289421 857442	757421 262695
GF202 GF201 GF203	GF202 GF202	GF201 GF203 GF203 GF203	GF200 GF204	GF203	GF202 GF204 GF203	GF203 GF201 GF203	GF204 GF203

09897798.070201

		1.45284688	-1.3256532			1400040	-1.5139649	-1.3275153					-1.0688623			-1.320812			1.25996075			1.01738552
932.9839 932.9599		932.6135	932.5876	932.4426		170 000	932.345	932.1987			931.9929		931.975		931.7167	931.5097		931.3249	930.9913	930.9566		930.7791
NDUFS2		GALGT				L	MOF									RMP		SKIV2L				GPR37
NADH dehydrogenase (ubiquinone) Fe-S protein 2 (49kD) (NADH-coenzyme Q reductase) ESTs	UDP-N-acetyl-alpha-D- galactosamine:(N- acetylneuraminyl)- galactosylglucosylceramide N- acetylglactosaminyttransferas	e (GalNAc-T) ESTs, Highly similar to terra	[M.musculus]	ESTs	member of MYST family	nistone acetyl transferases,	homolog of Drosophila MOF	ESTs	Human EST clone 251800	mariner transposon Hsmar1	sedneuce	ESTs, Weakly similar to	K01H12.1 [C.elegans]	ESTs, Weakly similar to ZINC FINGER PROTEIN 177	[H.sapiens]	RPB5-mediating protein	superkiller viralicidic activity 2	(S. cerevisiae homolog)-like	ESTs	ESTs	G protein-coupled receptor 37 (endothelin receptor type B-	like)
Hs.173611 Hs.195161		Hs.159481	Hs.59506	Hs.33533		:	Hs.42343	Hs.53031			Hs.42192		Hs.264915		Hs.85505	Hs.7943		Hs.89864	Hs.112929	Hs.272056		Hs.27747
Hs.96310 Hs.44147		Hs.573	Hs.59506	AA022496 Hs.33533			AA491297 Hs.22767	Hs.113922			Hs.42192		AA460720 Hs.13275		AA993513 Hs.85505	Hs.7943		H51554 Hs.89864	AA620973 Hs.112929	AA678078 Hs.119351		Hs.27747
H57306 N30069		R05336	W93861	AA022496			AA491297	R91583			N72213		AA460720		AA993513	AA450020 Hs.7943		H51554	AA620973	AA678078		R52852
204740 258666		125092	357465	364352			824647	196569			291247		796756		1623128	788309		179776	1049131	430623		41658
GF201 GF201		GF200	GF202	GF201			GF203	GF203			GF201		GF202		GF204	GF203		GF201	GF202	GF204		GF200

-1.2251591		-1.9519913	-1.3756185		-1.0661982		-1.2217406	-1.290084		1.23943109	-1.2843387
930.7784	929.7402 929.7286 929.3354	929.0149 928.9685	928.6509 928.6509 928.0731	927.7756	927.2769	927.2014	927.0949	927.0321 926.8788 926.7173 926.3412	926.0588	925.8096	925.6164
OAT	VDAC3 CTRL		CD1D			TCF6L1	PSMA4	NCF4	VAV3	KIAA0871	DKFZP586I1023
ornithine aminotransferase (gyrate atrophy) voltage-dependent anion	channel 3 chymotrypsin-like protease ESTs	ESTs ESTs	ES1S CD1D antigen, d polypeptide ESTs Homo sapiens mRNA; cDNA	DKFZp564E2282 (from clone DKFZp564E2282) Human clone 23722 mRNA	sequence transcription factor 6-like 1 (mitochondrial transcription	factor 1-like) proteasome (prosome,	type, 4 neutrophil cytosolic factor 4	(40kD) EST ESTs ESTs	vav 3 oncogene ADP-ribosylation factor-related	KIAA0871 protein ESTs	DKFZP586I1023 protein
Hs.75485	Hs.7381 Hs.150601 Hs.190384	Hs.185043 Hs.107988	HS.266619 HS.1799 HS.33433	Hs.109694	Hs.81360	Hs.75133	Hs.251531	Hs.196352 Hs.116199 Hs.271630 Hs.109154	Hs.267659	Hs.7972 Hs.229726	Hs.111515
AA446819 Hs.75485	AA460728 Hs.7381 AA026626 Hs.2596 AA706671 Hs.122212	AA100293 Hs.110737 R97798 Hs.107988	183864 HS.15051 AA451684 HS.1799 R96525 HS.33433	N63478 Hs.82721	N73130 Hs.81360	AA150777 Hs.95863	T96083 Hs.85513	AA465389 Hs.2870 AA628129 Hs.116199 H38159 Hs.107686 AA504125 Hs.109154	W91879 Hs.37331	AA410256 Hs.40850 AA700022 Hs.117363	T59873 Hs.105198
783696	796759 366541 1240057	511060 200151	789314 789314 199641	278053	248039	504826	120881	814123 1055721 191538 825218	415229 415229	753361 436047	76252
GF200	GF201 GF201 GF204	GF202 GF201	GF201 GF200 GF200	GF201	GF200	GF201	GF200	GF203 GF204 GF201	GF201	GF203 GF204	GF203

-1.4220933 -1.6707818 1.13838503	1.36133289	1.15970167	1.25426614	0101010	1.07840849	-1.2492212	7007007	-1.1631394	-1.1725214	-1.4882764		1.29774083	1.67367185			1.19038284				-1,0358566	1.08946999
925.4647 925.4006 924.7623	924.4003 924.302	924.2508 924.2208	924.2072	924.0564	924.0541 923.9736	923.8232	923.7263	923.6932	923.4592	923.4568		923.17	923.0235	922.872	922.6026	922.6014	921.8242	921.6995	921.6864	921,421	921.2732
	UST	77704417	NIAAU/4/		APOE													TPM1	KIAA0575		ARHI
ESTs, Weakly similar to alternatively spliced product using exon 13A [H.sapiens] ESTs	ESTs uronyl 2-sulfotransferase	ESTs ESTs	KIAAU/4/ protein ESTs	ESTs	ESTS apolipoprotein E	ESTs	ESTs	ESIS	ESTs	ESTs	Homo sapiens J domain	(JDP1) mRNA, complete cds	EST	ESTs	ESTs	ESTs	ESTs	tropomyosin 1 (alpha)	KIAA0575 gene product	ESTs	ras nomolog gene tamily, member I
Hs.86032 Hs.97694 Hs.191537	Hs.35699 Hs.134015	Hs.59554 Hs.269066	Hs.268682	Hs.30901	Hs.125554 Hs.169401	Hs.54957	Hs.37464	Hs.44628 Hs.46839	Hs.48480	Hs.98942		Hs.260720	Hs.62003	Hs.234058	Hs.31330	Hs.88495	Hs.107102	Hs.77899	Hs.193914	Hs.114076	Hs.194695
N35341 Hs.34567 AA399640 Hs.97694 AA278849 Hs.88522		W94591 Hs.59554 N39449 Hs.45009	AA454699 HS.8309 R19152 Hs.119690	H09143 Hs.30901	AA884157 Hs.125554 AA478589 Hs.100455	6	_	N34824 Hs.44628 N48271 Hs.46839	60	AA437213 Hs.98942		T95268 Hs.16940	AA040591 Hs.62003		H28985 Hs.31330	AA278766 Hs.88495	R28188 Hs.107102	R87122 Hs.34100	N75569 Hs.25680	AA701893 Hs.114076	W72033 Hs.58153
272018 729948 703544	200396 505335	358046 276920	129868	46506	1468456 753610	754532	232955	276450	565734	757430		120138	376164	267135	49922	703736	134658	197374	299332	434799	345680
GF202 GF202 GF203	GF203 GF201	GF202 GF201	GF201 GF202	GF201	GF204 GF200	GF203	GF204	GF202	GF202	GF202		GF200	GF202	GF201	GF201	GF203	GF204	GF201	GF201	GF203	GF202

-2.2813747 -1.3468077 -2.4843082		-1.5384789	2.20010056 1.5862522	1.10005652 -2.3840259 -2.0965588 -1.0734549
921.1981 920.8297 920.6897 920.6068	920.5387 920.4799 920.1099 920.0845	919.9587 919.4584 919.0981	918.7006 918.6111 918.3778 918.0397	917,4951 917,4703 917,3819 917,2879 916,3465
. w	o :=	CLN2 SSBP2	D MDH2 KIAA0100	УDD19
Homo sapiens mRNA; cDNA DKFZp434C1915 (from clone DKFZp434C1915); partial cds EST ESTs ESTs ESTs Controller similar to controller and controller controlle	KD SUBUNIT (H.sapiens) ESTS Homo sapiens immunoglobulin lambda gene locus DNA, clone228A10 ESTS	ceroid-lipotuscinosis, neuronal 2, late infantilio (Jansky- Bielschowsky disease) ESTs single-stranded-DNA-binding protein	malate dehydrogenase 2, NAD (mitochondrial) ESTs ESTs ESTs ESTs	EST YDD19 protein EST ESTs ESTs enoyl-Coenzyme A, hydratase/3-hydroxyaoyl
Hs. 46531 Hs. 63182 Hs. 13306 Hs. 21820	Hs.169715 Hs.78457 Hs.43834 Hs.269522 Hs.107537	Hs.20478 Hs.105738 Hs.169833	Hs.111076 Hs.126245 Hs.22123 Hs.268971 Hs.151761	Hs.58966 Hs.25615 Hs.112609 Hs.31685 Hs.31585
AA706788 Hs.46531 AA055936 Hs.63182 H10028 Hs.13306 R61231 Hs.21820	AA620672 Hs.54676 AA035452 Hs.78457 N28665 Hs.43834 AA677671 Hs.119463 N59387 Hs.107537	AA664004 Hs.20478 AA873049 Hs.105738 AA451851 Hs.21815	രവവ	W86892 Rs.58966 AA628112 Hs.56286 AA608833 Hs.112609 AA882780 Hs.118393 N57499 Hs.31685 R02373 Hs.1531
451753 377535 46930 42660	1049174 471729 269292 460460 246228	855385 1476048 786283	1636908 1472329 1416099 450330 33827	416557 1055705 1048617 450410 277357 124597
GF203 GF202 GF201 GF203	GF204 GF204 GF201 GF201 GF201	GF201 GF204 GF203	GF204 GF204 GF203 GF203	GF202 GF203 GF203 GF203 GF203 GF200

	4 0020600	1.29/2639	-1.9755989		-1.8226141		-1.2182157					-2.248535	1.06085428	-1.1230343										-1.8606117			-1.1585268	-1.214056			1.13203709
•	916.8692	916.7943	916.7319		916.6954	916.5612	916.3771	916.0627	915.957	915.6623		915.6066	915.5749	915.2719							915.2296	914.9966	914.8652	914.8303			914.766	914.7039		914.441	914.2224
	FOCIET	MHCZIA									9		POX											KIAA0700				¥		PILR(BETA)	CUGBP2
APPENDIX A	ESTs	MHC class II transactivator	ESTs	Homo sapiens mining for	KIAA1435 protein, partial cds	ESTs	ESTs	ESTs	ESTs	EST	ESTs, Weakly similar to DY3.6	[C.elegans]	lysyl oxidase	EST	Homo sapiens cDNA	FLJ10982 fis, clone	PLACE1001692, moderately	similar to S-ACYL FATTY	ACID SYNTHASE	THIOESTERASE, MEDIUM	CHAIN (EC 3.1.2.14)	ESTs	ESTs	KIAA0700 protein	Homo sapiens cDNA	FLJ20284 fis, clone	HEP04227	hexokinase 1	paired immunoglobin-like	receptor beta CUG triplet repeat.RNA-	binding protein 2
	Hs.58452	Hs.3076	Hs.31444		Hs.44743	Hs.271996	Hs.24723	Hs.271641	Hs.10490	Hs.116130		Hs.61661	Hs.102267	Hs.208288							Hs.24309	Hs.39542	Hs.12387	Hs.13999			Hs.191228	Hs.118625		Hs.138661	Hs.211610
	W80447 Hs.58452	Ö	H16772 Hs.31444		AA450338 Hs.44743	T88816 Hs.15479	H97851 Hs.24723	H67707 Hs.38486	H99851 Hs.108841	AA626157 Hs.116130		AA256464 Hs.61456	H99075 Hs.108488	H77641 Hs.39787							AA470066 Hs.24309	W72466 Hs.39542	R59200 Hs.12387	R38214 Hs.124949			AA620802 Hs.112908	AA485271 Hs.3283		AA007560 Hs.58529	AA856739 Hs.82321
	415473	824547	50227		785521	109952	251727	210803	263906	745242		682072	262060	214233							730353	345416	41793	137369			1055520	840158		429044	1371759
	GF201	GF200	GF202		GF203	GF201	GF203	GF201	GF201	GF204		GF203	GF202	GF202							GF201	GF201	GF201	GF203			GF202	GF200		GF201	GF203

Homo sapiens cDNA

	1.0076227	1.21285254			-1.1644443		0000107	-1.4255238	-1.3967751							1.64652597		1.61336266	-1.1588005		1.41926252								1.19420527		
	914.186	914.0007		913.6412	913.508		040 0000	912,9288	912.8932			912.843	912.6032			912.0081		911.9793	911.7164		911.673			911.5261					911.5007	911.2689	
		FLJ20498		CASP6												PSMF1								TRAP150						FBP2	
FLJ11307 fis, clone PLACE1010053, highly similar to M.musculus Spnr mRNA for	RNA binding protein	hypothetical protein	caspase 6, apoptosis-related	cysteine protease	ESTs	Homo sapiens mRNA; cDNA	District Constitution of the constitution of t	UKFZp434FU/35)	EST	Homo sapiens mRNA; cDNA	DKFZp727C191 (from clone	DKFZp727C191)	ESTs	proteasome (prosome,	macropain) inhibitor subunit 1	(PI31)	ESTs, Highly similar to	HSPC007 [H.sapiens]	ESTs	ESTs, Weakly similar to line-1	protein ORF2 [H.sapiens]	thyroid hormone receptor-	associated protein, 150 kDa	subunit	Homo sapiens cDNA	FLJ20350 fis, clone	HEP13972, highly similar to	Z184_HUMAN ZINC FINGER	PROTEIN 184	fructose-1,6-bisphosphatase 2 FBP2	
	Hs.8215	Hs.97925		Hs.3280	Hs.15330		007100	HS.2/192	Hs.94488			Hs.41181	Hs.138717			Hs.75925		Hs.55097	Hs.6973		Hs.268911			Hs.108319					Hs.59053	Hs.61255	
	Hs.8215	Hs.80889		AA626710 Hs.118148	AA416697 Hs.15330			Hs.166/9	Hs.94488			AA621408 Hs.31839	Hs.46993			AA873845 Hs.75925		AA427901 Hs.55097	Hs.6973		Hs.15981			Hs.42619					W87749 Hs.59053	AA025150 Hs.61255	
	N53133	N34429		AA626710	AA416697			N/6944	N95041			AA621408	N49952			AA873845		AA427901	R15832		H51825			W85832					W87749	AA025150	
	246620	277390		745143	731258			246074	306621			1033388	282694			1473194		773483	53110		194006			416010					417229	365326	
	GF200	GF203		GF204	GF202			GF200	GF202			GF204	GF201			GF203		GF202	GF202		GF200			GF201					GF202	GF201	

1.11175646	1.2312505		1.25175908			-1.0219704	1.01127884	-1.4346993										-1.1675547			-1.0544913		-1.0989864				1.24318278			-1.5089796	
910.5515 910.3314	910.2936		910.2608	910.1771		910.0838	909.9219	909.7485		909.702					909.4895			909.1558	908.7029	908.6836	908.167	908.0198	962.706				907.522			907.3373	907.2206
				DKFZP434F195			LF3			P2RX5										CIN85											
ESTs EST	EST	Homo sapiens cDNA FLJ10649 fis, clone NT2RP2005835, weakly	similar to SHP1 PROTEIN	DKFZP434F195 protein	ESTs, Weakly similar to	putative [C.elegans] interleukin enhancer binding	factor 3, 90kD	EST	purinergic receptor P2X, ligand	gated ion channel, 5	Homo sapiens cDNA	FLJ20350 fis, clone	HEP13972, highly similar to	Z184_HUMAN ZINC FINGER	PROTEIN 184	Homo sapiens mRNA; cDNA	DKFZp434B0610 (from clone	DKFZp434B0610); partial cds	ESTs	c-Cbl-interacting protein	ESTs	ESTs	EST	Human protein immuno-	reactive with anti-PTH	polyclonal antibodies mRNA,	partial cds	Homo sapiens mRNA,	chromosome 1 specific	transcript KIAA0493	ESTs
Hs.72308 Hs.125687	Hs.46768		Hs.12865	Hs.33037		Hs.28393	Hs.256583	Hs.237686		Hs.77807					Hs.59053			Hs.112589	Hs.122574	Hs.153260	Hs.48787	Hs.118498	Hs.229119				Hs.44566			Hs.251108	Hs.187527
AA159356 Hs.72308 AA884827 Hs.125687	N47858 Hs.46768		AA456303 Hs.12865	H50186 Hs.33037		AA434400 Hs.28393	AA449048 Hs.101664	AA017066 Hs.60742		AA044267 Hs.77807					AA151111 Hs.85007			AA608775 Hs.112589	AA776747 Hs.122574	AA989257 Hs.109271	463436 Hs.48787	AA629039 Hs.118498	N58276 Hs.48190				AA088258 Hs.44566			R61518 Hs.22839	/88528 Hs.16176
593026 A 1468129 A			813161 A	179129 H		770869 A	785816 A	361175 A		486678 A					505183 A			1030649 Av	1292892 Av	1604005 Av	_	744001 A	247862 N				511091 A				417748 W
GF202 GF204	GF202		GF202	GF204		GF203	GF200	GF202		GF201					GF201			GF202	GF204	GF204	GF202	GF204	GF202				GF202			GF202	GF201

Westbrook et al	k et al.			APPENDIX A		Atty	Atty Docket No. 2172
GF201	344274	W73811 Hs.108316	Hs.123654	KIAA0824 protein	KIAA0824	906.9015	
GF204	1507359	AA905113 Hs.19814	Hs.19814	ESTs		906.8485	
GF202	767312	AA418524 Hs.104519	Hs.104519	phospholipase D2	PLD2	906.3167	-1.35356
GF201	278171	N63536 Hs.35839	Hs.29263	ESTs		906.2809	
GF202	796330		Hs.29863	ESTs		906.154	-2.0420773
GF202	344156	W69995 Hs.94808	Hs.94808	ESTs		905.5841	-1.2251084
GF200	240367	H89996 Hs.57419	Hs.57419	transcriptional repressor	CTCF	905.197	-1.0015865
GF200	813635	AA453673 Hs.77600	Hs.77600	arginase, liver	ARG1	904.6103	1.13550766
				chromodomain helicase DNA			
GF203	700332	AA283710 Hs.55165	Hs.36787	binding protein 2	CHD2	904.5753	1.31923904
GF204	435905	AA701428 Hs.114061	Hs.114061	ESTs		904.516	
GF202	1048694	AA620607 Hs.111591	Hs.111591	ESTs		904.4673	-2.0219205
GF200	134476	R27644 Hs.24167	Hs.24167	synaptobrevin-like 1	SYBL1	903.5646	1.07149599
GF204	1292108		Hs.69494	ESTs		903.4844	
GF202	29583	R42218 Hs.13333	Hs.13333	ESTs		903.4478	1.16697466
GF203	208487	H62199 Hs.124032	Hs.221127	ESTs		903.2943	-1.0273844
GF202	731337	AA416782 Hs.98258	Hs.98258	ESTs		903.2901	-1.1850413
				topoisomerase (DNA) II alpha			
GF201	366971	AA026682 Hs.100298	Hs.156346	(170kD)	TOP2A	903.2719	
				mitogen-activated protein			
GF201	796134	AA460969 Hs.7510	Hs.7510	kinase kinase 7	MAP3K7	903.2576	
GF203	753113	AA400710 Hs.71070	Hs.102859	ESTs		903.2018	-1.4011952
GF201	811035	AA485433 Hs.7724	Hs.7724	KIAA0963 protein	KIAA0963	903.1359	
GF201	855438	AA664077 Hs.78089	Hs.78089	ATPase, vacuolar, 14 kD	ATP6S14	903.0035	
GF201	731339	AA416783 Hs.86158	Hs.278573	H-2K binding factor-2	LOC51580	902.7877	
				brain-specific protein p25			
GF203	176572	H45295 Hs.115270	Hs.29353	alpha	p25	902.7331	-1.1092614
				conserved helix-loop-helix			
GF202	488499	AA047462 Hs.24067	Hs.198998	ubiquitous kinase	CHUK	902.7178	1.4295062
				Homo sapiens clone 24659			
GF201	809533	AA454584 Hs.29206	Hs.29206	mRNA sequence		902.5822	
GF204	744933	AA625812 Hs.116083	Hs.263150	ESTs		902.1578	
GF201	502287	AA156781 Hs.83992	Hs.83992	ESTs		902.1497	
GF203	786073	AA448672 Hs.99186	Hs.99186	EST		902.1217	-1.1418544
0001	1 455007	A A O 62 3 4 40 Hs 11 E 4	Us 1154	oviductal glycoprotein 1,	OVGP1	901 919	-2 252404
GFZU3	1430837	AA003448 115.11.54	t	CANCE	5		

-1.9069018	-1.636803 -1.12877 1.05403711 1.02640624	-1.6856188	1.08067399 -1.428142 -1.8369271	-1.0006491 -1.4338031 -2.0203591 -1.3239556
901.7398 901.2926 900.9083	900.9053 900.819 900.7828 900.6626	900.6512 900.6182 900.5283	900.3249 900.3053 900.0598 899.969 899.9549	899.9011 899.6119 899.1282 899.1047 899.0674 898.9833
	NUDT3 PLAT	YDD19	APRT TEGT	RNAC ERP70 KIAA1131
Homo sapiens patired mesoderm homeo box 1 (PMX1), mRNA ESTs	nudix (nucleoside diphosphate iniked moiety XJ-type motif 3 ESTs ESTs ESTs ESTs Page motif is a ESTs plasminogen activator, tissue plasminogen activator, tissue plasminogen motivator, tissue per motivatoral thread norien AD7c-	NTP (H.sapiens) ESTs YDD19 protein Horno sapiens cDNA FLJ20761 fis, clone	adenine phosphorbosyltransferase testis enhanced gene transcript ESTs ESTs ESTs	RNA oyclase homolog protein disulide isomerase related protein, intestinal- related) ESTs ESTs ESTS ESTS ESTS ESTS ESTS ESTS
Hs.30528 Hs.16808 Hs.82415	Hs.4815 Hs.19568 Hs.110294 Hs.274404	Hs.154431 Hs.99610 Hs.25615 Hs.107872	Hs.28914 Hs.74637 Hs.91958 Hs.21394	Hs. 113052 Hs. 93659 Hs. 32677 Hs. 269023 Hs. 56782 Hs. 210850
AA682609 Hs.117273 AA780055 Hs.16808 N39590 Hs.82415	AA256462 Hs 44950 R05832 Hs.19568 AA056534 Hs.110294 AA453728 Hs.213	167261 Hs.108860 AA464162 Hs.99610 AA463958 Hs.13259 AA708441 Hs.107872	AA598510 Hs.28914 AA629591 Hs.74637 AA629357 Hs.98162 N57554 Hs.91958 R39878 Hs.21394	R05309 Hs.113052 NS9626 Hs.393639 AA490829 Hs.105274 H93778 Hs.32677 H94474 Hs.108478 A4432070 Hs.21149
450846 451247 277063	682066 124795 489098 813841	66676 810354 810299 506018	897774 884766 743731 279972 26932	125148 248454 823992 190499 243172 28225 784117
GF204 GF203 GF202	GF202 GF200 GF202 GF200	GF201 GF202 GF201 GF204	GF200 GF201 GF203 GF203	GF200 GF204 GF203 GF203 GF203 GF203 GF203

1.3226218	1.07178438	-1.1586862	1.03331388	1.38551378	-1.7962446	-1.1639785			1.34602709		1.27380068		-1.2045758		-2.0033879		1.70454056	1.70454056	1.11732534	07000777	1.12358/43
898.7311	898.321 898.3702 898.3698	898.3468 898.092	897.5168	897.0518	896.8094	896.7119	896.6299		896.4922	896.2879	896.007		895.9739		895.9478	7/00:060	895.5351	895.5351	895.5095	1000	895.3607 895.198
S1P NMA	KIAA1193	I H2BFN				EFNB1					SLUG				GTF2IP1		CANX	CANX		i	ZNF184
site-1 protease (subtilisin-like, sterol-regulated, cleaves sterol regulatory element binding proteins) putative transmembrane nuclain	process KIAA1193 protein EST ESTs	H2B histone family, member N H2BFN EST	ESTs	ESIs ESTs	ESTs	ephrin-B1	ESTs	Homo sapiens cDNA FLJ10792 fis, clone	NT2RP4000560	ESTs	slug (chicken homolog), zinc finger protein	ESTs, Weakly similar to mitoden inducible gene mig-2	[H.sapiens]	general transcription factor II,	i, pseudogene 1	ESI	calnexin	calnexin	ESTs	zinc finger protein 184	(Kruppel-like) ESTs
Hs.75890 Hs.78776	Hs.101891 Hs.94074 Hs.29410	Hs.151506 Hs.116155	Hs.55497	Hs.225691 Hs.32094	Hs.144995	Hs.144700	Hs.130557		Hs.9725	Hs.35580	Hs.93005		Hs.180535		Hs.169921	HS.116058	Hs.155560	Hs.155560	Hs.47094	!	Hs.158174 Hs.198651
AA447393 Hs.75890		V68399 Hs.94213	V95414 Hs.55497	H56207 Hs.37265 4A774761 Hs.32094	00 Hs.124257	4A428778 Hs.45272	55 Hs.108836		53 Hs.114326		309 Hs.117884		90 Hs.18178		4A400128 Hs.110167	AA625552 Hs.116058	4A126356 Hs.79933	AA126356 Hs.75076	AA404564 Hs.115425		AA455712 Hs.5186 H65881 Hs.38427
784504 AA44		292399 N68399 745084 AA626343	_	203791 H56207 970685 AA77476	Ξ	_	261274 H98255		261811 H98853		204737 H57309		121530 T97890		-	Ī	•	511521 AA12	772373 AA40		814014 AA4557 211145 H65881
GF200	GF202 GF202 GF203	GF202	GF202	GF200 GF204	GF203	GF200	GF201		GF203	GF201	GF200		GF200		GF202	GF204	GF200	GF200	GF202		GF200 GF204

APPENDIX A ESTs, Weakly similar to

	-1.0746441	-1.0866777		1.31796642	-1.6392449	1.07404157	1.22307673		1,17612099	1 09797338	1.09797338
	894.8486	894.7496 894.3416	894.2505 893.9283 893.7439	893.7156 893.2075 893.0713	892.9343 892.7531	892.2073 892.1888	892.1595	892.0588	892.0195	801.8734	891.8734
		PBX2	PPP4R1	KIAA1083	ATP1A1 SH3GL1	FLJ20015	UNG	NRGN	DR1	A00000	PPP2CA
predicted using Genefinder	[C.elegans] pre-B-cell leukemia		protein phosphatase 4, regulatory subunit 1 ESTs ESTs	Homo sapiens cDNA FLJ20449 fis, clone KAT05575 KIAA1083 protein ESTs	ATPase, Na+/K+ transporting, alpha 1 polypeptide SH3-domain GRB2-like 1 ESTs, Weakly similar to hypothetical protein		ase 1 kinase C			n phosphatase 2 rly 2A), catalytic subunit,	hatase 2 catalytic subunit,
i a	Hs.39143 [C.	Hs.93728 tra Hs.194397 ES	pro Hs.3382 reg Hs.40545 ES Hs.43756 ES	Hs.130546 FL Hs.26334 KI Hs.118047 ES	AT Hs.190703 alp Hs.97616 SF ES	Hs.264897 [H Hs.80618 hy		Hs.26944 su do	Hs.16697 co		
	H69934 Hs.39143	T59641 Hs.93728 AA004321 Hs.15345	AA464237 Hs.28881 AA045709 Hs.40545 AA459282 Hs.43756	AA398348 Hs.97329 AA171421 Hs.26334 N51529 Hs.15838	AA873355 Hs.119404 AA398366 Hs.97616	AA452139 Hs.65932 AA701863 Hs.80618	H15111 Hs.78853	H49511 Hs.26944	AA132094 Hs.100656	A A E G G G G G G G G G G G G G G G G G	AA599092 Hs.75624
	239324 H6	80549 T5 428652 AA	810122 AA 488010 AA 810898 AA	726835 AA 594796 AA 281483 N5	1471841 AA 726768 AA	787856 AA	_	178825 H4	566760 AA		
	GF202	GF200 GF201	GF201 GF201 GF201	GF203 GF202 GF201	GF203 GF202	GF202 GF204	GF200	GF201	GF200		GF200

-1.0336248	-1.2104436 1.61920961 -1.2599091 -2.5454539		-1.0612268	-1.0470889	-2.0376547	-1.4761929	-1.0604351	-1.2260145	1 09412007		1.31742491	1.40936484
891.4918 891.282	891.1521 891.0657 891.0283 890.7763		890.4084	890.4005	890.1194	889.7123 889.5724	889.5718	889.4645	888 8409	888.7983	888.733 888.6288	888.2684 888.1466
NFKB1	KIAA0769			PPP4R1	MSH5			TLE3			PIR	RAD52 DKFZP586F1019
nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105) ESTs ESTs, Highly similar to similar to GTPase-activating proteins	[H.sapiens] ESTs ESTs KSTs KIAA0769 gene product	Homo sapiens BNPI mRNA for brain-specific Na-dependent inorganic phosphate	cotransporter, complete cds protein phosphatase 4,	regulatory subunit 1	mutS (E. coli) homolog 5	ESTs ESTs	EST	transducin-like enhancer of split 3, homolog of Drosophila E(sp1)	EST, Highly similar to similar to Cdc14B1 phosphatase IH canions	ESTs	Pirin ESTs	RAD52 (S. cerevisiae) homolog DKFZP586F1019 protein
Hs.83428 Hs.21320	Hs.74266 Hs.98638 Hs.112505 Hs.19056 Hs.10198		Hs.6535	Hs.3382	Hs.112193	Hs.86434 Hs.116318	Hs.22298	Hs.31305	He 997178	Hs.48784	Hs.79259 Hs.191322	Hs.89571 Hs.227209
AA451716 Hs.83428 H79318 Hs.105355	AA406233 Hs.74266 AA429885 Hs.98638 AA608524 Hs.112505 N70537 Hs.54275 H61552 Hs.106071		AA702627 Hs.6535	T62804 Hs.3382	AA621155 Hs.112193	AA428137 Hs.86434 AA884617 Hs.116318	R43001 Hs.22298	AA057738 Hs.31305	NA5108 He 46484	W55916 Hs.48784	AA111865 Hs.109923 AA702985 Hs.127281	N72452 Hs.89571 AA406566 Hs.9380
789357 235095	753252 781128 950577 299128 206052		384006	79353	1046542	773527 1468585	31652	510571	283001	321261	530219 447171	245296 753300
GF200	GF203 GF202 GF202 GF202 GF201		GF203	GF200	GF202	GF202 GF204	GF203	GF202	GEOUG	GF201	GF203 GF204	GF200 GF203

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						887.9188		887.839	887.7641	887.7638	887.7078	887.7051	887.604	886.9523				886.9508	886.9503	886.9314		886.7994	886.7061	
		Ø		Φ				HNRPA1			SRM300			HSPF1				ATP6B2				LHFPL2		
Human DNA sequence from	clone 141H5 on chromosome	Xq22.1-23. Contains parts of a	novel Chordin LIKE protein	with von Willebrand factor type	C domains. Contains ESTs,	STSs and GSSs	heterogeneous nuclear	ribonucleoprotein A1	ESTs	ESTs	RNA binding protein	EST	ESTs	heat shock 40kD protein 1	ATPase, H+ transporting,	lysosomal (vacuolar proton	pump), beta polypeptide,	56/58kD, isoform 2	ESTs	EST	lipoma HMGIC fusion partner-	like 2	ESTs	** * **
						Hs.82223		Hs.249495	Hs.24512	Hs.20567	Hs.197114	Hs.98777	Hs.116156	Hs.82646				Hs.1697	Hs.112851	Hs.46862		Hs.79299	Hs.37648	
						AA040424 Hs.82223		H15296 Hs.26903	N47468 Hs.41073	AA701909 Hs.20567	AA999947 Hs.7841	AA431987 Hs.98777	AA626350 Hs.116156	AA405571 Hs.43749				AA877194 Hs.1697	AA620287 Hs.112851	N48337 Hs.46862		AA863469 Hs.79299	H58949 Hs.37648	
						485854		49918	280750	435537	1636496	782211	745088	772429				1323203	1030726	279715		1469377	207771	

GF201 GF200 GF203 GF204 GF202 GF204 GF202

GF200

GF203 GF202 GF202

GF203 GF200

-1.1740287 -1.2379729

-1.2678536 -1.3199386

1.03264311

	-1.6914833	-1.6524026	1.30697201		-1.5535238	-1.0540035								-2.4324685	-1.8335006	
	886.9508	886.9503	886.9314		886.7994	886.7061		886.6865	886.5847	886.2745	886.2272	886.0855	886.0834	885.8464	885.7668	885.115
	ATP6B2				LHFPL2		-F	MAN1A2		KIAA0935			CXX1			MY047
(and adding to the land	56/58kD, isoform 2	ESTs	EST	lipoma HMGIC fusion partner-	like 2	ESTs	mannosidase, alpha, class 1A,	member 2	ESTs	KIAA0935 protein	EST	ESTs	CAAX box 1	ESTs	ESTs	MY047 protein
	Hs.1697	Hs.112851	Hs.46862		Hs.79299	Hs.37648		Hs.239114	Hs.11356	Hs.12183	Hs.119803	Hs.23096	Hs.250708	Hs.46832	Hs.182196	Hs.11000
	AA877194 Hs.1697	AA620287 Hs.112851	N48337 Hs.46862		AA863469 Hs.79299	H58949 Hs.37648		Hs.23337	Hs.11356	Hs.25012	AA704174 Hs.119803	Hs.23096	Hs.8031	Hs.46963	Hs.118044	Hs.11000
	AA877194	AA620287	N48337		AA863469	H58949		H97940	T63981	H11270	AA704174	R45980	W72596	N49746	N47994	T62031

260741 79763 47225 460889 35893 345621 282283 281585 85614

GF201 GF201 GF204 GF204 GF201 GF201 GF201 GF203

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APPENDIX A

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	-1.5457694	-1.6729362	1.32486202	-1.2643391	1.12812842	-1.6735634 2.07332516	-1.2990563	-1.8285999 -1.8180054 -1.1905252 -1.3755851	
	885.1058	885.0152 885.0031	884.916 884.6684	884.1204	884.0914 884.0632	883.9644 883.6545	883.5027 883.2374 882.9783 882.6635 882.4602 882.4176	882.2214 882.0257 881.7192 881.7081	
			UBE4B	POU2F1	SLC2A1 DKFZP4341225	MRF-1	MAN2B1 LOC51582	IL13RA1 KIAA0737 DTR	
ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!	[H.sapiens] Homo sapiens mRNA; cDNA DKFZp586A0618 (from clone	DKFZp586A0618) ESTs ubiquitination factor E4B	.02)	transcription factor 1 solute carrier family 2 (facilitated glucose	transporter), member 1 DKFZP4341225 protein	modulator recognition factor I EST mannosidase, alpha, class 2B,	member 1 ESTS ESTS antizyme inhibitor ESTS ESTS ESTS HONO sapiens mRNA for KIAA1342 protein, partial ods	interleukin 13 receptior, alpha 1 IL13RA1 KIAA0737 gene product diphtheria toxin receptor (heparin-binding epidermal growth flador-like growth ESTs	
	Hs.226564	Hs.4105 Hs.72020	Hs.24594 Hs.46741	Hs.182237	Hs.169902 Hs.87794	Hs.920 Hs.238643	Hs.108969 Hs.44736 Hs.268933 Hs.223014 Hs.180638 Hs.95605	Hs.250911 Hs.194035 Hs.799 Hs.57877	
	Hs.54974	AA609783 Hs.112767 AA886757 Hs.72020	Hs.108487 Hs.46741	Hs.62730	H58873 Hs.108181 AA626324 Hs.87794	AA789301 Hs.920 AA677863 Hs.117089	AA427691 Hs.108969 AA481754 Hs.44736 H80621 Hs.117901 N29619 Hs.82249 AA456027 Hs.8480 H01940 Hs.95605 AA778869 Hs.94042	RA1407 Hs.100871 AA633647 Hs.17630 R14663 Hs.799 AA457490 Hs.57877	
	N93601	AA609783 AA886757	W74337 N47589	H38522	H58873 AA626324	AA789301 Hs.920 AA677863 Hs.1170	AA427691 AA481754 H80621 N29619 AA456027 H01940 AA778989	R41407 AA633647 R14663 AA457490	
	308873	1031963 1500262	346292 280967	192694	207358 745569	1391644 430677	770454 810779 239793 257287 812153 150176 858680	30330 856568 35828 838296	
	GF202	GF202 GF204	GF201 GF202	GF200	GF200 GF204	GF203 GF203	GF201 GF201 GF204 GF203 GF203 GF203	GF203 GF203 GF200 GF200	

-2.3398351 1.54590084 -2.5253999	-2.1812847 1.40022802 -1.0397545	-1.5466207	-1.2291663	-1.1155153	-1.229663 -1.7450172 -1.4086048	-1.0743004
881.5027 881.2897 881.1862	880.9359 880.8824 880.7223	880.2979 880.2979	879.9883 879.8218 879.7979	879.7252 879.7252 879.3275 879.212	879.1755 879.1518 879.0032 878.8803	878.765
KIAA0252	B4GALT5 NRP1		SLC9A6	CAMK1 CAMK1 AVIL DHFR	NBL1 SSFA2	PLP1
ESTS, Highly similar to RNA helicase-related protein IH.sapiens] ESTS KIAAOS2 protein UDP-GattberaGisNAc beta 1,4-qualcusylitransferase,	polypeptide 5 neuropilin 1 ESTs ESTs, Weakly similar to oxidative-stress responsive 1	[H.sapiens] ESTs solute carrier family 9 (sodium/hydroden exchanger),	isoform 6 ESTs ESTs calcium/calmodulin-dependent	protein kinase I caclcum/calmodulin-dependent protein kinase II advillin dihydrofolate reductase euroblastoma candidate redion sunnession of	tumorigenicity 1 ESTs ESTs sperm specific antigen 2	proteolipid protein 1 (Pelizaeus: Merzbacher disease, spastic paraplegia 2, uncomplicated)
Hs.269595 Hs.172780 Hs.83419	Hs.107526 Hs.69285 Hs.16689	Hs.4789 Hs.12396	Hs.62185 Hs.61497 Hs.54618	Hs. 184402 Hs. 184402 Hs. 47344 Hs. 83765	Hs.76307 Hs.21757 Hs.125505 Hs.82767	Hs.1787
AA706964 Hs.120916 R62241 Hs.28304 AA704524 Hs.83419	AA504652 Hs. 107526 AA008867 Hs. 69285 H18470 Hs. 16689	R08769 Hs.20230 AA398234 Hs.12396	R45009 Hs.62185 AA042911 Hs.61497 N90403 Hs.54618	H29415 Hs.118414 H29415 Hs.96398 AA427733 Hs.47344 R00884 Hs.83765	AA598830 Hs.76307 R15946 Hs.21757 AA883790 Hs.125505 AA496804 Hs.82767	T75041 Hs.1787
451918 139764 451104	825641 489535 51214	127458 726901	20115 486850 305851	52629 52629 770840 123971	898305 53031 1461608 897655	22731
GF203 GF200 GF203	GF203 GF203 GF203	GF201 GF203	GF200 GF201 GF202	GF200 GF200 GF201 GF201	GF200 GF203 GF204 GF200	GF200

1.25657475 1.40516967 1.03376052 -1.0974131 1.1019105	1.03250346	-1.4094516		-1.1911192 -1.2439486 2.0524798 -1.7446437 -2.2475083 -1.9687569 -2.1317876 1.04172233
878.7635 878.5777 878.4839 878.3669 878.2917 878.2207	877.9555 877.8034	877.7031	877.4242 877.3253 877.1121	877.0436 877.025 876.7581 876.2844 876.2844 876.2575 876.1369 876.1369 875.9346 875.9348
FIBP			P4HB OMG	PTPRNZ LSP1 KIAA0856
fibroblast growth factor (acidic) intracellular binding protein ESTs ESTs ESTS ESTS ESTS ESTS ESTS ESTS	ESTS, weary similar to SCI protein [R.norvegicus] ESTS Homo sapiens mRNA; cDNA DKEZPA/34M0331 ffrom clone	DKFZp434M0331) procollagen-proline, 2- oxoglutarate 4-dioxygenase (proline 4-hydroxylase), beta polypeptide (protein disulfide	binding protein p55) ESTs oligodendrocyte myelin glycoprotein	protein tyrosine phosphatase, receptor type, N polypeptide 2 ESTs ESTs Wmphocyte-specific protein 1 ESTs KIAA0956 protein ESTS ESTS
Hs.7768 Hs.28212 Hs.186466 Hs.260041 Hs.268844	Hs.268713 Hs.187497	Hs.48219	Hs.75655 Hs.14014 Hs.194772	Hs.74624 Hs.24341 Hs.269536 Hs.97740 Hs.56729 Hs.75478 Hs.75478 Hs.121865 Hs.121865 Hs.124818
AA490046 Hs.7768 H48502 Hs.28212 T00522 Hs.119156 R16009 Hs.63802 R92199 Hs.117888 AA016285 Hs,125076	R45567 Hs.6286 AA046705 Hs.90544	N58405 Hs.48219	R27004 Hs.113338 AA780791 Hs.14014 H24006 Hs.1839	AA46450 Hs,74624 AA669978 Hs,117831 AA401436 Hs,97740 R83159 Hs,3048 W38812 Hs,109128 AA77731 Hs,121865 AA437148 Hs,124818 H69553 Hs,124818
839888 207098 110664 66474 195841 361227	35366 487383	248095	132702 1070324 51373	812968 / 211319 H 435705 / 743193 H 110788 T 129285 R 1292857 / 782275 / 782275 H 212473 H
GF202 GF200 GF202 GF200 GF202	GF202 GF202	GF200	GF204 GF204 GF201	GF200 GF200 GF203 GF202 GF204 GF204 GF204 GF204 GF204

	1.33492523	1 00001500	1.02391393			1.20694595				-1.0898195				-1.4884894		1.05437621		-2.3621834			-1.0078475	-1.6378145	-1.8214742				1.6501629	-1.6211556		1.10599937		1.31405779	-1.2947831		-1.1659238
	8/5.6402	075 5750	6/3.3/36	875.3112		875.1553		875.041	875.0332	874.9618			874.915	874.7906	874.5919	874.5659	874.1384	873.9656		873.9232	873.7723	873.5272	873.4483			873.4072	873.0601	872.9717		872.7618	872.7202	872.6188	872.6106		872.4066
	CDH	TDID4	4 L	SOXL		PLCB3NP		COPG2	ABLIM	KIAA0042				KIAA 1045						KLF7								KIAA0731		CBP2					
cadherin 1, E-cadherin	(epithelial)	information of receptor	IIII aciol 4	Sox-like transcriptional factor	pnospnolipase C, peta 3,	neighbor pseudogene	coatomer protein complex,	subunit gamma 2	actin-binding LIM protein	KIAA0042 gene product	Homo sapiens mRNA; cDNA	DKFZp761P039 (from clone	DKFZp761P039); partial cds	KIAA1045 protein	ESTs	ESTs	ESTs	ESTs	Kruppel-like factor 7	(ubiquitous)	ESTs	ESTs	ESTs	Homo sapiens mRNA; cDNA	DKFZp434H1228 (from clone	DKFZp434H1228)	ESTs	KIAA0731 protein	collagen-binding protein 2	(colligen 2)	ESTs	ESTs	ESTs	Homo sapiens clone 24760	mRNA sequence
!	Hs.194657	110.440704	18.110/04	Hs.32317		Hs.100623		Hs.258811	Hs.158203	Hs.3104			Hs.184390	Hs.7989	Hs.44159	Hs.95600	Hs.49014	Hs.58356		Hs.21599	Hs.189765	Hs.121562	Hs.125029			Hs.16085	Hs.186530	Hs.6214		Hs.9930	Hs.128629	Hs.119563	Hs.14931		Hs.61408
	H97778 HS.82004	10010111	AA449101 IS.00091	AA044662 Hs.111167		AA775290 Hs.100623		AA774034 Hs.115987	H16812 Hs.22231	AA477501 Hs.3104			H17273 Hs.26830	R42561 Hs.7989	AA459650 Hs.44159	AA115861 Hs.95600	AA158532 Hs.49014	W74216 Hs.58356		N49209 Hs.32170	T96851 Hs.119552	AA757873 Hs.121562	H63575 Hs.125029				R68514 Hs.28850	AA465202 Hs.8151		R71440 Hs.9930	AA018937 Hs.109558	T97717 Hs.119563	N76867 Hs.14931		AA455092 Hs.61408
	251019	705004	100000	488422		878631		858462	50471	739983			50302	31022	795536	564597	592410	346359		280249	121312	395809	206457			40075	137760	815108		142788	362875	121574	245745		812283
	GF200		00215	GF201		GF203		GF204	GF201	GF200			GF201	GF202	GF201	GF202	GF204	GF202		GF201	GF202	GF203	GF203			GF204	GF200	GF203		GF200	GF204	GF202	GF200		GF203

Atty Docket No. 21726/92526	872.2225	871.9046 871.8435 871.6581 1.08713222	871.4554 -1.5777749	871.4415 871.0686 -1.1360562	871.0412 870.8393 -1.8728926	8/0.8212 870.6415 1.0444941	870.3799 -1.0201926	870.0508 1.17097403 869.4472 -1.5269277 889.481	869.4203 869.3572	869.0569 -1.6254269	
		CPA3		or KIAA1091	IDH2 LOC51756	YDD19	2 MYBL2	نہ وہ ہ	KIAA0934		
APPENDIX A	ESTs	carboxypepinase As (mast cell) ESTs ESTs	ESTs, Moderately similar to putative transcription factor CA150 [H.sapiens]	ESTs, Highly similar to nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal [H.sapiens] KIAA1091 protein	isocitrate dehydrogenase 2 (NADP+), mitochondrial HE2 alpha1	YDD19 protein ESTs	v-myb avian myeloblastosis viral oncogene homolog-like 2 MYBL2	Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence ESTS	KIAA0934 protein mitogen-activated protein	Nildse nildse 7 ESTS Homo sapiens mRNA; cDNA DKFZp761J032 (from clone DKFZp761J032); partial cds	
	Hs.221794	Hs.646 Hs.97876 Hs.146261	Hs.262563	Hs.167418 Hs.26797	Hs.5337 Hs.274570	Hs.25615 Hs.205555	Hs.179718	Hs.5086 Hs.62777 Hs.22080	Hs.227716	Hs.93135 Hs.93135 Hs.6489	19.040
	R32325 Hs.106189	T64223 Hs.646 AA459285 Hs.97876 R25074 Hs.50984	AA447709 Hs.54139	W83369 Hs.27093 R60711 Hs.26797	AA679907 Hs.105969 AA400437 Hs.2717	AA774724 Hs.116561 N72600 Hs.124168	AA456878 Hs.74605	AA429281 Hs.5086 AA251143 Hs.62777 AA910431 Hs.128821	N29585 Hs.43999		77400177 113.0400
∢etal.	134916	80221 810904 35105	813787	415084 42008	869375 742576	970649 295623	815526	771000 683986 1505783	270645	813838	252
Westbrook et al.	GF201	GF201 GF201 GF200	GF202	GF201 GF202	GF201 GF202	GF204 GF203	GF200	GF200 GF203 GF204	GF201	GF203 GF203	10415

	-1.6760738	1.07978522	-1.0352677	1.49319021		-1.378866	-1.8032663											-1.6206691		1.36717412	
	-1.6	1.07	7.0	1.49		-1.3	-1.88											-1.6		1.36	
868.9476	868.8257	868.796	868.6259	868.1655		867.9918 867.8175	867.1362									867.0648		867.0573		866.9126	866.9094
DKFZP434B194		NDUFV3				EZH2	CAMLG							_							DNMT2
similar to tuffelin-interacting protein ESTs, Weakly similar to	receptors [C.elegans] NADH dehydrogenase (ubiquinone) flavoprotein 3	(10kD) Homo sapiens cDNA FLJ10874 fis. clone	NT2RP4001803	ESTs	enhancer of zeste (Drosophila)	homolog 2 ESTs	calcium modulating ligand	Human DNA sequence from clone RP1-37E16 on	chromosome 22 Contains the	3' part of the gene for a novel	VHS domain containing	protein similar to predicted	worm and human proteins, the	SH3BP1 gene for SH3-domain	binding protein 1, the gene for	a novel protei ESTs, Highly similar to	putative mitogen-activated protein kinase kinase kinase	[H.sapiens]	ESTs, Weakly similar to WASP-family protein	[H.sapiens]	methyltransferase 2
Hs.20225	Hs.43827	Hs.59745	Hs.30318	Hs.31818		Hs.77256 Hs.126957	Hs.13572									Hs.5790		Hs.41040		Hs.178186	Hs.97681
AA485750 Hs.104386	AA455262 Hs.43827	W96319 Hs.59745	AA469966 Hs.30318	N59265 Hs.31818		AA430744 Hs.77256 AA620894 Hs.116027	R40208 Hs.91706									AA400022 Hs.5790		R10185 Hs.91312		AA436009 Hs.119149	R95732 Hs.97681
811168	814817	358609	730412	289582		770992	27516									743182		128833		730772	198982
GF201	GF203	GF200	GF202	GF203		GF200 GF204	GF202									GF201		GF200		GF202	GF201

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-1.2800704	-1.0679676	-1.1199706	-2.8371511		1.19904829						-1.6489743	1.18058958		-1.1959827	-2.1015641	1.75457608	-1.3284632	-1.292593		1.67586085	1.81768655	-1.4133563 -1.7789217
866.8567	866.8299	866.7922	866.7552	866.6155	866.3477	866.2095		865.9736	865.8535		865.6466	865.4244	865.402	865.2346	865.1021	864.6872	864.6205	864.6128		864.4919	864.3723	863.5189 863.3002
	MAPK14			TCTEL1		LSM3					RAC2									P2RX4		LMOD1
ESTs	mitogen-activated protein kinase 14	ESTS Homo sanions clone 24747	mRNA sequence	expressed 1-like 1	ESTs	Lsm3 protein	ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	[H.sapiens]	EST	ras-related C3 botulinum toxin substrate 2 (rho family, small	GTP binding protein Rac2) ESTs, Highly similar to CGI-	138 protein [H.sapiens]	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	purinergic receptor P2X, ligand	gated ion channel, 4 ESTs, Highly similar to TRANSFERRIN RECEPTOR	PROTEIN [H.sapiens] Homo sapiens cDNA	FLAZU063 IIS, clorie COL03604 leiomodin 1 (smooth muscle) LMOD1
Hs.69331	Hs.79107	Hs.117979	Hs.13456	Hs.266940	Hs.38703	Hs.111632		Hs.194131	Hs.119882		Hs.173466	Hs.5836	Hs.99101	Hs.119484	Hs.122138	Hs.71944	Hs.167714	Hs.26790		Hs.9610	Hs.185726	Hs.118964 Hs.79386
AA424948 Hs.69331	AA404479 Hs.79107	H99108 Hs.117979	T78909 Hs.13456	N22889 Hs.114347		AA461098 Hs.5220		AA206456 Hs.111177	AA705242 Hs.119882		AA521232 Hs.73801	AA488986 Hs.5836	AA460346 Hs.99101	R26531 Hs.119484	AA780057 Hs.122138	AA151297 Hs.71944	N51030 Hs.114301	H11629 Hs.26790		AA670190 RG.1	R94591 Hs.20303	N72888 Hs.112351 AA441933 Hs.79386
768258	772261	261676	108864	266696	211747	796176		645669	461532		827132	824723	795907	132392	451252	505007	244194	48056		1035182	276286	291557 774078
GF203	GF200	GF203	GF203	GF204	GF200	GF201		GF204	GF204		GF200	GF203	GF201	GF202	GF203	GF202	GF202	GF203		GF200	GF200	GF203 GF203

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1.03759249 -1.9049569 -1.2918102 -1.5922466 1.17606388 -1.8946322	-1.4055428 1.72099269 -1.3390858	-1.5221564	-1.1432191	-1.2929769
863.1858 863.1581 862.788 862.6728 862.6612 862.3026 862.3026	862.275 862.2644 862.1312 861.9571 861.711	861.1615 861.0042 860.9326 860.9326	860.7571 860.6693 860.367	860.0991 859.8098 859.724
ODC1 KIAA0451	C18B11	DKFZP434D146	ZNF151	
omithine decarboxylase 1 ESTs, Weakly similar to p40 III.sapiens) ESTs ESTs KIAA0451 gene product ESTS ESTS	C18B11 homolog (44.3KD) ESTS ESTS ESTS ESTS, Weakly similar to Phospholipase C (H. sapiens) Homo sapiens cDNA FLJ10569 its, clone MTZPR2002618, weakly similar to PROTEIN ARCHINICS	DKFZP434D146 protein Homo sapiens cDNA FL20207 fis, clone COLF1609	First finger protein 151 (pHZ- 67) ESTs ESTs ESTs Weekly similar to finger	protein HzF ru, kruepper- related [H.sapiens] Homo sapiens mRNA for KIAA1139 protein, partial cds ESTs
Hs.75212 Hs.112671 Hs.41294 Hs.98170 Hs.18586 Hs.278585 Hs.50015	Hs. 10620 Hs. 207777 Hs. 44807 Hs. 55138 Hs. 97542	Hs.26006 Hs.240845 Hs.129014	ns.22354 Hs.33532 Hs.125653 Hs.237861	Hs.55606 Hs.274408 Hs.24951
AA460115 Hs.75212 AA609245 Hs.112671 H95819 Hs.41294 AA418856 Hs.88170 AA709023 Hs.28158 R81636 Hs.28852 R81636 Hs.28852	88	AA169724 Hs.26006 R56877 Hs.61540 H41285 Hs.129014	24 45	AA454174 Hs.55606 H09167 Hs.101678 AA421018 Hs.24951
796646 1031516 243135 730009 506523 147533 294685	131988 450836 273054 308228 1292096	610124 41305 192521	755373 1466423 590539	795319 46415 731348
GF200 GF202 GF203 GF203 GF203 GF204 GF204	GF202 GF203 GF202 GF202 GF202	GF202 GF204 GF204	GF204 GF202 GF202	GF201 GF201 GF202

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		-1.5810838	-1.1025414			1.07.320041			-2.3193458				-2.0140673	-1.2620887					0 10100100	2.13133432		*******	-1.14/3314					
859.6985 859.3722		859.3052	859.1893			859.130Z 859.069			858.5753	858.5001			858.3581	857.7596	857.7452	857.6375		857.6165	4066	657.4033	1000.700	0070	857.0438	856.9059	856,8153	856.774	856.7505	
		PPP1R11				ERPHOLZ13-21 IDN3			SCA7					EDNRA		QARS		EEF1E1	0000	02110				KIAA0610				
ESTs ESTs	protein phosphatase 1, egulatory (inhibitor) subunit		ESTs	orotein with polyglutamine repeat; calcium (ca2+)	nomeostasis endoplasmic	eticulum protein DN3 protein	spinocerebellar ataxia 7	phy	tinal degeneration)	ESTs	ESTs, Weakly similar to KRAB-	containing zinc-finger protein	(RAZ1 [M.musculus]	endothelin receptor type A		etase	eukaryotic translation	elongation factor 1 epsilon 1	splicing tactor, arginine/serine-	rich 6	9 9	Homo sapiens cDNA	-LJZU39Z fls, clone KAIA4653	KIAA0610 protein ESTs, Weakly similar to	Dachs/ F7.g	ESTS	ESTs	
Hs.124180 E			Hs.159204 Hs.67270			Hs.6430 r Hs 225767	,		_	Hs.122515 F			Hs.109540	•	Hs.18397	-	•	Hs.172247		HS.6891			HS.2/04/	Hs.118087	Hs 5250	Hs.48673		
W71983 Hs.58130 AA155668 Hs 26407		4A485501 Hs.82887	N52255 HS.44838 AA703434 HS.67270			AA481554 Hs.6430 N62911 Hs 48664			AA704255 Hs.108447	AA778551 Hs.122515			4A126222 Hs.109540	AA452627 Hs.76252	AA626315 Hs.18397	4A634166 Hs.79322		N91962 Hs.32119		AA169645 HS.6891	A009769 HS.20494		AA//8//1 Hs.122064	R33103 Hs.12102	44459853 Hs 5250	V62946 Hs.48673	4A461529 Hs.23830	
345582 W			284343 N 450140 A			815285 A				1048893 A.			511491 A	788285 A	745570 A	868400 A		306921 N		59451/ A			-	135800 R	795798	_	`	
GF201	; ;	GF200	GF201 GF203			GF200	3		GF203	GF204			GF202	GF200	GF204	GF201		GF201	9001	GF202	GFZUI		GF203	GF201	GE201	GF201	GF201	

-1.324245	-1.0201868	1.27705949 -1.073933 -2.7957706	1.14919536	-1.0894706	1.26492146
856.7049 856.6334 856.3477 -	(O, C)	855.5238 855.485			854.3303 854.1952 854.0145
		PMS2L12	RUNX1 PRKACB	PTPRO SLC35A2	
ESTs. Weakly similar to weak similarity to ribosomal protein 1.14 [C.elegans] ESTs ESTs ESTs	ESTS ESTS, Weakly similar to	neuronar trireac protein AU/c- NTP [H.sapiens] costmeiotic segregation ncreased 2-like 12 ESTs	unt-related transcription factor (acute myeloid leukemia 1; amf1 oncogene) orotein kinase, cAMP- dependent, catalytic, beta	protein tyrosine phosphatase, receptor type, 0 solute carrier family 35 (UDP-galactore transporter), member 2 ESTs, Weakly similar to IIII ALU SUBFAMILY SC WARNING ENTEY IIII	H.sapiens] ESTs, Moderately similar to NRD2 convertase [H.sapiens] Homo sapiens clone 25088 mRNA sequence
Hs.39387 L Hs.38034 E Hs.255120 E Hs.125519 E			Hs.129914 8 Hs.87773 0	Hs.258609 r Hs.21899 r Hs.98763 E	Hs.138580 [Hs.106083 P Hs.4863 r
AA932558 Hs.39387 W92766 Hs.38034 AA388365 Hs.101937 AA88384 Hs.125519	H65044 Hs.38340 AA470082 Hs.104839	Hs.101677 Hs.89672 Hs.31755	AA/08348 HS.120110 AA146826 HS.129914 AA459980 HS.87773		Hs.39242 Hs.106083 Hs.4863
AA932558 W92766 AA398365 AA883884	H65044 AA470082	R91033 N68166 H46922	AA146826 AA459980	R42433 H51549 AA431797	H71224 H80171 R42984
1570318 357037 726695 1467988	210525 730407	194872 292213 178029	589484 796442	30175 179753 782549	214583 230116 32489
GF204 GF201 GF203 GF203	GF200 GF202	GF200 GF200 GF203	GF203 GF203 GF203	GF201 GF201 GF202	GF201 GF200 GF204

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-1.5373185	-1.3531756 -1.0437872 -1.1293058	-1.6466263	-1.4370793	1.20786303	-1.4031234	
853.7455 853.3828	853.3199 853.1525 853.0608	852.9902 852.7299 852.6324	852.317 852.1708 852.1177	851.955 851.9186 851.8433	851.7491 851.7344 851.6987	851.6946 851.4251
KIAA0660	YDD19 KIAA0958	васн1	PSMA4 LDPL KIAA1128	KIAA0851	CREG MATR3	TASR
Ras-GTPase activating protein SH3 domain-binding protein 2 KIAA0660 EST Homo sapiens cDNA FL110662 fis. clona	NT2RP2002701 YDD19 protein KIA40958 protein BBTB and CNC homology 1,	transcription factor 1 transcription factor 1 ESTs FOSTs FOS	Myte, 4 leupaxin KIAA1128 protein ESTs, Moderately similar to IIII ALU SUBFAMILY SX ANARNING FNTRY IIII	Haspiens ESTIS, Weekly similar to IIII ESTIS, Weekly similar to IIII ALU CLASS A WARNING ENTRY IIII [H.sapiens] KIAA0851 protein	cellular repressor of E1A- stimulated genes matrin 3 Homo sapiens mRNA; cDNA DKFZp8800221 (from cione DKFZp8800221)	arginine protein ESTs
Hs.6727 Hs.46633	Hs.274351 Hs.25615 Hs.22982	Hs.154276 Hs.42207 Hs.104098	Hs.251531 Hs.49587 Hs.81897	Hs.266537 Hs.93961 Hs.5867	10 89	Hs.3530 Hs.20798
AA151214 Hs.13455 N49587 Hs.46633	AA293441 Hs.77480 N21321 Hs.42978 AA456013 Hs.22982	Al016618 Hs.115416 H96605 Hs.42207 AA194893 Hs.104098	AA733040 Hs.104670 W49781 Hs.49587 AA282236 Hs.88992	AA130228 Hs.110159 AA419608 Hs.111963 H29044 Hs.5867	T71991 Hs.5710 H93622 Hs.109511 AA453495 Hs.23285	H11042 Hs.4214 AA004819 Hs.20798
504979 Av 277736 N	725558 Av 265503 N2 812142 Av	1638852 AI 251517 H6 665093 AA	399536 AA 325128 W 712907 AA	504187 AV 752625 AV 52604 HE		47096 H-
GF201 GF202	GF203 GF202 GF203	GF204 GF202 GF203	GF203 GF201 GF203	GF202 GF202 GF201	GF201 GF202 GF201	GF201 GF201

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1.34716789 -1.0199526 -1.1864291 1.04706961	1.15191657 2.07801836 1.06941965	-1.5081356 -1.5812989 -1.5974363	1,19030143	1,25453177 -1,4040739 1,27220238 -1,2574367
851.3899 851.2 851.0643 850.9997	850.932 850.5176 850.4286 850.2954	850.2653 849.9769 849.7888	849.1317 849.0836 848.885 848.8544 848.7618 848.7618	847.8038 847.7509 847.6417 847.5854 847.478 847.2897
KIAA0786 CYP26A1 KIAA0160	OXA1L	A GTF3A KIAA0763	KIAA0696	SPUVE
ESTs latrophilin cytochrome P450, subfamily XXVIA, polypeptide 1 KIAA0160 protein	oxidase (glochrome c) assembly 1-like ESTs ESTs	general transcription factor IIIA GTF3A ESTs, Weakly similar to Prodos protein [Dralanogaster] KIAA0763 gene product KIAA07	Torino septents intriver, torino septents intriver, torino septents (KIAA1136 protein, partial cots ESTs F-box protein Fbw1b; beta-transduon repeat-containing protein 2 ESTs ESTs Hymon sessions of DNAA	FLZ02211 is, close OOLF1807 Contribution of Court 1807 Seatine professe, umbilical endothelium ESTs ESTs
Hs.46722 Hs.24212 Hs.150595 Hs.197803	Hs.151134 Hs.43387 Hs.72045 Hs.165142	Hs.75113 Hs.139179 Hs.4764	Hs.21896 Hs.16917 Hs.116287 Hs.161756 Hs.21229 Hs.269837	Hs.27728 Hs.154737 Hs.172241 Hs.21964 Hs.25935 Hs.177376
N49384 Hs.46722 AA705981 Hs.124162 R51021 Hs.23161 AA521347 Hs.79880	R97137 Hs.102021 N23399 Hs.43387 AA152296 Hs.72045 R08772 Hs.20231	AA456147 Hs.75113 N71758 Hs.116356 AA418726 Hs.4764	H52009 Hs.21896 H62009 Hs.45064 AA84302 Hs.116287 AA865590 Hs.127248 AA705250 Hs.120920 H58000 Hs.37455 R43481 Hs.22358	AA054542 Hs.55979 AA911832 Hs.76607 AA136565 Hs.43085 N66093 Hs.21964 RES635 Hs.25935 AA599043 Hs.55204
277611 1239859 38642 826137	199995 268384 491238 127462	796388 290667 767819	39442 209182 1276477 1470169 461525 204442 32393	489444 1457276 564801 278404 40108 950382
GF203 GF203 GF202 GF200	GF200 GF201 GF202 GF200	GF203 GF203 GF202	GF203 GF201 GF204 GF204 GF204 GF204	GF201 GF204 GF202 GF203 GF202

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APPENDIX A

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1.11536261	1.29399822	1.35732127			-1.0577656	-1.2026226	-1.2496317			-1.5847963			-2.1630057				1.10246046	-1.0263667	1.19648456	-1.1547454		-2.8291459		1.09887994			1.23398925	1.34875187	-1.895728	
847.2581	846.9525	846.6381	846.4815		846.4149	846.3596	846.2837		845.9523	845.9043	845.6538	844.4897	843.9534				843.9111	843.8683	843.7377	843.262	843.1243	842.7432		842.6674	842.6476	842.601	842.5947	842.5603	842.5254	842.5128
G22P1	ADK				PSEN1	KIAA0094	KIAA0978		KCNAB3	FRZB	HIS1	ZNF254		_						KTN1		KIAA0867		SLC12A4) KHK	IL7R	FLJ20498	LOC51596
thyroid autoantigen 70kD (Ku	adenosine kinase	EST	ESTs	presenilin 1 (Alzheimer	disease 3)	KIAA0094 protein	KIAA0978 protein	potassium voltage-gated channel, shaker-related	subfamily, beta member 3	frizzled-related protein	HMBA-inducible	zinc finger protein 254	ESTs	ESTs, Moderately similar to IIII	ALU SUBFAMILY SB1	WARNING ENTRY !!!!	[H.sapiens]	EST	ESTs	kinectin 1 (kinesin receptor)	EST	KIAA0867 protein	solute carrier family 12	transporters), member 4	ESTs	ESTs	ketohexokinase (fructokinase) KHK	interleukin 7 receptor	hypothetical protein divalent cation tolerant protein	CUTA
He 197345	Hs.94382	Hs.114078	Hs.23180		Hs.3260	Hs.82007	Hs.3686		Hs.24379	Hs.153684	Hs.15299	Hs.86371	Hs.97791				Hs.4094	Hs.94046	Hs.72580	Hs.211577	Hs.113160	Hs.52081		Hs.10094	Hs.26052	Hs.91815	Hs.81454	Hs.237868	Hs.97925	Hs.107187
A A A 86311 Hs 35884	R12473 Hs.94382	AA701923 Hs.114078	AA700926 Hs.23180		W86875 Hs.58933	H73080 Hs.82007	AA485878 Hs.26909		H23225 Hs.99784	H87275 Hs.71675	W68585 Hs.15299	AA205649 Hs.86371	AA400273 Hs.97791				AA111979 Hs.4094	N54085 Hs.94046	AA159605 Hs.72580	AA459106 Hs.82709	AA700554 Hs.113160	AA282938 Hs.52081		AA452982 Hs.10094	R53558 Hs.26052		T61308 Hs.81454	AA487121 Hs.109703	AA505150 Hs.97925	Al004315 Hs.107187
849809	128243	435570	453137		416407	234907	840471		51986	223661	342551	646891	742666				530237	247366	593174	814303	432670	713238		789014	39959	33940	77897	841238	825833	1631849
00000	GF200	GF203	GF204		GF202	GF200	GF202		GF201	GF200	GF201	GF204	GF202				GF202	GF202	GF202	GF203	GF204	GF203		GF200	GF201	GF201	GF200	GF202	GF203	GF204

0.00	Atty Docket No. 2172	-1.7361737	-2.0401254		-1.7386425		-1.2254349		-1 4462976	1 11760853	-1.3937583			1.08712644		-1.163256	1.26966443	1.03040507					1.73212311		-2.0004445	-1.1045939		1.06390698	-1.3399516	1.25824578
*	Affy	842.4753	842.3318		842.0483		841.8298	77.17	841.7314	841 2744	841.2409		841.2309	841.1506	841.111	840.9671	840.923	840.5399	840.2926	840.2707		840.0507	840.0468	840.0311	839.9758	839.7733	839.5433	839.4525	839.3422	839.3187
0000		TULP2					l P53BP1		VDD19	2	LOC51284		LAIR1											API5L1		DNM2	RNASEHI			
TOWOZZO, BOZZOBOO	APPENDIXA	tubby like protein 2 ESTs	ESTs	ESTs, Moderately similar to IIII ALU SUBFAMILY SC WARNING ENTRY IIII	[H.sapiens]	tumor protein 53-binding	protein, 1	HOITIO SAPIETIS (CIOTIE SZZI7 1)	YDD19 protein	ESTS	toll-like receptor 7	leukocyte-associated Ig-like	receptor 1	ESTs	ESTs	EST	ESTs	ESTs	EST	ESTs	Homo sapiens clone 23718	mRNA sequence	ESTs	API5-like 1	ESTs	dynamin 2	ribonuclease HI, large subunit RNASEHI ESTs, Highly similar to	HSPC002 [H.sapiens]	ESTs	ESTs
		Hs.104636 Hs.19321	Hs.12397		Hs.190305		Hs.170263	11000	Hs 25615	Hs 20596	Hs.179152		Hs.115808	Hs.169979	Hs.193928	Hs.86752	Hs.68138	Hs.269235	Hs.120382	Hs.267992		Hs.6580	Hs.220864	Hs.227913	Hs.97970	Hs.167013	Hs.25292	Hs.76907	Hs.115335 Hs.271783	Hs.77978
		AA884015 Hs.104636 R02178 Hs.19321			N50949 Hs.57489		AA521389 Hs./9/64		72333 HS.76394		_		AA991196 Hs.115808	478083 Hs.39832	4A780676 Hs.122728	AA218915 Hs.86752	4A084323 Hs.68138	4A010208 Hs.110242	AA719380 Hs.120382	T74257 Hs.76809		R42813 Hs.7009	H68170 Hs.38698	AA608881 Hs.115994	AA406226 Hs.97970	AA780897 Hs.82458	AA057723 Hs.25292	169532 Hs.76907	4A682304 HS.115335 4A021259 Hs.33609	4A405739 Hs.77978
	ж өт а.	1468310			281127		82/013	000		_	_		1606315 /	240406	868004	629805	547786	430205	1292755 /	84713		32229 F	230013	1048609	742887	1155191	512410		•	742977
-	Westbrook et al.	GF203 GF204	GF202		GF203		GF200	700	GF200	GF203	GF202		GF204	GF200	GF204	GF202	GF203	GF202	GF204	GF201		GF201	GF200	GF204	GF202	GF203	GF204	GF200	GF204 GF203	GF202

-2.2323664 1.27636716 -2.4373501	-1.2573359	-1.0976363	-1.4481058 1.94749581 -1.1013541	1.82009202	1.28090515
839.2146 839.1186 838.8396 838.7964 838.627	838.4299	838.0103	837.8873 837.8089 837.5861	837.3574 836.9978 836.8013 836.7524	836.4703 836.361 836.1503 836.0438 835.9146
KIAA0176	RPS5P1 LCP2		GSTM3 LOC51259	API5L1	DSCAM DKFZP586L151 KIAA0128
ESTs ESTs KIAA0176 protein ESTs ESTs rithsomel protein S5	pseudogene 1 pseudogene 1 ymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 78(x) ESTs, Weakly similar to putative protein FR-X-Bdelta4	[H.sapiens] Homo sapiens HSPC183 mRNA, complete cds olutathione S-transferase M3	(brain) hypothetical protein ESTs, Highly similar to peroxisomal D3,D2-enoyl-CoA isomerase [H.sapiens]	ESTs API5-like 1 Horno sapiens mRNA; cDNA DKFZp434C2016 (from clone DKFZp434C2016) ESTs	Down syndrome cell adhesion molecule DK/ZPS881.51 protein KIAA0128 protein, septin 2 ESTs
Hs.98331 Hs.122518 Hs.4935 Hs.184492 Hs.126744	Hs.237225 Hs.2488	Hs.239154 Hs.274417	Hs.26745 Hs.26745 Hs.180716	Hs.126224 Hs.227913 Hs.17110 Hs.268596	Hs.49002 Hs.43658 Hs.90998 Hs.64753 Hs.180958
AA421048 Hs.98331 AA778847 Hs.122518 R44371 Hs.4935 AA608528 Hs.94940 N71059 Hs.126744	781454 AA428607 Hs.17376 1552481 AA927372 Hs.2488	AA418029 Hs.32368 AA160498 Hs.109113	R63106 Hs.2006 N36985 Hs.26745 AA399269 Hs.111904	AA872885 Hs.126224 AA451935 Hs.21466 AA971641 Hs.17110 T91083 Hs.14395	N64532 Hs.49002 AA489616 Hs.43658 AA868745 Hs.123282 H14374 Hs.25870 T82819 Hs.15035
731373 / 452906 / 34616 F 950587 / 294587 /	781454 /	592491	137940 F 273625 P 726483 /	10 10	290429 R 823656 / 1460653 / 48520 H
GF202 GF204 GF200 GF202 GF204	GF202	GF203 GF202	GF200 GF203 GF202	GF204 GF204 GF204 GF204	GF201 GF202 GF204 GF204 GF200

	1.09127599	1.68055152	1.21806369	1.20543178 1.69475875	1.03387361	1.33209022		1.08383992 -1.3525276 -1.6693921
835.8508	835.7021 835.612	835.544 835.3904	835.1767	835.0974 834.9724 834.8063 834.7403	834.5464	834.5442 834.4341 834.2024	834.1522 833.4677 833.2899 833.2447	832.2952 832.2188 832.0244
YWHAZ	GLCLC	KIAA0606 KIAA0673	CHP1	VAV1		EIF3S10 DKFZP586I1023 DKFZP564A122	FLOT1	DKFZP434B194 CDSN
tyrosine 3- monooxygenasedtryptophan 5- monooxygenase activation protein, zeta polypeptide	glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8KD) GLCLC ESTS KIAA0606 protein; SCN	Circadian Oscillatory Protein (SCOP) KIAA0673 protein	protein 1 ESTs, Weakly similar to CGI-	101 protein [H.sapiens] vav 1 oncogene ESTs	EST eukaryotic translation initiation factor 3. subunit 10 (theta.	150/170kD) DKFZP58611023 protein DKFZP564A122 protein Homo sapiens apoptosis-	3) mRNA, partial cds ESTs ESTs flotillin 1	ESTs similar to tuftelin-interacting protein corneodesmosin
Hs.75103	Hs.151393 Hs.269234	Hs.38176 Hs.106487	Hs.22857	Hs.14587 Hs.116237 Hs.268852 Hs.64095	Hs.231680	Hs.198899 Hs.111515 Hs.187991	Hs.177677 Hs.119923 Hs.10362 Hs.179986	Hs.46786 Hs.20225 Hs.507
AA609598 Hs.112245	H56069 Hs.1673 AA033991 Hs.58468	48501 Hs.15460 422952 Hs.21266	N30747 Hs.22857	AA883518 Hs.125467 T65770 RG.68 R93153 Hs.35110 AA884420 Hs.64095	AA278594 Hs.88461	AA916914 Hs.82131 AA773196 Hs.13623 N31577 Hs.107725	T63520 Hs.63697 AA705814 Hs.119923 AA464251 Hs.10362 AA456611 Hs.8751	AA199586 Hs.46786 AA911900 Hs.20225 W95595 Hs.94990
1031744 A	203721 H 429932 A	207087 H 51932 H	257960 N	1467420 A 80384 Tf 197051 Ri 1466971 A		1473792 A. 845771 A. 271699 N.		647437 A 1457350 A 357785 W
GF201	GF200 GF201	GF200 GF201	GF203	GF204 GF200 GF200 GF204	GF203	GF203 GF204 GF201	GF201 GF204 GF201 GF201	GF202 GF203 GF202

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Ally Docket No. 217	832.0178	831.7443 1.00176701 831.7443 -1.1136204	831.7207 -1.1291709 831.6135 1.81364095	831.0611 -1.8938241		830.8454 1.00097375	830.6312 -1.0233243 830.4984 -1.0024049	·		830.2148 -1.7269531 830.0439 1.77672918		829.9079	828.428Z	829,2823 -1.0053256	829.0761 1.02407011 828.7634 -1.4731287	828.7524
	83	83	83 KIAA0918 83	83 83		83	83 VHI 83	-	<iaa1067 83<="" p=""></iaa1067>	83	3		KIAAU/88 82	SLC17A1 82	8 88	85
APPENDIX A	ESTs ESTs, Moderately similar to MIXED LINEAGE KINASE 2	[H.sapiens] ESTs	Homo sapiens mRNA for KIAA1377 protein, partial cds KIAA0918 protein	ESTS Homo sapiens cDNA	FLJ10191 fis, clone HEMBA1004756, weakly similar to Human transporter	protein mRNA ESTs, Weakly similar to	C10G11.5 [C.elegans]		_	EST	ESTS, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!		KIAAO/88 protein solute carrier family 17 (sodium phosphate), member	٠. ر	flanking sequence ESTs Homo sapiens mRNA for	KIAA1424 protein, partial cds
	Hs.22209	Hs.166919 Hs.272139	Hs.188790 Hs.58009	Hs.22672 Hs.193974		Hs.165655	Hs.43864 Hs 174007	Hs.81071	Hs.243901	Hs.138746 Hs.17719		Hs.262420	Hs.181043	Hs.100001	Hs.7838 Hs.221132	Hs.11611
	AA931725 Hs.22209	T98615 Hs.18419 AA004803 Hs.110214	-	44460/ Hs.226/2 4A417618 Hs.6615		AA680367 Hs.116968	13 Hs.108990 4 Hs 78160			6 Hs.48707	_	AA878307 Hs.125389	AA953648 Hs.15313	1 Hs.100001	AA460329 Hs.110218 H57111 Hs.37399	AA454021 Hs.11611
		T98615 AA00480	AA401311 W69435	H44607 AA41761		AA680	W15533	N79484	AA127058	N63076	C704N			N73241	AA460329 H57111	AA454
ok et al.	1572196	122178 429122	743150	33022 746163		430510	322794	301122	502200	284741	660	-	1564976	246522	795790 204814	795277
Westbrook et al.	GF204	GF200 GF202	GF202 GF202	GF201 GF203		GF203	GF200	GF200	GF202	GF202	20210	GF204	GF204	GF200	GF202 GF200	GF201

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Auy	828.7498	828.7154	828.6355	828.4769	828.4601	828.2574	828.1208	827.9943	827.9024		827.6964	1202.120	827.1383	827.1514	826.8871	826.8281	825.9827			825.8068	825.7937		825.6055	825.5834			825.0117		824.9967	824.829	000	024.020	024.4137	824.2100	04.0.450
		SEC14L1				CTSC							i S										PKD1						EVIS	RBM3		ICEDIL			
APPENDIX A	ESTs	SEC14 (S. cerevisiae)-like 1 ESTs	ESTS	ESTs	ESTs	cathepsin C	ESTs	ESTs	ESTS	nomo sapiens minina lor	KIAA1321 protein, partial cds	200	cytochrome c-1	ESTs	ESTs	ESTs	ESTs	Homo sapiens cDNA	FLJ20258 fis, clone	SOLF7250	ESTs	oolycystic kidney disease 1	autosomal dominant)	ESTs	ESTs, Moderately similar to	SH3-containing Grb-2-like 1	H.sapiens]	ecotropic viral integration site		RNA binding motif protein 3	ranscription elongation factor	B (SIII), polypeptide 1-like	ESIS	EST	10:1
		Hs.75232			_	•		60	Hs.47314			4/			_	Hs.48849	Hs.14658	_		Hs.28907	Hs.51891	_		Hs.169457			Hs.183294			Hs.182225		_	Hs.13205	HS.18612	HS.39043
	4	R55992 Hs.75232	AA284283 HS:37692 AA284283 HS:103087	N62595 Hs.48578	T96644 Hs.111511	AA644088 Hs.10029	_		N51682 Hs.47314			198156 HS.116461	AA447774 Hs.697	AA677880 Hs.14521	R45976 Hs.113483	AA400277 Hs.48849	N89973 Hs.14658			AA464955 Hs.5399	H17046 Hs.51891			R53527 Hs.26047			H85475 Hs.10070		W47387 Hs.26929	AA054287 Hs.61840					W8/585 HS.59043
k et al.	712379	40704	325012	288846	121326	845355	283982	239662	279058		814329	121/20	813830	430687	35788	742659	305677			810088	50689		245526	39843			249753		324180	380797	!	490947	269416	418049	41/202
Westbrook et al.	GF203	GF200	GF201	GF201	GF202	GF201	GF203	GF201	GF202		GF203	GFZUZ	GF200	GF203	GF203	GF202	GF201			GF201	GF201		GF204	GF201			GF203		GF201	GF200		GF202	GF203	GF201	GFZ0Z

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Atty	823.824	823.7372 823.7125	823.6121 823.4996	823.4706	823.3567	822.8524	822.5282	822.0363	821.9415	821.9004	821.782	821.7105	821.6631	821.5832	821.4109	821.38	821.2456		RZ0.8Z51	820.8199		820.7762	820.6049	820.326	820.1846	820.1265
	DKFZp586O1922	CTSK KIAA0129	NDUFA2	KIAA0599	COPEB		rcons	TADA2L	PheHB			SYT5		KIAA0088			KIAA0963			GATA1		PCANAP1		KIAA0582	ALCAM	
APPENDIX A	hypothetical protein	tosis)	subcomplex, 2 (8kD, B8) ESTs	KIAA0599 protein core promoter element binding	protein	ESTs	protocadnerin 8 transcriptional adaptor 2	(ADA2, yeast, homolog)-like obenylalanyl-tBNA synthetase	beta-subunit	ESTs	ESTs	synaptotagmin 5	ESTs	KIAA0088 protein	ESTs	ESTs	KIAA0963 protein	ESTs, Weakly similar to	C44B9.1 [C.elegans] GATA-binding protein 1 (globin	transcription factor 1)	prostate cancer associated	protein 1	ESTs	KIAA0582 protein activated leucocyte cell	adhesion molecule	ESTs
	Hs.155090	Hs.83942 Hs.179703	Hs.163867 Hs.98009	Hs.198037	Hs.4055	Hs.130838	HS.19492	Hs.125156	Hs.9081	Hs.164557	Hs.193737	Hs.23179	Hs.177948	Hs.76847	Hs.97896	Hs.23163	Hs.7724	:	Hs.12244	Hs.765		Hs.118258	Hs.98129	Hs.79507	Hs.10247	Hs.22469
	Hs.25409	Hs.83942 Hs.44361	AA425211 Hs.79854 AA406094 Hs.98009	Hs.9019	AA055585 Hs.76526	Hs.130838	Hs.19492	AA664041 Hs.116931	4A465180 Hs.9081	Hs.6970	4A406071 Hs.97974	Hs.23179	4A459937 Hs.97458	Hs.76847	4A420989 Hs.97896	Hs.23163	4A476273 Hs.106781	:	Hs.12244	Hs.765		Hs.102672	AA412435 Hs.98129	AA443147 Hs.6875	Hs.10247	Hs.22469
	H08753	R01515 N32542	AA425211 AA406094	T49576	AA055585	N59757	H29216	AA664041	AA465180	R56863	AA406071	H39018	AA459937	H67274	AA420989	R45380	AA476273		R49442	R06446		N52554	AA412435	AA443147	R13558	H10051
k et al.	45645	123926 270975	773287	96929	510381	248528	52594	822288	815072	41092	743029	192271	795687	229537	731254	35783	770672		38350	126368		244796	731444	796747	26617	46933
Westbrook et al	GF201	GF200	GF204 GF202	GF201	GF201	GF203	GF201	GF204	GF203	GF204	GF202	GF201	GF201	GF200	GF202	GF203	GF201		GF202	GF200		GF201	GF202	GF201	GF200	GF201

	1.02206234	.00820269	1.55581266	-1.6960054	-1.2820006	-1 3884484	-1.0722666		1.11129937		-2.3199401			-1.5122956	-1.3629755		1.21593094	-1.122843		1.51045747		-2.0818786	-1.1221435	1.34332238	
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820.1174	820.0994 820.0406	819.9532	819.868	819.6445	819.481	819.1751	818.4605	818.3592	818.1776	818.0576	817.9655	817.8994	817.8958	817.8691	817.7364		817.4728	817.376		817.3503		817.2417	817.2302	817.1692	817.0256
		GNB5		KIAA0726	KIAA0870				HPCA									KIAA0089		MCM3			RNASE6PL		CYP4B1
ESTs Homo sapiens mRNA; cDNA DKFZb434E0626 (from clone	DKFZp434E0626) ESTs	guanine nucleotide binding protein (G protein), beta 5	ESTs	KIAA0726 gene product	KIAA0870 protein	ESIS	ESTS	ESTS	hippocalcin	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to Similarity with snail BR-1	protein [C.elegans]	KIAA0089 protein	minichromosome maintenance	deficient (S. cerevisiae) 3	FLJ10533 fis, clone	NT2RP2001056	ribonuclease 6 precursor	ESTs	cytochrome P450, subtamily IVB, polypeptide 1
Hs.13297	Hs.30957 Hs.269088	Hs.275353	Hs.26438	Hs.107809	Hs.18166	Hs.55098	Hs.23210	Hs.116335	Hs.114215	Hs.13528	Hs.112784	Hs.57483	Hs.31652	Hs.97799	Hs.35031		Hs.8715	Hs.82432		Hs.179565		Hs.67619	Hs.8297	Hs.16552	Hs.687
Hs.13297	Hs.123873 Hs.47862	AA708886 Hs.115241	Hs.26438	Hs.107809	3	Hs.55098	Hs.23210	5 Hs.116335	Hs.89692	Hs.13528	4 Hs.112784	Hs.57483	4A047568 Hs.31652	AA400434 Hs.97799	Hs.35031		4A459249 Hs.8715	AA485401 Hs.82432		AA455786 Hs.82479		4A427953 Hs.112030	AA405000 Hs.8297	AA458625 Hs.16552	AA291484 Hs.687
R43572	R49126 N54793	AA70888	R55640	R87698	AA449823	N95059	R42871	AA608845	H19068	90806N	AA609914	N46335	AA04756	AA40043	R93069		AA45924	AA48540		AA45578		AA42795	AA40500	AA45862	AA29148
22908	38598 244305	384567	154795	180785	788629	305302	31475	1048672	171936	303139	1031113	279232	376789	742555	196826		814443	840333		809557		773509	712341	813390	724888
GF201	GF203 GF201	GF203	GF200	GF203	GF203	GF201	GF203	GF204	GF200	GF201	GF202	GF201	GF201	GF202	GF203		GF203	GF200		GF200		GF202	GF200	GF203	GF201

-1.1685048	-1.1433371	-1.2273992	-1.1939357 -1.9981344	-1.2463073	-1.3431185	-1.3476188	-1.0032525	1.25793161
816.9238	816.6705	816.5618 816.4612	816.2583 816.2086	816.1898 816.1636	816.081	816.0008 815.8588	815.6918	815.6655 815.6221 815.6194
GYS1		UBE2G2	ТВН	BDKRB2	HIRIP4			PPT1 IL1R1 SH3GL2
glycogen synthase 1 (muscle) GYS: ESTs EST, Weakly similar to !!!! ALU SUBSAMILY J	(H.sapiens) Ubiquitin-conjugating enzyme	LECTS (110111010g0us to year) UBC7) ESTs	thyrotropin-releasing hormone TRH ESTs ESTs, Weakly similar to !!!!	ENTRY !!!! [H.sapiens] oradykinin receptor B2 ESTs, Weakly similar to coded	for by C. stegans conva ykz0f8.5 [C. elegans] HIRA interacting protein 4 (dnaJ-like)	Homo sapiens clone 23555 mRNA sequence EST ESTs, Moderately similar to	M. Sapiens S. P. Sapiens S. P. Sapiens S. P. Sapiens S. P. Sapiens S. Sapiens	informacinose, ried of infantile) interfeukin 1 receptor, type I SH3-domain GRB2-like 2
Hs.772 Hs.193235	Hs.140853	Hs.192853 Hs.13277	Hs.182231 Hs.250786	Hs.129869 Hs.250882	Hs.169577 Hs.21189	Hs.8077 Hs.238784	Hs.183294	Hs.3873 Hs.82112 Hs.75149
446 Hs.772 966 Hs.4246	671 Hs.22192	AA443634 Hs.108912 T89077 Hs.13277	AA069596 Hs.65233 AA496247 Hs.73619	AA055399 Hs.106452 AA194043 Hs.54421	AA496002 Hs.27345 AA626868 Hs.115986	R43604 Hs.8077 AA788918 Hs.122373	AA486445 Hs.27259	AA063637 Hs.3873 AA464525 Hs.82112 R20729 Hs.75149
45632 H08446 46477 H09966	32186 R42671	771295 AA44 22328 T890	382787 AA06 796867 AA48	377491 AA06 665674 AA19	768515 AA49 745216 AA62	32696 R436 1020543 AA78	842927 AA48	365973 AA06 810213 AA46 26249 R207
GF200 GF201	GF202	GF202 GF204	GF200 GF202	GF201 GF203	GF202 GF204	GF203 GF204	GF202	GF201 GF200 GF201

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APPENDIX A	W58344 Hs.103120 Hs.103120 ESTs ESTs, Weakly similar b predicted bing denelinder	AA608631 Hs.88347 Hs.88547 [Calegans] 815.4804 1.7842746 AA608411 Hs.5759 Hs.128554 KAA0824 protein KIAA0824 1815.3824 1.0568214 N23390 Hs.128497 Hs.128497 ESTs 815.0168 2.03101894	Hs.64254 Hs.117780 Hs.28241 Hs.28241 Hs.63515 Hs.273644	AA644679 Hs.5120 Hs.5120 Oyloeni, cytoplasmic, light PIN 814.2916 H15685 Hs.107514 Hs.76359 catalase CAT 814.1255 H1man finger protein (ZMF127-XQ) gene and 5'.	AA427395 Hs.28031 Hs.7838 flanking sequence 814.0408 globasium large conductance 814.0408 calcium-activated channel,	AA029299 Hs.2417 Hs.93841 subfamily M, beta member 1 KCNMB1 813.9421 AA620479 Hs.28620 Hs.161489 ESTs 813.9279 -1.1559908 v-ral siminal loukemia viral oncogene homolog B (ras	W39343 Hs,79960 Hs,250811 related; GTP binding protein) RALB 813.8195 -1.1828657 AA907727 Hs,65732 Hs,65732 ESTs R13.6956 NGFI-A binding protein 2	5 Hs.159223 (ERG1 binding protein 2) NAB2 813.4072 NGFI-A binding protein 2	AA444487 Hs.80436 Hs.159223 (ERG1 binding protein 2) NAB2 81134072 -1.3363067 N22711 Hs.8172 ESTS 813.1699 813.1699 Rs.126956 Hs.126956 Hs.126956 Hs.26959 Symptophysin-like protein SYPL 812.4284 AA1505607 Hs.76136 Hs.26956 interleukin 1, beta IL1B 812.4284	AA481269 Hs.49232 Hs.178381 ESTs 812.2524 1.14960186 AA873159 Hs.2296 Hs.288571 apolipoprotein C-l APOC1 812.2496 -1.1988125
		E =		တ	AA427395 Hs.26031	AA029299 Hs.2417 AA620479 Hs.28620		AA434487 Hs.11115		
	GF202 341643	GF202 950768 GF202 510060 GF203 268338		GF201 853938 GF201 49410	GF201 771048	GF201 470122 GF202 951242	GF200 322617 GF204 1505908	770868	GF200 770868 GF201 266531 GF204 1468063 GF201 770444 GF201 491763	GF203 815242 GF203 1472689

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1.04856672 1.34210153 -1.6015239 -2.2585045 -1.3740838 -1.2866422 -1.4110092 -2.7560513 -1.0439948 1.7800237 -1.3023658 810.1394 312,1146 812.1124 811,5893 811.4019 310.9293 310.8508 310.2458 309.9522 309.7787 809,6378 809.3552 311.5957 311.1472 310.9609 310.8183 310.7672 809.3984 311.3267 C210RF37 KIAA0733 CBFA2T3 NDUFS3 FGF12 specific factor 4, 30kD subunit CPSF4 SOS1 PMX1 HGS PNA 립 human growth factor-regulated cleavage and polyadenylation chromosome 21 open reading paired mesoderm homeo box son of sevenless (Drosophila) 5'(3')-deoxyribonucleotidase; 30kD) (NADH-coenzyme Q ubiquinone) Fe-S protein 3 ibroblast growth factor 12 tyrosine kinase substrate domain, alpha subunit 2; core-binding factor, runt ESTs, Weakly similar to FAK1-binding protein 2; NADH dehydrogenase 3B-associated KRAB putative [C.elegans] translocated to, 3 KIAA0733 protein ipoprotein lipase 1 omolog 1 reductase) epressor rame 37 ESTS ESTS ESTS ESTS ESTS ESTS ESTS Hs.117035 Hs.266476 Hs.180878 Hs.124752 Hs.154993 4s.155606 Hs.109727 Hs.110099 Hs.108873 Hs.24756 Hs.26299 Hs.67201 Hs.46707 Hs.21371 4s.98076 1s.9911 Hs.5273 Hs.6820 Hs.6351 AA677112 Hs.117035 AA281930 Hs.110099 Hs.107547 AA457253 Hs.109727 Hs.108873 AA074666 Hs.78825 Hs.98673 4A633835 Hs.83122 Hs.24756 AA142842 Hs.28781 Hs.26299 AA463444 Hs.67201 Hs.46707 Hs.21371 AA410190 Hs.98076 AA634381 Hs.5273 Hs.9911 AA293744 Hs.1873 AA775379 Hs.6351 172683 H99460 N20338 N56968 N51823 119129 340373 155569 277513 281846 754485 726236 868169 262313 264646 504372 811764 454219 838692 878699 712600 232697 743811 544664 50930 73550 28927 GF202 GF203 GF203 GF200 GF204 GF204 3F201 3F201 GF202 GF201 GF203 GF203 GF202 GF203 GF203 3F201 GF200 3F201 3F201

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809.2006 809.0189 808.7076	808.6608 808.5283	808.5035 808.0562 807.6451 807.5668	807.5148	807.3604	807.2863 807.1772 806.9421	806.9008	806.7912 806.6512	806.5589
MLL74	MAD4	вход	CYP	SCYA2		GPS2		CDH11
myeloid/ymphold or mixed- lineage leukemia (frithorax (Drosophila) homolog); translocated to, 4 EST ESTS, Weakly similar to !!!! ALIU SUBSAMIL'Y SO MATANING EKTEY. !!!		Astrinis) box polypeptide o (RNA helicase) ESTs ESTs	Clk-associating RS-cyclophilin CYP small inducible cytokine A2 (monocyte chemotactic protein 4 homologies).	je) ESTs, Weakly similar to	riybolistical protein [H.sapiens] ESTs G nrotein nathway sunpressor		NT2RP4001966 EST	osteoblast)
Hs.100469 Hs.50424 Hs.226071	Hs.165357 Hs.102402	Hs.171872 Hs.184067 Hs.105791 Hs.73232	Hs.77965	Hs.340	Hs.11500 Hs.23606 Hs.76639	Hs.7301	Hs.41793 Hs.231713	Hs.75929
AA010818 Hs.108205 N74052 Hs.50424 N70756 Hs.49921	H94934 Hs.14907 AA416970 Hs.25230	AA458473 Hs.112056 AA417622 Hs.88865 H92773 Hs.105791 AA171426 Hs.73232	AA458502 Hs.97482	AA425102 Hs.340	AA479883 Hs.11500 H11760 Hs.23606 N66156 Hs.76639	AA971634 Hs,3244	AA775291 Hs.41793 N50782 Hs.47113	H96738 Hs.75929
359597 296748 298091	230247 730036	809600 746169 197221 594806	809621	768561	772880 48033 278523	1584503	878633 283870	251685
GF201 GF202 GF202	GF200 GF202	GF202 GF203 GF203 GF202	GF201	GF200	GF202 GF203 GF203	GF204	GF204 GF202	GF200

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GF203 GF200	825740 785293	AA504844 Hs.1098 AA476543 Hs.37189	Hs.1098 Hs.37189	DKFZp434J1813 protein similar to rat HREV107 Homo sapiens cDNA F1.10991 fis. clone	DKFZP434J1813 HREV107	806.5323 806.184	-1,2532538 -1.3623807
GF202 GF204 GF201	773640 360388 210486	7 22	Hs.61508 Hs.240728 Hs.100407	PLACE1002072 ESTs programmed cell death 4	PDCD4	806.0536 805.8318 805.7225	1.4109241
GF201 GF203 GF202 GF200	133860 433328 285680 549101	R27975 Hs.24237 AA700583 Hs.113163 N67570 Hs.110293 AA083577 Hs.105973	Hs.269401 Hs.156933 Hs.110293 Hs.275245	ESTs ESTs ESTs EST HR (histone cell cycle		805.718 805.3971 805.2611 805.2578	1.16173261 -1.0687563 2.10268388
GF200 GF200 GF202	52327 163528 609209	H23459 Hs.75349 H14208 Hs.78482 AA167120 Hs.72652 B00822 Hs.75621	Hs.172350 Hs.78482 Hs.189991 Hs.270246	regulation colocatory of carevisiae) homolog A paralemmin EST §	HIRA PALM	805.1575 805.0069 804.9442 804.892	-1.0193905 -2.037249 -1.1264094 1.43256216
GF200 GF201 GF203	246869 417761 399563		Hs.62112 Hs.59197 Hs.120332	zinc finger protein 207 ESTs EST EST ESTs, Weakly similar to Similarity with snail BR-1	ZNF207	804.7919 804.7617 804.517	1.1384791
GF203	785642	AA449068 Hs.66493	Hs.66493	protein [C.elegans] ESTs, Weakly similar to		804.2888	-1.8531472
GF203 GF203 GF200 GF202 GF201 GF201	430717 416404 42880 266823 786680 366358	AA678095 Hs.125084 W86868 Hs.124744 R59697 Hs.25283 N24115 Hs.43266 AA451895 Hs.79274 AA026276 Hs.61339	Hs.201392 Hs.124744 Hs.25283 Hs.43266 Hs.79274 Hs.61339	receptor HG38 [H.sapiens] ESTs cyclin-dependent kinase 8 ESTs annexin A5	CDK8 ANXA5	804.2675 804.1707 804 803.5592 803.5749 803.2943	1,31364303 -1,045169 -1,161823 -1,2657874
GF201 GF200	855390	AA663995 Hs.83879 AA449762 Hs.23517	Hs.155462 Hs.256583	minichromosome maintenance deficient (mis5, S. pombe) 6 interleukin enhancer binding factor 3, 90kD	e MCM6 ILF3	803.0984	1.07848409

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1.01221351	801.2465 801.1014 800.8508		EST Homo sapiens cDNA FLJ10718 fis, clone NT2RP3001096, weakfy similar to Ratus norvegicus leprecan mRNA ESTs	Hs.49609 Hs.42824 Hs.111911	N69100 Hs.49609 AA873182 Hs.42824 AA400108 Hs.111911		GF202 292982 GF204 1472797 GF202 742707	GF202 GF204 GF204
	801.2727		CAMP-DEPENDENT PROTEIN KINASE INHIBITOR, MUSCLE/BRAIN FORM [H.sapiens]	Hs.106106	AA004415 Hs.24196			GF2
-2.0057241	801.8618		Homo sapiens CAC-1 mRNA, partial cds	Hs.109748	11 Hs.109748	20 H03961	GF203 151620	GF
-1.7600641	802.1563 801.9045 801.8776	SEZ6L	seizure related gene o (mouse)-like ESTs	Hs.194766 Hs.11962 Hs.58742	H29013 Hs.100212 AA620708 Hs.11962 W85822 Hs.58742	(0	GF201 49937 GF204 1049216 GF202 415988	GF2 GF2 GF3
-1.8493421	802.2007		Homo sapiens mRNA; cDNA DKFZp586A0618 (from clone DKFZp586A0618)	Hs.4105	AA292086 Hs.4105		GF203 725405	GF
1.20637176	802.8101 802.6219 802.608		ESTs ESTs ESTs	Hs.167388 Hs.42254 Hs.75013	13 Hs.52199 17 Hs.42254 12 Hs.6491	7 R43093 42 N32057 6 R45292	GF201 32737 GF201 260142 GF202 35626	GF201 GF201 GF202
-1.5826718	802.8997	KIAA0257	KIAA0257 protein ESTs, Weakly similar to serine/threonine-specific protein kinase [M.musculus]	Hs.75912 Hs.6163	AA479691 Hs.75912 AA412184 Hs.106499		GF201 740742 GF202 729929	GF.
Atty Docket No. 21	Attj		APPENDIX A				Westbrook et al.	We

Westbrook et al.

1 91 46741	-2.5229287	-1.3973973	1.00896021	-1.4673215					-1.2688339		1.09193424		-1.5275518		-1.5868288		1.23846751				-2.847792				-1.638589					2.885094		
000	800.1439	800.0637	799.9986	799.8196	799.799			799.7519	799.6081		299.076		798.9343		798.8458		798.83			798.7471	798.7044			798.3994	798.1788			798.1478	797.9284	797.8915	797.7857	
	LOC51628			DKFZP434D1335					DKFZP586K0524				KCNQ3		TNRC3					NEDD5				MAPRE3	GSR				20D7-FC4	RPL15	FGF2	ı 3
Homo sapiens cDNA FLJ11302 fis, clone	CGI-68 protein	ESTs	ESTs	DKFZP434D1335 protein	ESTs	Homo sapiens mRNA; cDNA	DKFZp434N103 (from clone	DKFZp434N103)	DKFZP586K0524 protein	ESTs, Weakly similar to zinc	finger protein [H.sapiens]	potassium voltage-gated channel, KQT-like subfamily,	member 3	trinucleotide repeat containing	e	Homo sapiens mRNA for	KIAA1325 protein, partial cds	neural precursor cell	expressed, developmentally	down-regulated 5	ESTs	microtubule-associated	protein, RP/EB family,	member 3	glutathione reductase	Homo sapiens mRNA; cDNA	DKFZp434M2216 (from clone	DKFZp434M2216)	hypothetical protein	ribosomal protein L15	(basic)	(comp)
1070	Hs.8054	Hs.191935	Hs.267007	Hs.8258	Hs.135995			Hs.107056	Hs.27239		Hs.270435		Hs.40866		Hs.21858		Hs.42768			Hs.155595	Hs.25777			Hs.172740	Hs.121524			Hs.199429	Hs.128702	Hs.74267	He 56066	
7054 0 10704	5	_	_	_	N63951 Hs.48901			AA431753 Hs.107056	AA448941 Hs.3745		N71457 Hs.50037		H08545 Hs.40866		N59721 Hs.21858		H99959 Hs.42768			AI025015 Hs.112179	R51305 Hs.25777			R42830 Hs.126928	AA777289 Hs.121524			AA708915 Hs.107496	AA035310 Hs.114796	4A434088 Hs.74267	W51760 Hs 103067	
100254	_	_	_		289417 N6			-	785744 AA		294916 N7		45636 HC		246722 N5		262834 H9			1631713 Alk	38883 R5				448619 AA				471664 AA	837904 AA	324383 W	
000	GF202	GF200	GF200	GF203	GF201			GF201	GF200		GF200		GF203		GF200		GF202			GF204	GF203			GF204	GF203			GF204	GF201	GF202	GE201	3

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1.02315836	1.38095393					-1.1464367			-1.2274521			1.67952068					1.16449488	-1.9387939	1.36847708				
797.709	797.5562	797.2697	797.1766	797.143		797.0732		796.7642	796.5574		796.3694	796.1578			796.1046		796.0448	795.6904	795.6557			795.6012	
CACNB3				SCLY	47		<u></u>	RBBP6	불		SF3B1								JAG2			SSR3	
calcium channel, voltagedependent, beta 3 subunit Homo sapiens cDNA FLJ20139 fis, done	COL07179	ESTs	ESTs	putative selenocysteine lyase	ESTs, Highly similar to RAS- RELATED PROTEIN RAB-1A	[M.musculus]	retinoblastoma-binding protein	9	hepatic leukemia factor	splicing factor 3b, subunit 1,	155kD	ESTs	ESTs, Weakly similar to	predicted using Genefinder	[C.elegans]	Homo sapiens clone 23718	mRNA sequence	ESTs	jagged 2	signal sequence receptor,	gamma (translocon-	associated protein gamma)	
Hs.250712	Hs.121559	Hs.53455	Hs.171689	Hs.44049		Hs.5566		Hs.85273	Hs.250692		Hs.13453	Hs.212433			Hs.57844		Hs.6580	Hs.267194	Hs.166154			Hs.28707	
R36947 Hs.118081	R96579 Hs.121559	AA454165 Hs.53455	N72848 Hs.42555	AA991864 Hs.44049		AA476287 Hs.5566		AA016290 Hs.85273	W00959 Hs.1488		AA876198 Hs.14571	AA033832 Hs.61687			AA705409 Hs.57844		AA620503 Hs.6580	R45257 Hs.128786				AA453487 Hs.27034	
25922	199577	795322	291464	1610453		770685		361239	296587		1256764				462159		951265	22716	156033			795353	
GF202	GF203	GF201	GF201	GF204		GF202		GF201	GF200		GF204	GF202			GF204		GF202	GF203	GF203			GF201	

	-2.66754	1.77900817	1.41672646	1.0197663		1.1081671	1.55845703	1.55845703
	795.5457 795.5186 795.4601 795.2872	795.2372	795.1492	794.8989	794.5703	794.265 794.2552 793.9955 793.9784	793.973	793.973
	KIAA0592	MGST1		DDX3	COL5A1		HLA-DQA1	HLA-DQA1
Human DNA sequence from done 967Mz1 on chromosome 20pp. 2-13. Contains the CHGB gene for othorogram in SCG1, a B (secretogram in 1, SCG1), a pseudogene similar to part of KIAA0172, the gene for a movel profesi similar to redicted wom, vests and	plant proteins, ESTs ESTs KIAA0592 protein	microsomal glutathione S- transferase 1	ESTS ESTS DEAD/H (Asp-Glu-Ala-	Asp/His) box polypeptide 3 EST	collagen, type V, alpha 1 ESTs ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!!	[H.sapiens] ESTs ESTs ESTs	major histocompatibility complex, class II, DQ alpha 1 HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1 HLA-DQA1
	Hs.88959 Hs.268903 Hs.99578 Hs.13273	Hs.790	Hs.95097	Hs.147916 Hs.45093	Hs.199172 Hs.199172	Hs.260556 Hs.144504 Hs.99601 Hs.49423	Hs.198253	Hs.198253
	R56840 Hs.92625 W84714 Hs.108070 AA775818 Hs.99578 AA970720 Hs.13273	Hs.790	AA677492 HS.125168 R32893 Hs.95097	AA626845 Hs.14990 N40953 Hs.45093	AA777053 Hs.121891 AA775877 Hs.121832	AA628209 Hs.116213 AA497010 Hs.75817 AA609872 Hs.99601 AA463628 Hs.49423	Hs.53875	Hs.83231
	R56840 W84714 AA775818 AA970720	AA495936 Hs.790	AA677492 R32893	AA626848 N40953	AA777053 AA775877	AA628209 AA497010 AA609872 AA463628	T63324	T63324
	138255 415688 878488 1573087	768443	460247 135610	7451 88 277189	378271 878557	1055664 897547 1031050 811834	80109	80109
	GF203 GF201 GF204 GF204	GF200	GF204 GF203	GF201 GF202	GF204 GF204	GF204 GF204 GF204 GF203	GF200	GF200

-1.9814348	2.07177417			-1.1468107 1.03070877	-1.5331512		-9 117301E	-1.212896	-1.2335351		1.02460598		-1.3503636	1 23980074	2.03320072	-1.170993		-1.0183504
793.8692 793.8548 793.8037	793.7375	793.6827	793.5677 793.3736	793.2919 793.1572	793.1459		793.1408	792.9399	792.7355		792.6981		792.488	792 0061	791.8349	791.7549	791.6219	791.5994
		ADAM17	KIAA0554				NR3C1				MMP2		TIAM2	ATR:	DPYSL4			
Homo sapiens CAC-1 mRNA, partial cds ESTs ESTs	Homo sapiens cUNA FLJ10511 fis, clone NT2RP2000656	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)	ESTs KIAA0554 protein	ESTs ESTs	ESTs	nuclear receptor subfamily 3,	group C, member 1	ESTs	ESTs	matrix metalloproteinase 2 (gelatinase A, 72kD oelatinase, 72kD type IV	collagenase)	T-cell lymphoma invasion and	metastasis 2	AI-billuing transcription racio	dihydropyrimidinase-like 4	ESTs	Homo sapiens mRNA; cDNA DKFZp761H171 (from clone DKFZp761H171): partial cds	EST
Hs.109748 Hs.28329 Hs.16312	Hs.106768	Hs.64311	Hs.97721 Hs.168350	Hs.268617 Hs.23492	Hs.199647		Hs.75772	Hs.47823	Hs.220888		Hs.111301		Hs.12598	Hs 1018/12	Hs.100058	Hs.268839	He 238679	Hs.20794
R33498 Hs.51335 AA452134 Hs.28329 R09056 Hs.16312	AA490502 Hs.106768	AA878951 Hs.125734	AA448187 Hs.97721 T74566 Hs.12196	R08153 Hs.16629 R23260 Hs.23492	54		N30428 Hs.82010				AA936799 Hs.111301		AA450024 Hs.12598	A A 281616 He 1018/19	AA757754 Hs.100058	W01211 Hs.50454	H992738 Hs 106879	
136351 786545 127487	823907	1493278	782806 84695	127173	950410		271198	244815	296168		1474174		788317	719093	395708	296838	263002	129567
GF201 GF203 GF201	GF203	GF204	GF201 GF201	GF200 GF203	GF202		GF201	GF200	GF200		GF203		GF202	CESO	GF203	GF200	CE901	GF200

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-1.1434953		1.02756412 -2.1651511	-1.5705335	1.13410974		-1.4617089	-1.7795629
791.5091 791.4973 791.4803	791.321	791.1937 791.1815	791.1296 790.9443 790.8888 790.7688	790.5321	790.5059	790.4344 789.5647 789.3742 789.1639	788.9542 788.9045
SSI-3	TIM23		KLHL3	HSPC195		TOMM70A KIAA0697	MAX
STAT induced STAT inhibitor 3 ESTs ESTs translocase of inner mitochordrial membrane 23	(yeast) homolog Homo sapiens mRNA; cDNA	DKFZp8864191) EST Homo sapiens cDNA FLJ11336 fis, clone PLACE1010661, weakly	simila to restrator econico PROTEIN PBS13 ESTs kelch (Drosophila)-like 3 FSTs	hypothetical protein ESTs, Moderately similar to SH3 domain-binding protein SNP70 [H.sapiens]	ESTs, Weakly similar to KIAA0693 protein [H.sapiens] translocase of outer mitochondrial membrane 70	(yeast) homolog A ESTs KIAA0697 protein ESTs	ESTs MAX protein
Hs.107055 Hs.183957 Hs.90463	Hs.11866	Hs.77135 Hs.112679	Hs.22383 Hs.117029 Hs.7388 Hs.43936	Hs.15093	Hs.9774	Hs.21198 Hs.22660 Hs.12329 Hs.53652	Hs.97927 Hs.42712
AA001219 Hs.25379 AA682242 Hs.117219 T40905 Hs.90463	T68317 Hs.11866	W05442 Hs.77135 AA609289 Hs.112679	R51067 Hs.22383 AA677082 Hs.117029 R51524 Hs.101108 N30868 Hs.43936	24	က	R94191 Hs.108493 AA888225 Hs.22660 AA664111 Hs.12329 AA431715 Hs.53652	N94043 Hs.97927 H99639 Hs.42712
362278 1293121 61412	83279	299442 1031562	37385 454188 38582 258120	139354	841307	198312 1492287 855625 782244	293457 262821
GF203 GF204 GF202	GF201	GF200 GF202	GF202 GF204 GF203	GF200 GF203	GF201	GF200 GF204 GF204 GF201	GF200 GF201

cofactor biosynthesis protein A biosynthesis protein C mRNA, Homo sapiens molybdenum and molybdenum cofactor Hs.42915

CLPTM1 cleft lip and palate associated transmembrane protein 1 complete cds Hs.106671

1.17410714

788.5337

ESTs, Weakly similar to hU1-70K protein [H.sapiens] STS Hs.269085

Hs.38931

Hs.101727 4s.110258 Hs.107961

H16171 N54540 T57221

GF204 3F201 GF201

244931 48704 73222

AA705112 Hs.42915

462595

GF203

788.1205 788.2097 788.1682

> ESTs, Weakly similar to !!!! MARNING ENTRY !!!! ALU SUBFAMILY J

H.sapiens]

Hs.127343 Hs.237562

AA954669 Hs.127343

1554917

GF204

Hs.50421

N74042

296719

GF202 GF201 GF201 GF202 GF202 GF202 GF201 GF201 3F204 GF201

-1.6709973

787.6738 787.6639

787.9597

POLYADENYLATE-BINDING KIAA0758 protein [H.sapiens] ESTs, Moderately similar to ESTs, Weakly similar to

4s.57887

AA126828 Hs.57887

502068

PROTEIN 1 [H.sapiens] ESTs EST

4s.251946 4s.268783

Hs.109818 Hs.112830

T50370

5059 50975 17426

H17134 H11086

1.08135728

787.5079 787,4545 87.0806 786.8504 786.8496 786.8182 786.8039

787.631

-1.2308912 -1.4302357

Huntingtin interacting protein E HYPE

Hs.234961

AA609955 Hs.112793

031182

N45031

322923 146531

4s.31023 4s.55878

Hs.31023

RBM8 glycoprotein hormones, alpha RNA binding motif protein 8 ESTS EST

> 4s.144022 Hs.119689 4s.177998 4s.272674

Hs.113721 Hs.55878 AA448402 Hs.65648

379342

781366

AA677403 Hs.119689

454908 704440 739450

4s.65648

CGA OKFZp434H1215 (from clone Homo sapiens mRNA; cDNA polypeptide

DKFZp434H1215); partial cds ESTS ೮

L3 pigment

4s.44055

AA477227 Hs.110379

N35025

271471

GF201

GF203 GF203

AA279648 Hs.10069 Hs.44055

-1.6760767 786.6159 786.7964 786.558

-1.1673138

			APPENDIX A			
809528	_	Hs.103682	ESTs		786.2944	10000
253725	N21972 Hs.43052	Hs.43052	ESTs		785.9579	-1.158/965
462652	AA704999 Hs.119861	Hs.119861	ESTS		785.7839	
_	N3431Z TS: 107.43	18.209004	ESTs, Highly similar to BasGAP-related protein		3	
432114	AA679303 Hs.125194	Hs.272113	[H.sapiens]		785.7636	
			Homo sapiens partial mRNA for NICE-4 protein, 3' end.			
245015	N52646 Hs.8127	Hs.273229	clone 1056f5		785.6834	-1.7130927
588139	Q	Hs.19107	ESTs		785.6501	1.10314902
			ESTs, Weakly similar to !!!!			
			ALU SUBFAMILY J WARNING ENTRY !!!!			
41888	R67283 Hs.22529	Hs.22529	[H.sapiens]		785.5647	-1.1350506
			NIMA (never in mitosis gene			
462926	AA682321 Hs.80896	Hs.153704	ed kinase 2	NEK2	785.5185	1.15445027
285798	N69332 Hs.54245	Hs.54245	ESTs		785.4093	1.31949969
			CGG triplet repeat binding			
815208	AA481248 Hs.107587	Hs.86041	protein 1	CGGBP1	785.3777	-1.0714875
810957	AA459399 Hs.41393	Hs.32312	KIAA0356 gene product	KIAA0356	785.1245	
			membrane cofactor protein			
			lymphocyte cross-reactive			
796997	AA463544 Hs.83532	Hs.83532		MCP	785.1172	1.58794186
773265	AA425325 Hs.98427	Hs.98427	ESTs		785.0964	1.19680524
277003	N34967 Hs.11614	Hs.11614	ESTs		784.5983	
			nucleosome assembly protein			
92026	AA463251 Hs.21365	Hs.21365	1-like 3	NAP1L3	784.4346	1.2406045
52339	H23278 Hs.8037	Hs.8037	ESTs		784.4246	
455156	AA676822 Hs.117093	Hs.117093	ESTs		784.4149	
			Homo sapiens cDNA FLJ11265 fis, clone			
770000	001001 -11 010101 - 1	0277700	DI ACE1000159		204 4050	10001001

Homo sapiens cDNA

1.13938584	2.14786426		2.14786426			-1.5903064		1.02583798		2.03453773	-1.2379535			1.63774926	-1.1347312				1.08521001				-1.0889404	-1.4022227		-1.2502533				1 58028677	1002600:1
784.1786	784.1149		784.1149	784.0931	783.9967	783.887	783.8513	783.8367		783.808	783.7247			783.4122	783.403		783.3802		783.3029		783.2513	783.1656	782.9795	782.9681		782.5276			782.3878	789 9984	102.3204
							DKFZP566H073				TUBB2						E1B-AP5		PTHR1							CYP3A7			EIF2S3		
FLJ11223 fis, clone PLACE1008209	Human clone 23933 mHNA sequence	Human clone 23933 mRNA	sedneuce	EST	ESTs	ESTs	DKFZP566H073 protein	ESTs	Homo sapiens cDNA	FLJ20653 fis, clone KAT01739	tubulin, beta, 2	ESTs, Weakly similar to	katanin p80 subunit	[H.sapiens]	EST	E1B-55kDa-associated protein	2	parathyroid hormone receptor	-	ESTs, Moderately similar to	CGI-92 protein [H.sapiens]	ESTs	EST	ESTs	cytochrome P450, subfamily	IIIA, polypeptide 7	eukaryotic translation initiation	factor 2, subunit 3 (gamma,	52kD) FSTs Highly similar to	UCDCO16 [U canions]	norcoro [n.sapieris]
Hs.92308	Hs.239483		Hs.239483	Hs.120019	Hs.55028	Hs.191956	Hs.7158	Hs.109843		Hs.180059	Hs.251653			Hs.19574	Hs.49193		Hs.155218		Hs.1019		Hs.55046	Hs.154054	Hs.68270	Hs.72080		Hs.172323			Hs.211539	112 474774	HS.1/1//4
AA188999 Hs.92308	H56918 Hs.113403		H56918 Hs.74850	AA707494 Hs.120019	AA644547 Hs.55028	AA609606 Hs.112732	AA953999 Hs.7158	W33182 Hs.109843		N67039 Hs.15661	AA888148 Hs.100155			ထ္ထ	N66399 Hs.49193		T88731 Hs.108373		AA872602 Hs.1019		AA181978 Hs.55046	H98683 Hs.102378	AA083207 Hs.68270	AA704483 Hs.72080		H67678 Hs.117846			AA464708 Hs.29910	100000	AA491249 HS.8461
626462	204614		204614	1291999	845435	1031741	1573520	321807		295985	1492104			950395	285466		109879		1323328		624667	262023	549035	450744		211234			810237		82423/
GF202	GF200		GF200	GF204	GF204	GF202	GF204	GF202		GF200	GF203			GF202	GF202		GF204		GF203		GF204	GF201	GF202	GF203		GF203			GF201	000	GF203

-1.6958282 -1.4282342 -2.3450581	-1.9983515	-1.4663062	-1.869028 -2.2956246	1.1287689	-1.5280467	-1.067394
780.0511 780.0242 779.9313 779.8821	779.3 779.178 779.1145 778.5292	778.3268	777.4113 777.4113 777.4077 777.4077	777.347 777.2776 777.2058	777.1325 776.9899 776.9131	776.9012
AZM	YDD19 DKFZP586l1023	PVR	KIAA0537 TIMM8B	KIAAU362 GTF2IRD1	BAI3 GRIA1	KIAA0063 PSMD10
Homo sapiens cDNA FLJ10018 fis, clone HEMBA1000631 alpha-2-macroglobulin ESTs ESTs	YDD19 protein ESTs DKFZP58611023 protein ESTs	38 protein [H.sapiens] poliovirus receptor ESTs, Moderately similar to !!!! ALU SUBFAMIL'S SQ WARNING ENTRY !!!!	[H.sapiens] KIAA0537 gene product translocase of inner mitochondrial membrane 8 (yeast) homolog B	KIAA0362 protein ESTs GTF2I repeat domain- containing 1 ESTs brain-specific anglogenesis	inhibitor 3 ESTs glutamate receptor, ionotropic, AMPA 1	KIAA0063 gene product proteasome (prosome, macropain) 26S subunit, non- ATPase, 10
Hs.99722 Hs.74561 Hs.122681 Hs.179696 Hs.18449	Hs.25615 Hs.182362 Hs.111515 Hs.42826	Hs.99168 Hs.171844	Hs.200598 Hs.200598 Hs.268561	Hs.25515 Hs.70488 Hs.21075 Hs.27222	Hs.8074 Hs.130825 Hs.7117	Hs.3094
AA620346 Hs.12370 AA775447 Hs.74561 AA780083 Hs.122681 AA621206 Hs.112951 AAA621206 Hs.142951	AA478315 HS.44755 AA680070 HS.72477 AA625574 HS.111515 V20229 HS.42826	AA448281 Hs.99168 AA412284 Hs.6879	AA702764 Hs.114031 N64374 Hs.94158 AA024637 Hs.105994	H28922 Hs.25515 R44397 Hs.23694 AA019591 Hs.21075 H10034 Hs.27222	Hs.8074 Hs.130825 Hs.7117	
AA620346 AA775447 AA780083 AA621206	AA478315 AA680070 AA625574 N20229	AA448281 AA412284	AA702724 N64374 AA024637	H28922 R44397 AA019591 H10034	H17398 R70546 H23378	AA757576 R77104
1030929 878182 1033716 744407	740965 430368 745296 264604	782843 731459	383945 290199 365157	49873 34626 363377 46617	50491 142331 52228	395604
GF201 GF203 GF204 GF202	GF204 GF204 GF203 GF203	GF202 GF201	GF203 GF202 GF201	GF200 GF203 GF200 GF201	GF201 GF204 GF200	GF203

		987886	-2.6566265		1.38099235	-1.5281712	-1 2600973		1.26694511	1.33400511		-1.7137078
776.6019	776.2266	775.9595	775.7037	775.617	775.5729	775.5525	775.485	775.241	774.8495 774.7141	774.6503	774.6396	774.5832
FABP7	ATP6A1		CD4 STAG3	ACTN4	HRG			ACK		EPHX2	RFC4	
fatty acid binding protein 7, brain ATPase, H+ transporting, yysosomal (vacuolar proton purmo), aloha polyoeotide.	70kD, isoform 1 Homo sapiens cDNA FLJ20079 fis, clone	COL03057	CD4 antigen (p55) stromal antigen 3	, alpha 4	ESTs histidine-rich glycoprotein	ESTs, Moderately similar to zinc finger protein [H.sapiens] ESTs, Moderately similar to IIII ALU SUBFAMILY SQ MARNING FATRY IIII	[H.sapiens]	ES IS activated p21cdc42Hs kinase ESTs, Weakly similar to IIII ALU SUBFAMILY J	WADNING ENTRY [H.sapiens] ESTs	epoxide hydrolase 2, cytoplasmic replication factor C (activator	1) 4 (37kD) ESTs, Weakly similar to	putative p150 [H.sapiens]
Hs.26770	Hs.5119	Hs.165948	Hs.17483 Hs.20132	Hs.182485	Hs.119220 Hs.1498	Hs.117270	Hs.71367	Hs.110059 Hs.153937	Hs.205048 Hs.42279	Hs.113	Hs.35120	Hs.272150
N46862 Hs.82480	AA504160 Hs.52210	4A775574 Hs.121826	AA451863 Hs.17483 AA453028 Hs.99300	4A702768 Hs.119196	4A428308 Hs.119220 H70473 Hs.1498	AA682587 Hs.117270	AA130861 Hs.71367	AA033983 Hs.110059 AA427891 Hs.80493	AA053682 Hs.63055 N29356 Hs.42279	R73525 Hs.113	N93924 Hs.108133	AA700024 Hs.114685
279195 N46	825170 AA		786308 AA		773591 AA 212649 H7	450809 AA		429909 AA 773478 AA	510397 AA 259072 N2	156473 R7	309288 N9	436051 AA
GF201	GF201	GF204	GF203	GF204	GF204 GF200	GF203	GF204	GF202 GF201	GF202 GF201	GF200	GF201	GF203

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774.4086	773.9 773.8608 773.7081 773.5887	773.5684	773.4097 773.2042	773.1701 773.1638	773.1249 773.1221 773.0264	772.965 772.9553	772.653 772.6169
	NME1 CUL5 KIAA1382			SNRPD1	MP1	NCK1	G3BP KIAA0231
ESTs, Weakly similar to putative serine/threonine protein kinase [H.sapiens] ESTs, Weakly similar to T08D2.6 [C.elegans]	non-metastatic cells 1, protein Cullin S appressed in Cullin S ESTs armino acid transporter 2 ESTs, Moderately Similar to !!!!	(H.sapiens) Homo sapiens cDNA FI.110583 fis. clone	NT2RP2003629 ESTs small nuclear	_	A; cDNA		Ras-GTPase-activating protein SH3-domain-binding protein KIAA0231 protein
Hs.123426 Hs.66309	Hs.118638 Hs.101299 Hs.88780 Hs.234433	Hs.90421	Hs.105633 Hs.97967	Hs.86948 Hs.231209	Hs.111730 Hs.6361 Hs.86636	Hs.62601 Hs.54589	Hs.220689 Hs.199243
1456315 AA862997 Hs.123426 700830 AA283819 Hs.66309	AA644092 Hs.118638 AA857851 Hs.79982 AA487236 Hs.88780 AA598996 Hs.24156	R88709 Hs.30816	T99853 Hs.105633 AA406210 Hs.97967	AA286670 Hs.99660 AA195253 Hs.43853	AA781507 Hs.111730 AA676885 Hs.6361 AA459110 Hs.86636	AA629033 Hs.65536 AA280214 Hs.54589	AA449834 Hs.79310 N79669 Hs.7938
1456315	845363 1475120 841480 897733	194908	123229 742867	701087 665496	855175 897142 814320	744010 712683	788645 289502
GF204 GF203	GF202 GF204 GF202 GF202	GF203	GF200 GF202	GF204 GF203	GF203 GF204 GF203	GF201 GF200	GF200 GF200

222996 N90630 Hs.75544 Hs.75644 profess, et apolypeatide between nuclear heterogeneous heterogeneous nuclear h	PPN2 yrosine 3- nonoxygenase/tryptophan 5- nonoxygenase activation	772.2557	557	
Hs.2694 Hs.2694 Hs.20026 Hs.20026 Hs.2173694 Hs.271582 Hs.2625 Hs.2625 Hs.26361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.78361 Hs.7	lypeptide YWHAH	Н 772.1717		-1.1510293
Hs.2624 Hs.20026 Hs.20014 Hs.173594 Hs.211582 Hs.25625 Hs.25625 Hs.75390 Hs.75391 Hs.186700 Hs.26300 Hs.186700 Hs.26300 Hs.186700 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300 Hs.26300	ein M HNRPM rrosine kinase,	M 772.1482		-1.3175372
Hs.26014 Hs.173594 Hs.211582 Hs.25625 Hs.26625 Hs.78961 Hs.16273 Hs.186500 Hs.256348 Hs.186500 Hs.256348 Hs.265982 Hs.265982 Hs.265982 Hs.265982 Hs.265982 Hs.265982	1 NTRK1	1 772.0813		-1.459224
Hs.173594 Hs.211582 Hs.25625 Hs.82961 Hs.7830 Hs.7831 Hs.11915 Hs.18600 Hs.2348 Hs.78473 Hs.265982 Hs.265982		J		
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2 Hs.25625 Hs.82961 Hs.82961 Hs.73961 Hs.121915 Hs.121915 Hs.86907 Hs.86907 Hs.86907 Hs.86907 Hs.86907	oiypeptide MYLK	771.7544		-1.3945534
Hs.82961 Hs.3530 Hs.78361 Hs.118273 Hs.121915 Hs.253248 Hs.76173 Hs.85077 Hs.856982 Hs.165982 Hs.165982 Hs.165761	cDNA clone 32, weakly yYLINOSITOL ESTERASE (EC 3.14.10)	771.6482	482	
Hs.3550 Hs.78361 Hs.118273 Hs.121915 Hs.234600 Hs.234600 Hs.234600 Hs.26592 Hs.26592 Hs.165761	ntestinal) serine-		817	
Hs./8861 Hs./18273 Hs./121915 Hs.22248 Hs.76173 Hs.265982 Hs.265982 Hs.185761		771.528		4 0750050
Hs.186600 Hs.28248 Hs.76173 Hs.85077 Hs.265982 Hs.185761	delweb			0000000
Hs.76173 Hs.85077 Hs.265982 Hs.185761		771.3353 771.3353 771.3167		-2.2629115 -1.5792871
Hs.265982 Hs.185761	HSU5252: similar to IIII WARNING	2521 777.1075 770.9632	·	1.04899025
	.sapiens]	770.7555 770.6808		1.22466077 1.22085427

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-1.6812759 1.1941079 -1.9700867	-1.026367	1.07267175	1.0091071 -1.2956322 -1.2956322	1.12089928	-1,3522681
768.2035 767.9639 767.8639	767.7939 767.7065 767.6646	767.5118 767.5094 767.4877	767.4757 767.4388 767.1195 767.1195	766.4095 766.3795 766.3035 766.1556 766.0814 766.0187	765.9881
SUPT6H RANBP2	ITGAE	KIF5B TUBA3 MYL1	CD48 CAPN1 KNS2 KNS2 DKFZP56411922	UTRN JUND CAST NCOA3	DDX1 COL4A3BP
suppressor of Ty (S.cerevisiae) 6 homolog FAN binding protein 2 ESTs Homo sapiens clone 22849 and 23755 unknown mRNA, partial cds integrin, ablah E (antigen CD103, human mucosal	lymphocyte antigen 1; alpha polypeptide) ESTs ESTs	kinesin family member 5B Tubulin, alpha, brain-specific myosin, light polypeptide 1, alkali, skeletal, fast CDAR anthon, Recell	carbon anger (1700) calpain, large polypeptide L1 kinesin 2 (60-70kD) kinesin 2 (60-70kD)	ESS ESS utrophin (homologous to dystrophin) jun D proto-oncogene ESS calpastatin nuclear receptor coactivator 3	DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 1 collagen, type IV, alpha 3 (Goodpasture antigen) binding protein
Hs.12303 Hs.199179 Hs.167688 Hs.13377	Hs.851 Hs.62772 Hs.97553	Hs.149436 Hs.272897 Hs.90318	Hs.901 Hs.2575 Hs.117977 Hs.117977 Hs.72157	Hs.238/69 Hs.182817 Hs.17401 Hs.2780 Hs.247043 Hs.225977	Hs.78580 Hs.21276
R85545 Hs.12303 H78788 Hs.82707 N34961 Hs.124014 AA774824 Hs.13377	4A425451 Hs.851 AA156795 Hs.62772 AA429573 Hs.97553	AA865469 Hs.116402 AA865469 Hs.119079 T52894 Hs.90318	705416 Hs.901 115456 Hs.2575 4A410207 Hs.114587 4A410207 Hs.80494 4A464691 Hs.72157	AA7/8345 Hs.12201/ H03591 Hs.30424 AA046321 Hs.17401 AA418670 Hs.2242 H79011 Hs.122726 W46433 Hs.72155	AA428518 Hs.78580 N62348 Hs.42839
R85545 H78788 N34961 AA77482	AA425451 Hs.851 AA156795 Hs.627 AA429573 Hs.975	AA64421 AA865469 T52894	R05416 H15456 AA41020 AA41020	AA7.7834; H03591 AA04632; AA41867; AA89456; H79011	AA428511
180195 230100 276977 970734	773332 502444 781461	845502 1470060 68103	125134 49560 754436 754436 810224	379307 151418 376764 767784 1416777 233666 323988	773192
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765.6185 765.6052 765.4882	765.4419	765.0468	764.9092	764.8608	764.8544	764.8151 764.8151	764.7958 764.7694	764.7282
HE3-ALPHA KIAA0407		B4GALT1	KIAA0106				EGFL1	KIT
human epididymis-specific 3 alpha KIAA0407 protein N-acetyltransferase, homolog	or S. cerevisiae And r KIAA0077 protein UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase,	polypeptide 1 anti-oxidant protein 2 (non- selentium glutathione peroxidase, acidic calcium- independent phospholipase	A2) Homo sapiens mRNA for	KIAA1434 protein, partial cds Homo sapiens cDNA FLJ20355 fis, clone HEP15804, highly similar to AF121883 Homo sapiens	sorting nexin 14 ESTs, Moderately similar to tetracycline transporter-like	protein [M.musculus] ESTs Horn sapiens chromosome Xq28 psHMG17 pseudogene, complete sequence; and melanoma antigen family A1 (MAGEA1) and zinc finger	protein 275 (ZNF275) genes, complete cds EGF-like-domain, multiple 1 v-kit Hardy-Zuckerman 4 feline	sarcoma viral oncogene homolog
Hs.2718 Hs.200480	Hs.75935 Hs.75935	Hs.198248	Hs.120	Hs.171917	Hs.46801	Hs.43773 Hs.43773	Hs.9786 Hs.55173	Hs.81665
AA778629 Hs.2718 AA496565 Hs.111811	H55220 H8.113492 AA291412 H8.75935	AA778196 Hs.130728	AA598874 Hs.120	AA702748 Hs.117994	N48004 Hs.125726	AA481152 Hs.4220 AA497045 Hs.43773	AA406125 Hs.9786 AA411204 Hs.55173	N24824 RG.24
1048985 755952	154720 725223	448380	897983	447299	281632	823577	742837 754653	269806
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1.15545823	1.01327071		1.12269626	-1.1090245	2.29291453			1.49177653					-1.4415276		1.19328167	-1.6670485		-1.0392391		
764.7205	764.6243 764.5241	764.4969	764.4747	764.4587	764.3019	764.3017	764.0594	764.0041		763.9615		763.8676	763.8001	763.7462	763.5634	763.4487	763.3588	763.2262 763.1793		763.1587
FGFR4	MAGEA2			GABPA				CUGBP2		MTF1				LTF			POR1			FLJ10852
fibroblast growth factor receptor 4	melanoma antigen, family A, 2 MAGEA2 ESTs Homo sapiens mRNA for	TL132	ESTs, Weakly similar to ORF YGR101w [S.cerevisiae] GA-binding protein	transcription factor, alpha subunit (60kD)	ESTs	ESTs, Moderately similar to DII3 protein [M.musculus] Homo sapiens cDNA	NT2RP3001081	binding protein 2	metal-regulatory transcription	factor 1	ESTs, Weakly similar to CGI-	78 protein [H.sapiens]	mRNA sequence	lactotransferrin	ESTs	ESTs	partner of RAC1 (arfaptin 2)	ESTs ESTs	hypothetical protein similar to	priotein AKR1
Hs.165950	Hs.36980 Hs.166520	Hs.234573	Hs.13094	Hs.78	Hs.71577	Hs.127792	Hs.24129	Hs.211610		Hs.211581		Hs.42954	Hs.188882	Hs.347	Hs.268899	Hs.61364	Hs.75139	Hs.184987 Hs 271766	3	Hs.95744
AA446994 Hs.1421	AA905896 Hs.36980 AA417252 Hs.98213	AA437374 Hs.111065	T69473 Hs.13094	N24732 Hs.43567	AA417355 Hs.71577	1469966 AA865362 Hs.127792	AA459405 Hs.24129	AA701933 Hs.21653		AA448256 Hs.94683		N21153 Hs.42954	AA598834 Hs.7268	AA677706 Hs.347	R06754 Hs.119642	N35369 Hs.12897	AA425908 Hs.75139	AA156112 Hs.28718 W85782 Hs 18529		AA459681 Hs.95744
784224	1505360 731202	770337	66894	265716	731198	1469966	810970	435573		782824		264868	898313	460487	126540	272049	769603	589861		795561
GF200	GF204 GF202	GF201	GF200	GF202	GF202	GF204	GF201	GF203		GF201		GF201	GF202	GF201	GF202	GF203	GF201	GF202	3	GF201

	Atty Docket No. 21726/92526	1.61680791	1.30811775	1.04504316													-1.6640587	-1.3842804	-2.1629425			1.14465755						-1.2476151		-1.0810682			1.00159233
	Atty E	763.0626	762.9517	762.7734	762.7689			762.5871		762.1384						762.0643	762.0275	762.0244	761.9627	761.814	761.7833	761.7629		761.6816	781 8930	761 5883	761.459	761.0987	761.084	760.645		760.3538	760.032
no Hiera Mariff Spails South Study		DKFZP434N093		PLCD1	18620			SCYA3		CYLC2												SSDP		TGN51					G10				
W. thear there had the had the the their short that the	APPENDIX A	DKFZP434N093 protein	ESTs	phospholipase C, delta 1	(20kD)	small inducible cytokine A3	(homologous to mouse Mip-	1a)	cylicin, basic protein of sperm	head cytoskeleton 2	Homo sapiens cDNA	FLJ10279 fis, clone	HEMBB1001242, highly	similar to Homo sapiens	topoisomerase-related	function protein mRNA	ESTs	ESTs	EST	ESTs	ESTs	sequence-specific single- stranded-DNA-binding protein	trans-Golgi network protein	(46, 48, 51kD isoforms)	profess Highly Silling to Colfey	FISTS	ESTS	ESTS	maternal G10 transcript	ESTs	Homo sapiens mRNA; cDNA DKFZp434H2218 (from clone	DKFZp434H2218)	ESTs
		Hs.33363	Hs.32646	Hs.80776	Hs 183487			Hs.73817		Hs.3232						Hs.25534	Hs.66817	Hs.30469	Hs.203660	Hs.58628	Hs.125676	Hs.266914		Hs.14894	II. 5000	Hs 252588	Hs.188897	Hs.94329	Hs.114034	Hs.18826		Hs.45114	Hs.44737
		Hs.20900	AA521035 Hs.32646	755490 Hs.80776	AA479795 Hs 96649			AA677522 Hs.73817		Al018066 Hs.3232						4A029273 Hs.25534	4A426032 Hs.66817	4A448663 Hs.30469	Hs.23258	3 Hs.58628	4A884742 Hs.125676) Hs.59628		Hs.100593	4 A C C C C C C C C C C C C C C C C C C	Hs 113146			0	Hs.18826			Hs.44737
			_		AA4797												AA4260	_	_	W81008	_	W91960		T81338	030344	R02259	N73092	N76117	AA4060	R11527			N35603
	ok et al.	277732	826353	154600	740604			460398		1642124						470140	757241	786076	130392	347296	1467283	415197		109437	745500	124510	291961	299427	743041	128297		282162	272288
	Westbrook et al.	GF203	GF203	GF203	GF201			GF201		GF204						GF204	GF202	GF203	GF202	GF201	GF204	GF202		GF201	CESO	GE204	GF201	GF202	GF201	GF200		GF201	GF202

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1.66544324			-1.9850266 1.70463975	1.23832356	-1.0504964	-1.416076									-1.44/814/	-2.3930243		1.17857069	1.06288998				
759.9619	759.8476	759.7626	759.7256 759.7166	759.6525	759.6348	759.4575	759.0974	1118.84/		758.6428		758.5732			758:3882	758.3851		758.3123	758.159	758.124		758.0251	
INPP5A		PPP2R1A	EIF1A	KIAA0942			HDAC2			VCY								AMPD3					
inositol polyphosphate-5- phosphatase, 40kD ESTs, Weakly similar to hypothetical protein	[H.sapiens] protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha	isoform eukaryotic translation initiation	factor 1A ESTs	KIAA0942 protein	ESTs	ESTs	nistone deacetylase 2	ESIS	variable charge, Y	chromosome	Homo sapiens mRNA full	EUROIMAGE 1035904	Homo sapiens mRNA; cDNA	UKFZp564CU53 (from clone	DKFZp564C053)	ESTs	adenosine monophosphate	deaminase (isoform E)	ESTs	ESTs	ESTs, Weakly similar to microtubule-vesicle linker	CLIP-170 [H.sapiens]	
Hs.124029	Hs.13543	Hs.173902	Hs.4310 Hs.42948	Hs.6763	Hs.24880	Hs.263254	Hs.3352	HS.269586		Hs.170076		Hs.36353			Hs.42484	Hs.25287		Hs.83918	Hs.97591	Hs.31429		Hs.98640	
T58773 Hs.63458	AA453580 Hs.13543	AA114966 Hs.56126	AA281733 Hs.4310 W07745 Hs.42948	AA417363 Hs.22233	AA456136 Hs.24880	R54416 Hs.26113	AA127093 Hs.3352	AA/05201 Hs.120953		AA406064 Hs.97368		AA702272 Hs.114110			AA452248 Hs.42484	AA700785 Hs.25287		R01732 Hs.83918	AA398016 Hs.97591	H16572 Hs.31429		AA284277 Hs.20074	
77533	795210	490023	712436	731240	796351	39178	502669	462/62		743038		447892			/865/3	435743		124127	726647	49259		324510	
GF200	GF201	GF201	GF203 GF200	GF202	GF202	GF203	GF201	GF204		GF201		GF204			GF203	GF203		GF200	GF203	GF204		GF201	

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	-2.105237	-1.2312511	-2,48366 -1,4020391 -1,1282633	1.19378946	-2.0936086	1.18147327 1.58524326 1.28882592 -1,4839547	-2.5108669 1.43718507 -1.0983152
	757.9301 757.8763	757.6335	757.2357 757.2314 757.2296	757.1466 757.1281 756.6736 756.6664 756.6542	756.549 756.1823 756.0703 756.0629	756.0609 755.9716 755.8395 755.8348	755.7348 755.6372 755.2884
		FEZ2	DKFZP564K1964	LOC51763	PDCD5 KPNB2 KIAA0006	PTPRR ANXA4	НОХВ13
ESTS, Highly similar to PHOSPHORYLASE B KINASE ALPHA BEGIII ATORY CHAIN I IVER	ISOFORM [H.sapiens] ESTs fasciculation and elongation	protein zeta 2 (zygin II) ESTs	ESTs DKFZP564K1964 protein EST SKIP for skeletal muscle and	Notilely enriched mostrol phosphatase ESTs ESTs ESTS ESTS ESTS ESTS ESTS	ESTs programmed cell death 5 karyopherin (importin) beta 2 PAK-interacting exchange factor aloha	protein tyrosine phosphatase, receptor type, R EST annexin A4	Homo sapiens mRNA; cDNA DKFZp434K0926 (from clone DKFZp434K0926) homeo box B13 ESTs
	Hs.186807 Hs.116331	Hs.103419 Hs.6272	Hs.96849 Hs.3447 Hs.207867	Hs.178347 Hs.105176 Hs.251964 Hs.119848	Hs. 191912 Hs. 1367 Hs. 168075 Hs. 79307	Hs.198288 Hs.141211 Hs.77840 Hs.192057	Hs.22753 Hs.66731 Hs.54627
	AA682856 Hs.117239 AA629355 Hs.116331	AA043280 Hs.103419 W67140 Hs.6272	AA677457 Hs.96849 AA166810 Hs.3447 H40536 Hs.113904	4A449154 Hs.88557 4A481491 Hs.105176 434297 Hs.27666 AA704825 Hs.119848	AA7.00 100 HS. 117.394 N47240 HS. 107.170 AA453508 HS. 107.951 AA236617 HS. 79307	H23202 Hs.74555 H53553 Hs.36789 AA419108 Hs.77840 AA706315 Hs.119956	AA418729 Hs.22753 AA456069 Hs.66731 N90523 Hs.54627
	450388 AA6 743727 AA6		460218 AA6 593840 AA1 192147 H40	785415 AA4 815124 AA4 277097 N34 453200 AA7			767827 AA4 813481 AA4 306146 N90
	GF203 GF204	GF203 GF201	GF203 GF202 GF203	GF200 GF204 GF203 GF204	GF203 GF200 GF201 GF201	GF200 GF200 GF200 GF203	GF202 GF203 GF202

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-1.1591126		1.27208725	1.40077653 -1.3863084				-1.0367817		-1.067208 -2.1282552	-1.6490599	-2.4095895 1.036
753.5197	753.5061	753.418 753.3765	752.6719 752.6719 752.4512		751.7808	751.6819	751.5834	751.5342	751.5281 751.5121	751.5015 751.3729 751.0758	751.008 750.9346
MAPK3	I CRLF1	-	CD39		di		TTF1	d, nit PRKAG1			SAD1
mitogen-activated protein kinase 3	cytokine receptor-like factor 1 CRLF1	ESTs, Weakly similar to KIAA0805 protein [H.sapiens] ESTs	ESTS CD39 antigen ESTs	ESTs, Weakly similar to TWISTED GASTRULATION PROTEIN PRECURSOR	[D.melanogaster] ESTs, Weakly similar to LINE- 1 REVERSE TRANSCRIPTASE	HOMOLOG [H.sapiens] transcription termination	factor, RNA polymerase I	protein kinase, AMP-activated, gamma I non-catalytic subunit PRKAG1 ESTs, Weakly similar to PUTATIVE RHORAC GUANINE NUCLEOTIDE EXCHANGE FAGTOR	[H.sapiens] ESTs	ESTs ESTs ESTs	SnRNP assembly defective 1 homolog ESTs
Hs.861	Hs.114948	Hs.22549 Hs.37424	Hs.205353 Hs.263353 Hs.26343		Hs.131279	Hs.271988	Hs.54780	Hs.3136	Hs.107761 Hs.42251	Hs.12867 Hs.124963 Hs.127931	Hs.12820 Hs.48964
AA454819 Hs.861	AA706010 Hs.114948	82	H43238 HS.91387 H10011 Hs.106343 N62631 Hs.26343		Al018381 Hs.131279	AA464517 Hs.87538	AA709143 Hs.54780	AA018676 Hs.3136	N76361 Hs.107761 H96908 Hs.42251		
809939	379768	782851 204688	31807 46715 288903		1639916	810203	385003	362755	245147 251753	44303 156322	897732 290198
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Atty Docket No. 21726	-1.6538667 1.30644385	-1.0118249							-1.3898823						-1.5959331	-1.3267892	1.03401353			-1.0621892		4 05478000	1 26915401		-1.3704133	1.15618888	-1.9598057			1.60255752 -1.1078265
Atty	750.9329 750.895	750.8747	750.8482	750.8328		750.6702	750.3651		750.3614		750.1782	750.1302			750.1251	750.0496	749.9893			749.9589	749.8203	240.070	749 2709		749.2559	749.2345	749.0046			748.5325 748.5035
		H1F0				DEPP			SHMT1		BST1				MPP2	NHLH1	MT1E					74	OLAIM OLAIM				FLJ11127			
APPENDIX A	ESTs ESTs	tone family, member 0	ESTs	ESTs	decidual protein induced by	progesterone	ESIS	serine hydroxymathyltransfarasa 1	(soluble)	bone marrow stromal cell	antigen 1	ESTs	membrane protein,	palmitoylated 2 (MAGUK p55	subfamily member 2)	nescient helix loop helix 1	metallothionein 1E (functional) MT1E	ESTs, Weakly similar to	proline-rich protein	[M.musculus]	ES	signaling lymphocytic		Homo sapiens EST00098	gene, last exon	ESTs	hypothetical protein	ESTs, Moderately similar to ELONGATION FACTOR G,	MITOCHONDRIAL	PRECURSOR [R.norvegicus] ESTs
	Hs.128959 Hs.268913	Hs.226117	Hs.16026	Hs.55444		Hs.93675	Hs.47213		Hs.8889		Hs.169998	Hs.186608			Hs.23205	Hs.30956	Hs.74170			Hs.100132	HS.9/842	02000 -11	Hs.32970 Hs.41250		Hs.95867	Hs.23389	Hs.91165			Hs.41066 Hs.175511
	Hs.128959 Hs.69059	Hs.102168	4A011136 Hs.16026	Hs.55444		Hs.125149	AA147654 Hs.47213		Hs.8889		Hs.108476	AA873342 Hs.125226			Hs.23205	Hs.30956	AA872383 Hs.74170			Hs.100132	AA404229 HS.97842	02000 -11 000014	He 41250		AA398406 Hs.95867	Hs.23389	Hs.91165			N50802 Hs.41066 AA258057 Hs.104401
	R85939 H52361	H57830	AA011136	W44762		R39563	AA147654		R53294		N27179	AA873342			R60019	H09936	AA872383			H99035	AA404228	700014	HAG58G		AA398406	R22420	T98201			N50802 AA258057
et al.	180156	205445	359795	320857		137554	505597		39798		257422	1471828			42906	46356	1472735			261472	158280	7.07	253577	10007	726791	130572	121798			283943 703383
Westbrook et al.	GF203 GF200	GF200	GF201	GF201		GF204	GF201		GF200		GF201	GF204			GF202	GF200	GF203			GF202	GF204	000	GESOS	5	GF203	GF200	GF200			GF203 GF203

Westbrook et al.	ж et al.				APPENDIX A		Any	Atty Docket No. 21 /26/
GF202 GF201	714472 377107	AA293314 Hs.7416 AA054949 Hs.61307	Hs.7416 Hs.61307	Hs.7416 Hs.61307	KIAA0397 gene product ESTs	KIAA0397	748.0905 747.9911	-2.7147892
GF203 GF202 GF204	208387 212394 385028	H60895 Hs.15370 H68309 Hs.108295 AA709154 Hs.121000	Hs.15370 Hs.108295 Hs.121000	Hs.15370 Hs.76894 Hs.191514	KIAA1407 protein, partial cds dCMP deaminase ESTs Homo sapiens mRNA for	ОСТБ	747.9164 747.8981 747.8519	-1.6282667
GF203 GF201	769868 85643	AA430361 Hs.22880 T62060 Hs.75599	Hs.22880 Hs.75599	Hs.22880 Hs.75599	upeptuyr-peptuasse III (Dr.F.s. gene) antithrombin III PAX transcription activation domain interaction protein 1	AT3	747.7668 747.6487	-1.5061872
GF200	130820		Hs.105395	Hs.173854	like ESTs, Moderately similar to GTP-BINDING PROTEIN	PAXIP1L	747.6282	1.15390437
GF201 GF201 GF201	359038 293292 121406	W92400 H N64706 H T96688 H	Hs.18746 Hs.47982 Hs.17891	Hs.243010 Hs.137282 Hs.158225	TC10 [H.sapiens] ESTs PBX/knotted 1 homeobox 1 Homo sapiens cDNA FLJ10511 fis, clone	PKNOX1	747.6241 747.5571 747.5036	
GF201 GF202 GF201	491778 35182 490140	A4115275 Hs.23977 R43780 Hs.12876 A4136040 Hs.85382	Hs.23977 Hs.12876 Hs.85382	Hs.106768 Hs.12876 Hs.91448	NT2RP2000656 ESTs MKP-1 like protein tyrosine phosphatase Homo Sapiens mRNA,partial cDNA sequence from cDNA	MKP-L	747.4847 747.1916 747.1778	1.23861666
GF202 GF204 GF200 GF201	43101 1434909 172721 50018	AA857103 Hs.33432 H19668 Hs.94722 H16761 Hs.30555	Hs.26708 Hs.33432 Hs.94722 Hs.30555	Hs.26708 Hs.235782 Hs.94722 Hs.268782	selection, DCR1-17.0 organic anion transporter OATP-E ESTs	LOC51737	747.163 747.076 747.0452 746.9896	-1.2382672
GF202 GF202 GF202	813629 782804	AA668063 HS.123834 AA447738 HS.12796 AA448186 HS.99158	ns. 123934 Hs.12796 Hs.99158	ns. 125934 Hs.206521 Hs.99158	ESI YME1 (S.cerevisiae)-like 1 ESTs	YME1L1	746.5972 746.5234	-1.7750515 -1.2279166

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-1.0947244 -1.8681942 -1.973088 -2.2452958 -1.2310085	-1.1966324	-1.082004	1.90762224		-1.6260766	1.37442374	-1.3030330	-1.5141537	1.27760185	-1.0401429	1.47677707	-1.5809977
746.0402 746.0303 745.9135 745.5985 745.2476	745.0043	744.7924 744.751	744.4099 744.4055		744.2708	744.1638	743.9662	743.6821	743.6394	743.5925	743.5289 742.989 742.7527	742.2935
KIAA0569	FSRG1					CETP	AXIN2			APAF1		DES
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! H.saplens] KIAA0569 gene product ESTs ESTs	iemale sterile homeotic-related gene 1 (mouse homolog) ESTs, Highly similar to CGI-99	orotein [H.sapiens] ESTs	ESTs	ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	H.sapiens] cholesteryl ester transfer	protein, plasma	ESTS axin 2 (conductin, axil)	ESTs ESTs. Weakly similar to	C48B6.3 [C.elegans] apoptotic protease activating	actor ESTs. Highly similar to CGI-26	protein [H.sapiens] ESTs	desmin EST ESTs
Hs.270854 Hs.34871 Hs.54795 Hs.186509 Hs.19461	Hs.75243	Hs.110803 Hs.250691	Hs.24444 Hs.234545		Hs.4190	Hs.89538	Hs.4329/ Hs.127337	Hs.97973	Hs.21323	Hs.77579	Hs.24332 Hs.50699 Hs.71832	Hs.171185 Hs.47508 Hs.106440
AA065404 Hs.14495 AA90605 Hs.34871 W32483 Hs.54795 AA705072 Hs.119669 AA158244 Hs.78281	Hs.75243	ΟI	R31645 Hs.24444 4A421171 Hs.96992		Hs.4190	Hs.89538	Hs.43297 Hs.127337	4A405182 Hs.97973	AA469950 Hs.21323	Hs.77579	N74602 Hs.24332 N76097 Hs.50699 A 4 156424 Hs 7 1832	Hs.101107 Hs.47508 Hs.106440
AA055404 AA490605 N92483 AA705072 AA158244	H72520	AA463512 R25672	R31645 AA421171		R38670	R19276	N23029 R33824	AA405182	AA469950	N51014	N74602 N76097 AA15642	R51510 N52549 R53062
510380 824109 301878 461499 592802	214133	797024 132924	135010 731095		23334	129988	26665/ 135887	742930	730362	244146	295831 299404 505425	38783 244772 40227
GF202 GF203 GF202 GF203 GF203	GF200	GF202 GF204	GF200 GF202		GF203	GF203	GF202 GF204	GF202	GF202	GF203	GF200 GF201	GF203 GF202 GF204

-1.637203	-1.2816164	-2.0846586	-1.2621534	-1.4325805	1.06284125	-1.2939517		1.23586468		1.25449958				1.0919223							-1.1792938			
742.0645	741.9362	741.9282	741.9215	741.8241	741.5335	741.3008		741.0988		741.0531	741.0092	740.8841	740.3652	740.0392	740.0061		739.922	739.8682			739.8103		/39.6984	739.6653
					CCNE2					SCAMP3				9 9				DKFZP586E0820			MYCL1		AMPD3	a
EST	ESTs	ESTs	ESTs	ESTs	cyclin E2	EST	Homo sapiens cDNA FLJ10747 fis, clone	NT2RP3001799	secretory carrier membrane	protein 3	ESTs	ESTs	ESTs	ceruloplasmin (ferroxidase)	ESTs	Homo sapiens cDNA FLJ20783 fis. clone	COL03108	DKFZP586E0820 protein	v-myc avian myelocytomatosis	viral oncogene homolog 1,	lung carcinoma derived	adenosine monophosphate	deaminase (Isoform E)	Human DNA sequence from clone RP1-102H19 on chromosome 6q15-16.1. Contains an HSP60 (TCP-10;ph60 chapperoin family) pseudogene, three novel genes, ESTs, STSs and GSSs
Hs.98872	Hs.41271	Hs.206224	Hs.26057	Hs.121016	Hs.30464	Hs.98256		Hs.189782		Hs.200600	Hs.22851	Hs.108745	Hs.47342	Hs.111461	Hs.98898		Hs.246885	Hs.91146			Hs.92137		Hs.83918	Hs.126231
4A436455 Hs.98872	V51859 Hs.41271	4A169259 Hs.111051	AA456289 Hs.26057	AA703394 Hs.121016	4A425442 Hs.30464	4A416772 Hs.98256		Hs.76438		Hs.25361	Hs.22851	Hs.108745	Hs.47342	Hs.115009	4A626374 Hs.98898		Hs.22191	AA428451 Hs.9915			Hs.92137		AA669162 Hs.116668	1471779 AAB73204 Hs.126231
AA4364	N51859	AA1692	AA4562	AA7033	AA4254	AA4167		R53973		R72518	H15675	H95787	N51961	N50654	AA6263		R42668	AA4284			R62862		AA6691	AA8732
753026	281908	609930	813154	450068	773345	731330		40042		156045	49302	243083	282315	280782	745105		32083	771215			138917		854088	1471779
GF203	GF203	GF202	GF202	GF203	GF202	GF202		GF200		GF200	GF204	GF201	GF201	GF203	GF204		GF201	GF201			GF200		GF204	GF204

COMPLY SEXTOND

	-1.5708884	-1.0463959	1.8299671	-2.4188232	-1.1181683	1.22940221		-1.4170299		-1.4170299		-1.4573903		1.27850039	1.16163119		-1.2685298				
730	739.5466	739.525	739.4736	739.0842	738.9656	738.9539		738.8641		738.8641	738.8438	738.7767		738.551	738.4619		738.3603		738.1567	1	738.0754
FOC	5	PCDH1	ELANH2		CTSE			GYPB		GYPB				RUNX2	LSM6		KCNAB2				POLR2J
O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine;polypeptide-N-acetylglucosaminyl	inaristerase) ESTs ESTs protocadherin 1 (cadherin-like	,	protease inhibitor 2 (anti- elastase), monocyte/neutrophil ELANH2	EST	cathepsin E	ESTs FSTs	glycophorin B (includes Ss	blood group)	glycophorin B (includes Ss	blood group)	ESTs	ESTs	runt-related transcription factor	2	Sm protein F	potassium voltage-gated channel, shaker-related	subfamily, beta member 2	ESTs, Weakly similar to WDNM1 PROTEIN	PRECURSOR [R.norvegicus] polymerase (RNA) II (DNA	directed) polypeptide J	(13.3KD)
60000	ns.100233 Hs.114121 Hs.55144	Hs.79769	Hs.183583	Hs.168316	Hs.1355	Hs.101490 Hs 125690	20024	Hs.250653		Hs.250653	Hs.148312	Hs.226755		Hs.121895	Hs.42438		Hs.154417		Hs.56105	!	Hs.80475
007870	AA410291 Hs.114121 N95435 Hs.55144	AA443557 Hs.79769	354664 Hs.117507	4A449780 Hs.99222	194487 Hs.1355	H51056 Hs.101490	00021.51.0004007	AA455338 Hs.15798		AA455338 Hs.117967	AA884697 Hs.125668	N74377 Hs.50490		AA858175 Hs.121895	AA708261 Hs.42438		H14383 Hs.32974		AA149250 Hs.109911		AA663075 Hs.115075
_	754458 A 309929 N	771236 A	_	785980 A	_	194155 H	•	812126 A		812126 A	1467175 A	296184 N		1435638 A	397638 A		48631 H		503051 A		852568 A
Ç	GF203 GF201	GF200	GF200	GF203	GF200	GF200	5	GF200		GF200	GF204	GF200		GF203	GF203		GF200		GF201		GF204

Atty Docket No. 21726		-1.2081597	-1.2157203 -1.186488 -1.1754483		-2.0562799		1.59294107				-1.5917805	-1.7162212	-1.3437215			-2.4361818		1.14000591	1.8150824	-1.2030887	-1.6534072	1.02383981	
Affy	737.9569	737.9479	737.8083 737.701 737.5969		737.5068		737.3545	737.2874	737.2374		737.1789	737.0405	737.0157		736.9755	736.8818		736.8724	736.6472	736.6167	736.4961	736.4941	
					101F6	<u>.</u>	NDUFA4	CHK	CSNK1D									님		KIAA0831	KIAA0296	GP110	
APPENDIX A	ESTs Human pre-T/NK cell associated protein (3B3)	mRNA, 3' end ESTs, Highly similar to WS basic-helix-loop-helix leucine	zipper protein [H.sapiens] ESTs ESTs	ESTs, Weakly similar to SODIUM- AND CHLORIDE- DEPENDENT GLYCINE	TRANSPORTER 1 [H.sapiens] putative tumor suppressor	NADH dehydrogenase (ubiquinone) 1 alpha	subcomplex, 4 (9kD, MLRQ)	choline kinase	casein kinase 1, delta	Homo sapiens mRNA; cDNA DKFZp586F2423 (from clone	DKFZp586F2423)	ESTs	ESTs	Homo sapiens cDNA FI.110532 fis. clone	NT2RP2001044	ESTs	D component of complement	(adipsin)	ESTs	KIAA0831 protein	KIAA0296 gene product	cell membrane glycoprotein, 110000M(r) (surface antigen)	
	Hs.117215	Hs.143288	Hs.93334 Hs.4248 Hs.20243		Hs.107854 Hs.149443		Hs.108661	Hs.77221	Hs.75852		Hs.13659	Hs.193417	Hs.269537		Hs.21958	Hs.159348		Hs.155597	Hs.105229	Hs.103000	Hs.119273	Hs.90107	
	1293103 AA682226 Hs.117215	AA758962 Hs.31115	526 Hs.93334 183 Hs.4248 330 Hs.20243		N62464 Hs.107854 AA454950 Hs.5007		AA680322 Hs.108661	359 Hs.77221	Al002588 Hs.14910		AA115304 Hs.109287	AA210707 Hs.17246	AA700025 Hs.118188		AA709333 Hs.120771	AA609206 Hs.112664		AA233549 Hs.111938	AA489218 Hs.105229	W23581 Hs.55419	AA890161 Hs.101253	82 Hs.90107	
∢etal.	1293103 AA68	1321677 AA75	128426 R10526 202901 H54183 127843 R08830		292223 N62464 814773 AA45496	-	869538 AA68		1610490 Al00;		501453 AA11	682768 AA21	436055 AA70		384670 AA70	1031468 AA6C		-	825058 AA48	327732 W23	1461074 AA89	78869 T51182	
Westbrook et al.	GF204	GF203	GF200 GF200 GF200		GF201 GF203) 	GF202	GF201	GF204		GF202	GF203	GF203		GF204	GF202		GF200	GF203	GF202	GF203	GF200	

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	-1.1312065	1.09299717	-1.3298085 1.45769881	1.40264877	1.06965388	1.20221522	1.00951561	-1.1706446	-1.263485 -2.241495	1.1131231	-1.1002256	-1.6460876	-1.0077671	
736.4144	736.3995	736.0831	735.8508 735.696	735.6418	735.5684	735.5627 735.2545	735.2333	734.9417	734.9394 734.9345	734.8625	734.6288	734.5349	734.5048	734.3932
	CHD2	RAP1A	KIAA0797		SOX2	SNRPE DKFZP586M1523			ZNF75	TITF1	PCBP2	S100A4	RAB9	
ESTs	binding protein 2 RAP1A, member of RAS	oncogene family Homo sapiens mRNA; cDNA DKFZo434M1126 (from clone	DKFZp434M1126) SUMO-1-specific protease ESTs, Weakly similar to MYELIN P2 PROTEIN	[H.sapiens] SRY (sex determining region	Y)-box 2 small nuclear ribonucleoprotein polypeptide	E DKFZP586M1523 protein	EST Homo sapiens cDNA	FLJ20419 fis, clone KAT02435	zinc finger protein 75 (D8C6) ESTs	thyroid transcription factor 1	poly(rC)-binding protein 2 S100 calclum-binding protein A4 (calclum protein, calvasculin, metastasin,	murine placental homolog) RAB9, member RAS	oncogene family ESTs, Weakly similar to	unknown [H.sapiens]
Hs.100515	Hs.36787	Hs.865	Hs.97140 Hs.27197	Hs.182695	Hs.816	Hs.1066 Hs.22981	Hs.25922	Hs.11184	Hs.29159 Hs.26731	Hs.197764	Hs.63525	Hs.81256	Hs.28726	Hs.96413
AA485432 Hs.100515	R36144 Hs.25107	AA279680 Hs.865	AA398247 Hs.97140 AA621256 Hs.27197	AA676765 Hs.77993	AA451892 Hs.816	AA678021 Hs.1066 H22559 Hs.8006	R52522 Hs.25922	T71869 Hs.11184	AA450180 Hs.29159 AA707195 Hs.26731	T60168 Hs.89853	AA057533 Hs.108607	AA504780 Hs.11221	H98534 Hs.28726	AA670359 Hs.96413
811033	137211	704905	726663 744565	897042	786674	431803 51807	39973	85502	789152 451937	81427	510521	825847	250667	878417
GF201	GF203	GF200	GF203 GF202	GF203	GF200	GF202 GF204	GF202	GF202	GF200 GF203	GF200	GF202	GF203	GF200	GF204

-1.2345566 1.09319323 1.14758239	1.13661682	-1.5491278	-1.3545934	-1.7334342	-1.3210464	-2.6722857
734.3282 734.3091 734.0966 733.9315	733.4781	733.4396	733.3596	733.3126 733.293 733.155	733.1281	732.9888
MAD2L1 DKFZP566J153 T-STAR	CCNH	GAT			CSF2RB	SPOP
MAD2 (mitotic arrest deficient, yeast, homology-like 1 MKZP968J153 protein ESTs Sam68-like phosphotyrosine protein, T-STAR	eSTS you'll H Human DNA sequence from clone RP4-756623 on clone RP4-766623 on clone	o i Pase activating prote putative glycine-N- acyltransferase	Homo sapiens cDNA FLJ20497 fis, clone KAT08890	ES18, weakily similar to KIAA1015 protein [H.sapiens] ESTs colony stimulating factor 2	receptor, beta, tow-anning (granulocyte-macrophage) Homo sapiens mRNA for	KIAA1126 protein, partial cds speckle-type POZ protein
Hs.79078 Hs.183438 Hs.60435 Hs.13565	Hs. 109144	Hs.18508	Hs.5199	Hs.9521 Hs.104904 Hs.121874	Hs.265262	Hs.44087 Hs.129951
AA481076 Hs.79078 H45286 Hs.32419 AA447612 Hs.60435 AA670123 Hs.13565	AA132066 Hs.109144 AA454146 Hs.514	AA126901 HS./1049 AA704995 HS.18508	AA460432 Hs.5199	T52999 Hs.9521 AA430205 Hs.104904 AA776844 Hs.121874	R66326 Hs.118200	R53971 Hs.11687 AA256459 Hs.25194
814701 182818 782705 844703	795296	502106 462645	796469	68207 781401 1291687	141115	40040 682058
GF200 GF203 GF201 GF203	GF202 GF200	GF203	GF202	GF201 GF202 GF204	GF202	GF204 GF203

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Atty Docket No. 2172		1.22664359	1.14732585	-1.8646861	1.00298383	1.4784243	1.11596125						-1.8132678	-1.6470187						1.00320349	
Ail	732.8145	732.7296	732.5726 732.5574	732.4844	732.4474	732.3309 732.3076	732.0568	731.9994	731.8397		731.6386		731.114	731.024	730.915	730.908		730.6913		730.5535	
	P14	CDC20	KIAA0350				LOC51747	DKFZP434F011	KIAA0950		SEC61B		C20RF1					DPP4		KIAA0380	
APPENDIX A	protease inhibitor 4 (kallistatin) P14 cell division cycle 20.	S.cerevisiae homolog Homo sapiens mRNA; cDNA DKFZp434M0420 (from clone	DKFZp434M0420) KIAA0350 protein	ESTs Homo sapiens mRNA full length insert cDNA clone	EUROIMAGE 254679	ESTs ESTs	cisplatin resistance-associated overexpressed protein	DKFZP434F011 protein	lifeguard	protein translocation complex	beta	chromosome 2 open reading	frame 1	ESTs ESTs Hinhly similar to CGL47	protein [H.sapiens]	ESTs	dipeptidylpeptidase IV (CD26, adenosine deaminase	complexing protein 2) KIAA0380 gene product; RhoA	specific guanine nucleotide	exchange factor	
	Hs.159628	Hs.82906	Hs.273369 Hs.23263	Hs.269583	Hs.206927	Hs.70821 Hs.22361	Hs.3688	Hs.20495	Hs.182859		Hs.77028		Hs.14454	Hs.204810	Hs.102897	Hs.9587		Hs.44926		Hs.47822	
	N58558 Hs.117943	AA598776 Hs.82906	Hs.101465 Hs.23263	AA704794 Hs.121048	4A678259 Hs.104824	4A121271 Hs.70821 4A010128 Hs.22361	AA412738 Hs.3688	AA004667 Hs.20495	AA620986 Hs.128966		Hs.77028		AA489478 Hs.14454	Hs.117905	Hs.102897	Hs.9587		Hs.44926		Hs.47822	
	N58558	AA598776	H29783 H15077	AA70479	AA67825	AA121271 AA010128	AA412738	AA004667	AA620986		H73928		AA489478	H55764	N91246	T53170		W70234		N54420	
k et al.	248412	898062	52755 49344	452446	432008	490188 359135	730633	428786	1049143		214884		897448	203425	305843	68534		343987		244801	
westbrook et al	GF201	GF200	GF201 GF200	GF203	GF203	GF202 GF201	GF202	GF201	GF204		GF201		GF202	GF202	GF201	GF204		GF201		GF200	

1.12231787	1.14688053	-1.4757992	-1.0760975	-1.4880856 1.18956503	-1.8994561 -1.0750844	-1.0800327	1.00493369	1.60927724
730.0473 730.0139 729.9989	729.8457 729.7294	729.6293	729.5894 729.5303	729.2702 729.2679	729.2577 729.2255	729.1392	728.6732 728.3176	728.0919
CSF1R	SUI1	EIF3S6	KIAA0010	SLC29A1 DKFZP586I1023		TIF1GAMMA ARAF1	ITM2A	DKFZP434B187
colony stimulating factor 1 receptor, formerly McDonough leiline sarcoma viral (v-fms) oncogene homolog ESTs	putative translation initiation factor EST	eukaryotic translation initiation factor 3, subunit 6 (48kD) ESTs, Moderately similar to HMG-box transcription factor	[M.musculus] KIAA0010 gene product solute carrier family 29 (nucleoside transporters)	member and potency) member and potency) DKFZP586I1023 protein Homo sapiens Chromosome 16 RAC chose CIT9875K-A.	152E5 ESTs transcriptional intermediary	factor 1 gamma v-raf murine sarcoma 3611 viral oncogene homolog 1 Homo sapiens clone 628 internam mRNA complete	sequence integral membrane protein 2A ITM2A N-acety/glucosamine-	phosphate mutase; DKFZP434B187 protein
Hs.174142 Hs.192552 Hs.191204	Hs.150580 Hs.39762	Hs.106673	Hs.8619 Hs.155287	Hs.25450 Hs.111515	Hs.4900 Hs.36291	Hs.168005 Hs.77183	Hs.181349 Hs.17109	Hs.237323
AA284954 Hs.75116 AA504842 Hs.104540 AA682541 Hs.113196	AA988313 Hs.119598 H77479 Hs.39762	R61297 Hs.113512	AA464967 Hs.8619 AA284599 Hs.82640	AA129135 Hs.25450 AA458828 Hs.88001	6 _	T62575 Hs.5483 H59758 RG.14	AA412266 Hs.4261 AA775257 Hs.17109	AA496455 Hs.115679
713974 825736 431235	1607039 233734	42452	810096 713862	586650 814354	756378 207778	79739	730072 878596	755765
GF201 GF203 GF203	GF204 GF200	GF203	GF201 GF200	GF203 GF203	GF203 GF200	GF201 GF200	GF201 GF203	GF203

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1.049506	-1.4100212 -1.8375096 -1.7598977 -1.5676112	1,40187699		1,30172011	-1.2458584	-1.4864815	-1.5899207	-2.2119232 -1.8222956	-1.230118 1.09258817
728.0717	728.0171 728.012 727.8582 727.8198	727.605	727.2357 727.2367 727.228	727.1348	726.7676 726.4728	726.3667	726.0259	725.848 725.8238	725.7859 725.619
	ACTR1A	STHM	SQV/L KIAA0226 KSR				ZFP95	TAF2C1	SCYA18 KIAA0342
ESTs ARP1 (actin-related protein 1, veast) homolog A (centractin	alpha) ESTs ESTS ESTS	sialytransferase ESTs nucleotide-sugar transporter	similar to C. elegans sqv-/ KIA40226 gene product kinase suppressor of ras Homo sapiens cDNA FLJ10485 ffs, clone	NT2RP2000195 ESTs, Weakly similar to	semaphorin F [H.sapiens] ESTs. ESTs. Weakly similar to !!!! ALU SUBFAMILY SC WARNING FNTRY !!!	[H.sapiens]	zinc finger protein homologous to Zfp95 in mouse	TATA box binding protein (TBP)-associated factor, RNA polymerase II, C1, 130kD EST small inducible cytokine small inducible cytokine subfamily A (Cys-Cys), member 18 nullmonava and	activation-regulated KIAA0342 gene product
Hs.226284	Hs.153961 Hs.17121 Hs.5757 Hs 12921	Hs.107573 Hs.116278	Hs.90078 Hs.141296 Hs.152094	Hs.107528	Hs.99083	Hs.110067	Hs.110839	Hs.24644 Hs.46900	Hs.16530 Hs.16950
R02800 Hs.119621	AA456850 Hs.83816 AA598831 Hs.17121 AA425116 Hs.5757 W73738 Hs 12921	AA062814 Hs.9531 AA779418 Hs.116278	AA431179 Hs.90078 W94774 Hs.80892 H88143 Hs.91472	R01796 Hs.90265	AA236561 Hs.17424 AA446859 Hs.99083	W80457 Hs.110067	AA449189 Hs.110839	AA487148 Hs.24644 N49186 Hs.46900	AA495985 Hs.16530 AA127794 Hs.16950
124052 R02	815575 AA4 898307 AA5 768590 AA4		782140 AA4 358083 W94 220655 H88	124405 R01	687579 AA2 784200 AA4	415493 W80	785434 AA4	841261 AA4 280213 N49	768497 AA4 502067 AA1
GF200	GF203 GF203 GF203 GF203	GF200 GF204	GF201 GF201 GF201	GF200	GF203 GF202	GF203	GF202	GF200 GF202	GF200 GF200

Atty Docket No. 2172	Hs.90989 Hs.163648	165 Hs.55548 Hs.55548 unknown potein ill-majering 725.3969 EST. Highly similar to charge-out, autunda activity and charge-out, autunda activity automateur activity automateur activity	sapiens] 725.293	Hs.93121 Hs.93121 KIAA0761 protein KIAA0761 725.233	Hs.121049 Hs.188501 ESTs	Hs.42239 ESTs 7	7 Hs.44234 Hs.44234 ESTs 725.0757	Hs.118049 Hs.269674	Homo sapiens Chromosome	A A A A A A A A A A A A A A A A A A A	15,307,32 3c.574 72,002 15,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002 17,002	5 Hs.107666 Hs.155182 KIAA1036 protein KIAA1036	Hs.124147 ESTs 7	Hs.26813 CDA14 LOC51290 7			Hs.107485 Hs.7913 ESTs 7	AA436164 Hs.23171 Hs.181326 KIAA1073 protein KIAA1073 724.6688 -1.7919876	AA777242 Hs.77955 Hs.77955 ESTs 724.5881	AA630346 Hs.78093 Hs.154332 KIAA0212 gene product KIAA0212 724.517	Rho GTPase activating protein	AA916728 Hs.102336 Hs.102336 B ARHGAP8 724.5098 1.1184422	ESTs, Highly similar to gamma	00000	NS TRS. L 2002U TRS. L 2002U [T. Sathens] HS 4840 HS 4840 FSTS	Homo sapiens mRNA for	He 26788 He 267150	Talendo Original de la comprenditate del comprenditate de la comprenditate de la comprenditate del comprenditate de la comprenditate del comprenditate del comprenditate del comprenditate del comprenditate de la comprenditate del comprenditate del comprenditate del c
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	99 H91641	73 W33165	389018 AA855158	05 H51262	23 T98941	-	-	04 N57632			N74698	AA043965	_		-	•	N35592			•					>		R17758	8
Westbrook et al.	GF201 241699	GF201 321773	GF203 13890	GF200 194005	GF202 122723			GF203 246504		70000		' '		_	GF204 453298	GF204 460171	GF201 272262	GF202 754380	GF204 448232	GF201 854874		GF203 1473690		•	GF204 133471 GF201 22359		GF204 25302	

Westbrook et al.

APPENDIX A

ESTs, Moderately similar to !!!! ALU SUBFAMILY SC

	-2.8483032	-1.8764638	-2.2457108	-1.9874903	1.00264455						2.63501164	1.64538164		1.16768214		-1.5028694	1.19431926			-1.3329757		-1.1986069			1.09359565					1.00459965
	723.9584	723.8841	723.8314	723.7195	723.6573	723.6224	723.6104				723.4435	723.2261		723.1863		723.1067	723.0456			722.9989		722.8937		722.8898	722.8022			722.6896	722.5681	722.2753
			PKM2				NUP214							ARHD		CDW52	PEG3					POLA							NXL	
WARNING ENTRY !!!!	H.sapiens]	EST	pyruvate kinase, muscle	ESTs	ESTs	ESTs	nucleoporin 214kD (CAIN)	ESTs, Moderately similar to	B219/OB receptor isoform	HuB219.1 precursor	H.sapiens]	ESTs	ras homolog gene family,	member D	CDW52 antigen (CAMPATH-1	antigen)	paternally expressed gene 3	Homo sapiens cDNA	FLJ10447 fis, clone	NT2RP1000851	polymerase (DNA directed),	alpha	ESTs, Highly similar to	HSPC040 protein [H.sapiens]	ESTs	ESTs, Highly similar to	GROUP X PHOSPHOLIPASE	A2 PRECURSOR [H.sapiens]	thioredoxin ESTs. Weakly similar to DRB1	H.sapiens]
S	Hs.188908	Hs.47329 E	Hs.198281 p	Hs.105136 E	Hs.99069 E	Hs.188098 E	Hs.170285 n	Ш	6 0	I	Hs.252508 [F	Hs.59203 E	22	Hs.15114 m	0	Hs.276770 al	Hs.139033 p.	Ι	ш	Hs.94308 N	_	Hs.267289 a			Hs.179852 E	ш	ა დ	_	Hs.76136 #	Hs.103378
	AA598877 Hs.112477	151741 Hs.47329	4A101822 Hs.110342	AA482282 Hs.105136	4A446346 Hs.99069	4A779258 Hs.126432	4A401428 Hs.69968				754733 Hs.26004	W88745 Hs.59203		AA143436 Hs.15114		AA620591 Hs.25271	AA459941 Hs.17931			N74995 Hs.94308		AA707650 Hs.74090			N25745 Hs.63169			AA630435 Hs.125097	AA431967 Hs.93458	AA432152 Hs.103378
	897992 AA	281739 N5	489544 AA	824681 AA	781287 AA	452703 AA	743188 AA				154996 R5	417800 WE		591907 AA		951313 AA	796398 AA			299559 N7		451706 AA		•	268354 N2				782193 AA	781505 AA
	GF202	GF202	GF202	GF203	GF202	GF204	GF201				GF203	GF202		GF200		GF202	GF200			GF202		GF203		GF201	GF202			GF204	GF201	GF202

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1.15038708	1.09717571	1.01351679 -1.660402	-1.9629906 1.21277584 1.1429751	-1.4432467	1.02543996 -1.7870333 -1.3332009	-1.6893503	-1.4851334
722.0714 721.9582 721.6574	721.0952	721.0424 721.0424 720.9347	720.7714 720.6596 720.3804	720.375 720.3076 720.179 719.9316	719.9171 719.6626 719.652 719.4355 719.4149	719.1083 719.0442 719.0147 718.944	718.839 718.6512 718.5653
KIAA1008	PC4 RPL32	RARS KIAA0184		KIAA0523	TR OAS2 EDNRB	PAX3 EHD4	DKFZP564J157
ESTs ESTs KIAA1008 protein activated RNA polymerase II	transcription cofactor 4 ribosomal protein L32 Homo sapiens mRNA for	NIAA IZ 14 protein, partial cus arginyl-tRNA synthetase KIAA0184 protein	ESTs ESTs ESTs	KIAA0523 protein EST EST ESTs	ESTs. Weakly similar to C15H9: 5(c-biggars) thioredoxin reductase beta 2-5 oligoadenylate synthetase endothelin receptor type B ESTs	paired box gene 3 (Waardenburg syndrome 1) EH domain containing 4 ESTs	Homo sapiens cDNA RL20578 lis, clone REC00607 DKFZp664,157 protein Homo sapiens mRNA; cDNA DKFZp761,191 (from clone DKFZp761,191); partial cds
Hs.46564 Hs.250900 Hs.21738	Hs.74861 Hs.169793	HS.43149 HS.180832 Hs.196437	Hs.172516 Hs.37623 Hs.41371	Hs.16032 Hs.237173 Hs.104774 Hs.105040	Hs.167641 Hs.12971 Hs.264981 Hs.82002 Hs.260707	Hs.198 Hs.55058 Hs.165240 Hs.31570	Hs.7731 Hs.63042 Hs.6194
W96452 Hs.46564 W84658 Hs.122664 AA863115 Hs.127324	AA099534 Hs.74861 AA452125 Hs.24233	4A424754 HS.43149 4A455652 HS.74514 4A482038 HS.44770	AA609987 HS.112798 H58834 HS.37623 AA521327 HS.41371	418630 Hs.16032 400477 Hs.117578 4A412295 Hs.104774 4A459384 Hs.105040	W88995 Hs.112169 AA434130 Hs.106051 R72244 Hs.24815 M2914 Hs.108863 AI015453 Hs.22313	197691 Hs.198 AA12509 Hs.55058 AA150619 Hs.31855 AA644099 Hs.31570	AA449345 Hs.7731 Al014387 Hs.3452 R43547 Hs.6194
		768997 AV	`		417466 W 770570 AA 155806 R7 271050 N2 1641132 All	251555 HS 730288 AA 504940 AA 845380 AA	785732 AA 1635350 AI 32687 R4
GF201 GF202 GF204	GF201 GF202	GF202 GF203 GF203	GF202 GF200 GF203	GF203 GF204 GF202 GF201	GF202 GF200 GF203 GF201 GF204	GF204 GF202 GF201 GF204	GF202 GF204 GF202

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		1.00341025	-1.1966589	1.03036217	1.06834468	1.11745783	70700404	1.24481358				-1.3845081	1 0730166	1.28316587		
718.5032 718.3141 718.2485	200	718.1067	718.0659	718.0182 717.9984	717.6974	717.6436	717.3997	717.3064		717.2214	717.218	717.0428	716.8624	716.7438		716.5956
NET-6			MCM2	FLJ20152	SFRS5	PLAG1	0	YDD19		RPIA	ESR1		Š	21 ×		
tetraspan NET-6 protein ESTs	EST Homo sapiens putative oncogene protein mRNA,	partial cds minichromosome maintenance deficient (S. cerevisiae) 2	(mitotin) Homo sapiens mRNA; cDNA DKFZp58610521 (from clone	DKFZp58610521) hypothetical protein splicing factor, arginine/serine-	rich 5	pleiomorphic adenoma gene 1 PLAG: ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	[H.sapiens]	cyclin G1 YDD19 protein	ribose 5-phosphate isomerase A (ribose 5-phosphate	epimerase)	estrogen receptor 1	Homo sapiens cDNA FLJ20615 fis, clone KAT05373	ESTs	zyxin EST	Homo sapiens mRNA; cDNA DKFZp566N034 (from clone	DKFZp566N034); partial cds
Hs.102737 Hs.44189	18.1100/3	Hs.6817	Hs.57101	Hs.236463 Hs.82273	Hs.166975	Hs.14968	Hs.152659	Hs.25615		Hs.79886	Hs.1657	Hs.14595	Hs.18439	HS./58/3 Hs.112879		Hs.271606
AA669356 Hs.102737 N72185 Hs.44189	6/00/13	AA610004 Hs.6817	AA454572 Hs.57101	N25242 Hs.126698 AA446864 Hs.10756	AA598965 Hs.75469	AA418251 Hs.14968	Hs.112568	AA083032 Hs.79101 B12808 Hs 113619		Hs.107193	AA291749 Hs.1657	Hs.14595	Hs.18439	N71461 HS.5269 AA620669 Hs.112879		Hs.22169
AA66935 N72185	AA023/3	AA61000	AA45457	N25242 AA44686	AA59896	AA41825	R06284	AA08303 R12808		R73500	AA29174	H97861	R15104	AA62066		R41947
884836 291193	/45382	1032004	809530	267464 784212	898265	767638	126277	547058 25384		156330	725321	251751	25380	294926 1049168		31820
GF204 GF201	4024	GF202	GF200	GF204 GF202	GF200	GF200	GF201	GF200	5	GF201	GF201	GF203	GF204	GF203 GF202		GF201

1.02225953

-1.0965426

-1.4480702

GF200 GF201 GF201 GF201 GF204 GF204 GF204

Affy	716.5131	716.4364	716.4236	716.3831	716.3494	716.3325	716.1816	716.155		716.0265			715.9996	715.6656			715.5715	715.5623		715.522	715.2397	715.1332	715.0327		715.0283	714.6516	714.5361	714.4092		24.4.04.00	14.3130			714.2883
	NUMB		CTNS										SCYA1				AMT	CLCN7		CD86		PMP22	GL01		PLP2		ADORA3	KIAA1082						
APPENDIX A	numb (Drosophila) homolog	ESTs	cystinosis, nephropathic	ESTs	ESTs	EST	EST	ESTs	Homo sapiens mRNA; cDNA DKFZp586K1220 (from clone	DKFZp586K1220)	small inducible cytokine A1 (I-	309, homologous to mouse	Tca-3)	ESTs	aminomethyltransferase	(glycine cleavage system	protein T)	chloride channel 7	CD86 antigen (CD28 antigen	ligand 2, B7-2 antigen)	ESTs	peripheral myelin protein 22	glyoxalase I	proteolipid protein 2 (colonic	epithelium-enriched)	EST	adenosine A3 receptor	KIAA1082 protein	Homo sapiens cDNA	FLJ10/49 fls, clone	NIZHESOOLISIS EST Moderately similar to IIII	ALU SUBFAMILY SX	WARNING ENTRY !!!!	[H.sapiens]
	Hs.78890	Hs.269775	Hs.64837	Hs.95511	Hs.101439	Hs.116831	Hs.156968	Hs.23120		Hs.7974			Hs.72918	Hs.269364			Hs.102	Hs.80768		Hs.27954	Hs.117031	Hs.103724	Hs.75207		Hs.77422	Hs.21559	Hs.258	Hs.24125		77070	HS.2464		!	Hs.209479
	AA487149 Hs.78890	R00265 Hs.100746	N94331 Hs.94704	F41066 Hs.95511	410679 Hs.101439	AA634384 Hs.116831	AA884636 Hs.125606	AA459108 Hs.23120		AA677643 Hs.7974			AA931884 Hs.72918	AA451850 Hs.111174			N59532 Hs.102	H99364 Hs.80768		AA973397 Hs.27954	AA677106 Hs.117031	R26960 Hs.103724	AA136710 Hs.75207		AA464627 Hs.77422	R37472 Hs.21559	AA863086 Hs.258	H26156 Hs.24125			152152 HS.9392			AA788882 Hs.122369
et al.	841263 /	123246 F	_	62092 T	_	-	1468630 /	814309 /		897262			1570420 /	786281 /			248631 N	262251 H		1569006	454205 A	133273 F	491001 /		810504 /	28277 F	1455566 /	161950 H		7				1020504 /

GF204 GF203

GF204

GF203 GF201 GF204 GF203 GF200 GF203 GF200 GF203 GF203 GF200 GF202

GF204

-1.9732916 1.10339007 1.15089027 -1.7683978 -2.5123613 -1.4155535 1.12624324 1.24618098

	1.71780911	1.12591691	-1.2559329	1.48638245	-1.1854868	-1.6635041	-1.6256145	-1.7526762	1.05759114
714.093	713.8123	713.7851	713.737	713.4039 713.1044 713.0627 713.0455	713.0339	713.0196	712.9671 712.9135	712.579 712.5679	712.5517 712.4293 712.4293
СD63		SFPQ	SCYB10	HNRPL		TM7SF1	RBP4	ВМР8	GNG7
EST, Highly similar to hypothetical protein, similar to [H.sapiens] Code antigen (melanoma 1 antigen) ESTs, Highly similar to CMP-N.	aceyinleurarınınc addı hydroxylase [H.sapiens] splicing factor proline/glutamine rich frotomarimidine trad-binding	protein-associated) small inducible cytokine suhfamily B (Cvs-X-Cvs).	member 10 heterogeneous nuclear	ribonucleoprotein L ESTs ESTs EST	ESTs transmembrane 7 superfamily member 1 (upregulated in	Kidney) retinol-binding protein 4,	interstitial ESTs bone morphogenetic protein 8	(osteogenic protein 2) ESTs guanine nucleotide binding	~
Hs.248821 Hs.76294	Hs.99664	Hs.180610	Hs.2248	Hs.2730 Hs.203228 Hs.42747 Hs.125960	Hs.112547	Hs.15791	Hs.76461 Hs.13975	Hs.99948 Hs.167506	Hs.127828 Hs.62766 Hs.112763
R94456 Hs.35321 AA454563 Hs.25564	AA287350 Hs.99664	R96240 Hs.35544	AA878880 Hs.2248	AA398352 Hs.97606 H09729 Hs.30644 AA706701 Hs.42747 AA889427 Hs.125960	AA609482 Hs.112547	AA520979 Hs.15791	AA005202 Hs.17878 AA167016 Hs.13975	AA779480 Hs.99948 H42037 Hs.106366	H30255 Hs.127828 AA045323 Hs.62766 AA609767 Hs.112763
198256 F	701123 /	197913 F	1493160 /	726846 / 45463 + 1240101 / 1468093 / 4	-	826256 /	429083 <i>H</i> 593793 <i>H</i>	1032431 <i>A</i>	190059 H 487109 <i>H</i> 1031945 <i>H</i>
GF201 GF201	GF203	GF202	GF203	GF203 GF204 GF204 GF204	GF202	GF203	GF201 GF202	GF203 GF201	GF204 GF202 GF202

	-2.1037702	-2.1953304		-1.5544813		-2.3987353	-1.0385647	-1.4047344	20000057	-1.2785752		-1.3232987				1.48217141		-2.5714004
			10			_					~		_		_			
712.3259	712.2717	712.2297	712.0585	712.054 712.0047 711.9645	9	711.8893	711.765	711.7231	711.6292	711.613	711 5/138	711.4686	711.3431		711.2767	711.1972		711.1866
KCNH3	TNR	AGTRL2		HLA-DRB5	500	GADD34				DKFZP564A122	E1E464	ZNF198				ASPA		BSMAP
potassium voltage-gated channel, subfamily H (eag- related), member 3 ESTs	enascin R (restrictin, janusin) TNR	Homo sapiens mRNA for KIAA1158 protein, partial cds angiotensin receptor-like 2	ESTs, Weakly similar to KIAA0704 protein [H.sapiens] maior histocompatibility	sta 5	¥	damage-inducible 34 ESTs	ESTs	EST For-	ESTS	OKFZP564A122 protein	Sukaryotic translation imitation	zinc finger protein 198	ESTs	Homo sapiens cDNA FLJ10018 fis, clone	HEMBA1000531	aspartoacylase (aminoacylase 2. Canavan disease)	rane-	anchored protein
	-		ΩΣE		i 5n i	в ш	Ш							źŒ	I	g ci	בֿוֹ	ਲ
Hs.64064 Hs.119819	Hs.54433	Hs.4865 Hs.155986	Hs.21938	Hs.181366 Hs.114729		Hs./6556 Hs.7849	Hs.72569	Hs.46974	HS.112791 Hs 268644	Hs.187991	10.044500	Hs.109526	Hs.119937		Hs.99722	Hs 32042		Hs.5012
Hs.21178 Hs.119819		Hs.4865 Hs.37099	Hs.21938	AA485739 Hs.73508 AA001435 Hs.114729 M46344 Hs.12647	10210	4A460168 Hs./6556 V63284 Hs.7849	AA165512 Hs.72569	Hs.46974	4A609951 HS.112/91	Hs.114433	A A 450 407 Hz 05000	AA251581 Hs.109526	AA705858 Hs.119937		AA417742 Hs.99722	Hs 32042		Hs.101045
R38427 A1003755	H41574	AA134824 Hs.4865 H93249 Hs.3709	W81098	AA485739 AA001435		AA460168 N63284	AA165512	N49848	AA609951 T95909	N53236	A A 450 407	AA251581	AA705858		AA417742	N71653		R38431
26487	175767	502506 241880	347378	811139 362080	000	795893 290149	593280	282478	120924	246881	10000	684644	1292207		746230	295137		26182
GF204 GF204	GF203	GF201 GF200	GF204	GF201 GF203	20 20	GF203	GF202	GF202	GF202	GF203	1001	GF203	GF204		GF204	GE200		GF202

	-1.0479011		1.69887775	1.04476184		-1.6671799	-1.4518346	-1.3161678		1.07830467	-1.4300065			1.07880928	-1.0821739			-1.1009048	-1.3399886		-1.1908751	-1.2592365	-2.7460713	-2.6993866					-1.5819415	-2.5132623		
	711.076	711.0284	710.958	710.9492	710.8964	710.842	710.6019	710.5293		710.5005	710.3218	710.0161	709.9677	709.8995	709.8038			709.7913	709.7786	709.6061	709.4443	709.4346	709.4235	708.9542	708.8463	708.7843		708.7767	708.7195	708.587		708.4692
	C21orf4			ADM	KIAA0444		KIAA0152			SAH			KIAA0095		KIAA1096			SDHA				KIFC3				-		RRBP1	DKFZP58611023			
chromosome 21 open reading	frame 1	ESTs	ESTs	adrenomedullin	KIAA0444 protein	ESTs	KIAA0152 gene product	ESTs	SA (rat hypertension-	associated) homolog	ESTs	ESTs	KIAA0095 gene product	ar channel 1	KIAA1096 protein	succinate dehydrogenase	complex, subunit A,	flavoprotein (Fp)	ESTs	ESTs	ESTs	kinesin family member C3	ESTs	ESTs	ESTs	ESTs	ribosome binding protein 1	(dog 180kD homolog)	DKFZP586I1023 protein Homo sapiens mRNA for	KIAA1340 protein, partial cds	Homo sapiens cDNA FLJ10548 fis, clone	NT2RP2001969
	Hs.9042	Hs.127688	Hs.191349	Hs.394	Hs.158291	Hs.12420	Hs.181418	Hs.55592		Hs.181345	Hs.112703	Hs.144547	Hs.155314	Hs.74276	Hs.69559			Hs.469	Hs.16414	Hs.171939	Hs.272089	Hs.23131	Hs.167366	Hs.90973	Hs.7232	Hs.48353		Hs.98614	Hs.111515	Hs.51743		Hs.9622
	AA495922 Hs.9042	AA864224 Hs.127688	N50406 Hs.118043	AA446120 Hs.394	R53560 Hs.7443	AA505136 Hs.12420	AA488036 Hs.90438	W37733 Hs.55592		W01011 Hs.89659		N34751 Hs.44621	AA428939 Hs.89568	AA486518 Hs.74276	H51042 Hs.69559			H50345 Hs.7860	R12414 Hs.124245	W42945 Hs.91424	AA463221 Hs.99586	AA436460 Hs.23131	R41406 Hs.21982	AA680421 Hs.90973	AA464580 Hs.7232	AA026167 Hs.48353		AA464540 Hs.23378	AA699359 Hs.57562	H85476 Hs.51743		1592479 AA983267 Hs.9622
	768452	1470368	280592	774446	39962	825813	840620	321958		296529	743465	271378	769751	843121	194131			179336	128221	323322	797042	753038	30329	433220	810571	366663		810509	432560	249755		1592479
	GF203	GF204	GF203	GF203	GF204	GF203	GF200	GF202		GF200	GF202	GF201	GF201	GF200	GF200			GF200	GF202	GF201	GF202	GF202	GF202	GF203	GF201	GF201		GF201	GF203	GF202		GF204

Atty Docket No. 2172				1.24198299	1.11353086		1.3487888	1.3487888	1.00057971	1.15728507	-2.265125	-1.3386703			1,12027255 -1,2634123 -1,2991278 -1,4730691
Attı	708.2899	707.9968	707.8513	707.8261	707.6041	707.2631	707.1875	707.1875	707.142	706.9943	706.844	706.8112		706.7559	706.704 706.7032 706.5889 706.5013 706.4783
			TM4SF5	RGS6	ENO2	GRM3				APXL	ATF5				NCOFI2 ASS
APPENDIX A	E	Homo sapiens cDNA FLJ20396 fis, clone KAT00561	member 5	regulator of G protein signalling 6	enolase 2, (gamma, neuronal)	imilarto	VuMA protein [H.sapiens]	NuMA protein [H.sapiens]	Homo sapiens gene for serine/threonine protein kinase	apicai proteiri, Aeriopus iaevis- IIKe	activating transcription factor 5 ATF5 FSTs	STS	ESTs, Weakly similar to antennal-specific short-chain dehydronenase/reductase	[D.melanogaster]	
	Hs.117332 EST	Hs.103657 FL	Hs.184194 me	reg Hs.3221 sig	Hs.146580 en	Hs.3786 me	Hs.168516 Nu	Hs.168516 Nu	Ho.58241 sel	apic Hs.2391 like	Hs.9754 aci			Hs.8949 [D	Hs.120980 2 Hs.160786 arg Hs.34287 E5 Hs.46494 E5
	AA699724 Hs.117332	AA486092 Hs.10107	R95924 Hs.107967	R39325 Hs.3221	AA450189 Hs.75675	N62328 Hs.108060	AA598659 Hs.115973	AA598659 Hs.100002	W72870 Hs.58241	H49455 Hs.2391	AA496253 Hs.9754	H99659 Hs.7086	AA4902C0 IIS.02323	AA448177 Hs.8949	AA400234 Hs.120980 AA676466 Hs.76753 R89356 Hs.34287 N45223 Hs.46494 N31493 Hs.44249
k et al.	433310 A	840783 A	199358 F	24176 F	789147 A	287843 N	897901 A	897901 ₽	344959 V	178818 H	814158 A		974308	782783 A	743230 <i>H</i> 882522 <i>H</i> 196032 F 283122 N 272200 N
Westbrook et al	GF204	GF201	GF204	GF203	GF200	GF201	GF200	GF200	GF202	GF200	GF203	GF202	GFZU3	GF201	GF202 GF203 GF203 GF202 GF201

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	-1.2410869			1.37200227	1.00026344			-1.4458213		-1.5384379			-2.5568732			-1.6513437					-1.8189588	-1.7307193		-1.4711953				-1.084381		1.19232095	1.28666419
706.4575	706.3871		706.3846	706.3563	706.0265			705.9223		705.6745			705.4511	705.2068		705.1343	705.0829	705.0272		704.9875	704.9629	704.9101		704.8782	704.7295	704.702		704.6601		704.3109	703.972
			SUPT4H1	CHEK1				CDC10					PIP5K2A	DGS-D		ITPKB		PLG				IRF2		KMO		KIAA1009		C8ORF1			STHM
ESTs	ESTs	suppressor of Ty	(S.cerevisiae) 4 homolog 1 CHK1 (checkpoint, S.pombe)	homolog	ESTs	cell division cycle 10	(homologous to CDC10 of S.	cerevisiae)	Homo sapiens clone 25186	mRNA sequence	phosphatidylinositol-4-	phosphate 5-kinase, type II,	alpha	DiGeorge syndrome gene D	inositol 1,4,5-trisphosphate 3-	kinase B	EST	plasminogen	Homo sapiens cDNA	FLJ20668 fis, clone KAIA585	EST	interferon regulatory factor 2	kynurenine 3-monooxygenase	(kynurenine 3-hydroxylase)	ESTs	KIAA1009 protein	chromosome 8 open reading	frame 1	Human Chromosome 16 BAC	clone CIT987SK-A-101F10	sialyltransferase sialyltransferase
Hs.9614	Hs.109766		Hs.79058	Hs.20295	Hs.54639			Hs.184326		Hs.5985			Hs.108966	Hs.83775		Hs.78877	Hs.32085	Hs.75576		Hs.12920	Hs.112788	Hs.83795		Hs.107318	Hs.196244	Hs.202276		Hs.40539		Hs.5320	Hs.1075/3 Hs.107573
T53431 Hs.9614	AA757819 Hs.109766		AA988701 Hs.79058	N73242 Hs.20295	N90598 Hs.54639			AA400010 Hs.97748		AA045300 Hs.62760			T40568 Hs.124728	AA011681 Hs.83775		R94153 Hs.78877	H24458 Hs.32085	AA774309 Hs.51919		AA885140 Hs.124382	AA609934 Hs.112788	AA393214 Hs.83795		R44396 Hs.23693	_	W56794 Hs.56179		AA256275 Hs.88034		N50770 Hs.5320	AA497051 HS.10937 AA497051 HS.118009
68818	396192		1594019	246524	306269			742542		487086			60605	429721		276091	52004	858644		1466549	1031156	727551		34526	856887	340808		682085		280837	823590 823590
GF201	GF203		GF204	GF200	GF202			GF202		GF202			GF202	GF201		GF200	GF204	GF204		GF204	GF202	GF200		GF203	GF204	GF201		GF203		GF200	GF200

1.03097775 -1.1365059 -1.4378372	1.04117551	-1.2370214		-1.1314301		-1.4118207	1.29856174	1.05021966	1.05141263	1.2238 40	1.32191683 2.14702987
703.8765 703.8073 703.7759	703.1993	702.9698	702.7328	702.7163 702.6517	702.6376	702,5975	702.5356 702.0769 702.0596	701.9664	701.9584	701.5185	701.3402 701.041 701.0394
	NAKAP95	OXA1L	GEF-2	LOC51632	FABP5		MST1 GLB1		S I	ALEX3 BK384D8_1.C22.2.MRNA	DDR2
ESTs ESTs ESTs Homo sapiens mRNA; cDNA DKFZp564J142 (from clone	DKFZp564J142) neighbor of A-kinase anchoring protein 95	oxidase (cytochrome c) assembly 1-like	2 ESTs, Weakly similar to KERATIN, TYPE I CYTOSKELETAL 9	[H.sapiens] CGI-76 protein fatty acid binding protein 5	(psoriasis-associated) ESTs, Weakly similar to	KIAA0437 [H.sapiens]	macrophage stimulating 1 (hepatocyte growth factor-like) MST1 galactosidase, beta 1 ESTs	ESTs ESTs, Weakly similar to Hrs	[H.sapiens] ESTs	ALEX3 protein hypothetical protein discoidin domain receptor	family, member 2 ESTs ESTs
Hs.39526 Hs.165195 Hs.91384	Hs.227146 Hs.96200	Hs.151134	Hs.6518	Hs.8834 Hs.184325	Hs.153179	Hs.102652	Hs.278657 Hs.79222 Hs.16279	Hs.202589	Hs.16400 Hs.90372	Hs.180903	Hs.71891 Hs.72068 Hs.20255
4A426309 Hs.39526 173806 Hs.108278 316656 Hs.91384	N75017 Hs.102319 AA678308 Hs 96200	AA598582 Hs.111611	Hs.6518	4A625964 Hs.8834 4A476626 Hs.11498	Hs.106066	Hs.102652	Hs.76034 Hs.79222 Hs.16279	Hs.22015	Hs.16400 Hs.90372	HS.77059	AA243828 Hs.71891 AA150459 Hs.72068 N92947 Hs.20255
AA426309 H73806 R16656	N75017	AA598582	AA455108 Hs.6518	AA625964 Hs.8834 AA476626 Hs.1149	N47717	N50935	T47813 AA878899 W85881	R16524	T97471 R26929	T90560	AA243828 AA150459 N92947
769024 214713 129616	299664	897835	809850	745484 785417	281039	281103	71432 1493175 416092	128695	121458	110744	668442 491712 307740
GF203 GF202 GF200	GF201	GF200	GF201	GF204 GF203	GF201	GF203	GF200 GF203	GF200	GF200 GF200	GF202 GF201	GF200 GF202 GF201

1.61396541 -1.3233907 -1.6901073 -1.4096685 1.00872076	-1.1902763 -1.424297 -1.5359619 -2.3139656	-1.4343719	2.16859019	1.19708749
700.9675 700.8009 700.5167 700.4564 700.1402 700.138	699,5352 699,7362 699,4296 699,1893 698,886	698.7111	698.6708 698.4566	698.3455 698.0942 698.0343
DJ159A19.3 DJ328E19.C1.1 CRHBP	ALAS1 FOLH1	XRCC5	D6S81E	CDC7L1 HSPE1
ESTs, Highly similar to RNA-BINDING PROTEIN EWS Hit sapiens EST hypothetical protein hypothetical protein ESTs ESTs ESTs Conflictorpin releasing hommone-binding protein	Human Chromosome 16 BAC clone CH89/SK-A-363E6 ESTs ESTs aminolevulinate, delta-, syinthase 1 ESTs ESTs Area repel choosase (prostate- specific membrane antigen) 1 X-ray repel complementing defective repair in Chinese	hamster cells 5 (double-strand- break rejoining; Ku autoantigen, 80kD)	HLA-B associated transcript-1 D6S81E ESTs CDC7 (cell division cycle 7, S.	cerevisiae, hornolog)-like 1 heat shock 10kD protein 1 (chaperonin 10) ESTs
Hs.48306 Hs.45034 Hs.10700 Hs.218329 Hs.106510 Hs.131375 Hs.120963	Hs.24103 Hs.11261 Hs.220823 Hs.78712 Hs.81446 Hs.1915	Hs.84981	Hs.55296 Hs.47004	Hs.28853 Hs.1197 Hs.270740
AA480982 Hs.48306 N39603 Hs.45034 T60121 Hs.90659 AA488858 Hs.100461 HR801 Hs.106510 W88978 Hs.131375 AA706815 Hs.120963	R26707 Hs.24103 AA538825 Hs.11261 R06738 Hs.19779 AA453891 Hs.78712 H81935 Hs.81446 N64840 Hs.82586	AA775355 Hs.84981	AA682749 Hs.11404 N50039 Hs.47004	N62245 Hs.28853 AA448396 Hs.1197 N95499 Hs.82117
814618 277083 76355 843276 128668 416525 451795	133238 868168 126508 813651 239937 284701	929828	1293145 282633	287749 781341 308467
GF203 GF202 GF201 GF203 GF203 GF204 GF204 GF206	GF203 GF203 GF200 GF200 GF204	GF203	GF204 GF202	GF201 GF200 GF201

1.21792511	-1.4288211 -1.6526794 1.02624963	-1.2868199 -1.4186963 -1.2775717 -2.3193379	-1.5087272	1.39262374
697.9943 697.9575 697.9418	697.9384 697.7088 697.7082 697.6191	697.4235 697.4166 697.2963 697.2633 697.2548	696.5391	696.4787 696.376 696.3212
NRIP1	BAIAP2	NEDD1 DKFZP434A043	EPB41L1 LOC51706 CHNZ MPST	CRYZ NGFR
ESTs, Highly similar to MULTIDRUG RESISTANCE PROTEIN 3 [H.sapiens] nuclear receptor interacting protein 1	Hunnan clone 23/59 mHwA, partial cds ESTs BAIT-associated protein 2 ESTs neural precursor cell partial precursor cell partials precursor cell	opproposal consequences of con	band 4.1-ilke 1 yoytochrome b5 reductase 1 (BSR, 1) chimerin (chimaerin) 2 chimerin (chimaerin) 2 sulfurtransferase Homo sapiens cDNA ELLI 101 filis, done ELLI 101 filis, done PLACE(E003174, moderately similar to LIBOUTINA.	18 KD (EC 6.3.2.19) 10 KD (EC 6.3.2.19) orgatallin, zeta (quinone reductase) nene growth factor receptor (TNFR superfamily, member 16)
Hs.260061 Hs.155017 Hs.124185	Hs.118666 Hs.161585 Hs.7936 Hs.192924	Hs.121033 Hs.98205 Hs.24435 Hs.102708 Hs.36189	Hs.26395 Hs.5508 Hs.15202 Hs.74097	Hs.21275 Hs.83114 Hs.1827
R53935 Hs.73812 AA458503 Hs.79108 AA030006 Hs.124185	Hs.113381 Hs.59492 Hs.7936 Hs.37303	AA693510 Hs.121033 AA417089 Hs.98205 AA043945 Hs.24435 AA481540 Hs.102708 R99938 Hs.36189	R71689 Hs.26365 AA999976 Hs.5508 T63420 Hs.88804 AA416693 Hs.115446	Hs.21275 Hs.83114 Hs.1827
R53935 AA458503 AA030006	R38171 W93709 R60328 H56372	AA693510 AA417089 AA043945 AA481540 R99938	R71689 Hs.2638 AA999376 Hs.5508 T63420 Hs.88800 AA416693 Hs.1154	Al015196 Hs.21275 R13434 Hs.83114 R55303 Hs.1827
39920 809627 470220	23759 357364 42271 203782	1276346 731128 486288 815279 201784	155575 1636523 81558 731241	1623328 28475 154790
GF201 GF200 GF204	GF204 GF202 GF202 GF203	GF204 GF202 GF203 GF203 GF200	GF200 GF204 GF203 GF204	GF204 GF200 GF201

1.32087431		1.13647073 1.18219221 -1.3672739 -1.3017368 1.06355179	1.08919339	1.38642246					-1.4720822
696.2874	696.236	696.2343 696.0902 696.019 695.9835 695.7675	695.7329 695.6296	695.4738	695.1097	695.1097 695.1097	695.1097 695.1097 695.1097	695.1097 695.1097 695.1097 695.1097	694.9564 694.9415 694.9141 694.8478
SSR1	S100A4	n GPP130	НХВ	CDH17	EDN1	EDN1	EDN1 EDN1	EDN1 EDN1 EDN1	CDK5
signal sequence receptor, alpha (franslocon-associated protein alpha) \$100 calcium-binding protein A4 (calcium protein, calvacculin matastasin	murine placental homolog)	type II Golgi membrane protein GPP130 ESTs EST EST	hexabrachion (tenascin C, cytotactin) ESTs	cadherin 17, Ll cadherin (liver- intestine)	endothelin 1	endothelin 1 endothelin 1	endothelin 1 endothelin 1 endothelin 1	endothelin 1 endothelin 1 endothelin 1	ESTs. Highly similar to ESTs. Highly similar to KIAA0831 protein [H.sapiens] ESTs ESTs cyclin-dependent kinase 5
Hs.250773	Hs.81256	Hs.143600 Hs.277901 Hs.8750 Hs.112711 Hs.187616	Hs.204133 Hs.205015	Hs 89436	Hs.2271 Hs.9271	Hs.2271 Hs.2271	Hs.2271 Hs.2271 Hs.2271	Hs.2271 Hs.2271 Hs.2271 Hs.2271	Hs.17875 Hs.18291 Hs.141566 Hs.166071
AA450360 Hs.75186	W67199 Hs.28582	AA877669 Hs.97235 AA599741 Hs.112519 AA489068 Hs.8750 AA609467 Hs.112711 AA703375 Hs.120948	Hs.84261 Hs.39313	AA08861 He 89436	HKG.1g114	HKG.2g114	HKG.1g114 Hs.2271	HKG.2g114	M90067 Hs.17875 W73161 Hs.58291 NA684 Hs.94163 AA401479 Hs.111721
AA450360	W67199	AA877669 AA59974: AA489068 AA609467	T77595 H72259	AAORRE	H11003	H11003	H11003 H11003	H11003 H11003 H11003	M90067 W73161 N64684 AA401479
785616	343400	1161013 1070062 824792 743579 450025	23185 213535	511909	47359	47359 47359	47359 47359 47359	47359 47359 47359 47359	31251 418081 344373 290067 742595
GF200	GF201	GF203 GF203 GF203 GF202 GF203	GF200 GF200	GE200	GF201	GF201 GF201	GF201 GF201 GF201	GF201 GF201 GF201 GF201	GF201 GF201 GF202 GF202 GF201

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	-2.3127299	1.09798712	1.00534512		1.0273279	1.53884867							-1.976727			-1.0284193				1.48488247				-1.2235001	1.15475557						1.48569176
	694.7227	694 655	694.3311	694.1547	694.0748	693.9158	693.892		693.8672	693.8304		693.7941	693.7215	693.653		693.6038	693.4904			693.4318	693.243	693.1088	693.0766	692.9611	692.9407				692.8254		692.8005
									SLC30A4			PILR(BETA)		KIAA0351		HNRPR					ZNF273		KIAA0403						PPP2R3		GABRD
ESTs, Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!	[H.sapiens]	Calledoulli	ESTS	ESTs	ESTs	ESTs	ESTs	solute carrier family 30 (zinc	transporter), member 4	ESTs	paired immunoglobin-like	receptor beta	ESTs	KIAA0351 gene product	heterogeneous nuclear	ribonucleoprotein R	ESTs	Homo sapiens mRNA full	length insert cDNA clone	EUROIMAGE 50374	zinc finger protein 273	ESTs	KIAA0403 protein	ESTs	ESTs	protein phosphatase 2	(formerly 2A), regulatory	subunit B" (PH 72), alpha isoform and (PB 130), heta	isoform	gamma-aminobutyric acid	(GABA) A receptor, delta
	Hs.188810	Hs 21291	Hs.191950	Hs.16525	Hs.79793	Hs.65009	Hs.26136		Hs.112282	Hs.260032		Hs.138661	Hs.40918	Hs.170307		Hs.15265	Hs.261335			Hs.168541	Hs.89732	Hs.83427	Hs.185140	Hs.42465	Hs.5285				Hs.28219		Hs.113882
	H62421 Hs.108239	44460719 HS.21261	AA707167 Hs.120913	4A609738 Hs.16525	153268 Hs.79793	AA025055 Hs.65009	AA988298 Hs.26136		AA868038 Hs.112282	R02015 Hs.77791		AI017695 Hs.47622	H86461 Hs.40918	AA402863 Hs.29963		AA486402 Hs.15265	AA128008 Hs.71035			AA599073 Hs.21998	N69908 Hs.89732	AA827378 Hs.83427	Hs.34829	Hs.42465	4A436565 Hs.5285				Hs.100645		Hs.118329
	H62421	AA460818	AA70716	AA609738	H53268	AA025058	AA988298		AA868038	R02015		AI017695	H86461	AA40286;		AA486402	AA128008			AA59907;	N69908	AA827378	N48178	H97927	AA43656				T89372		W81526
	236413	706248	451394	1031918	202559	365056	1607018		1461161	124246		1636712	223012	741795		842861	501876			950409	297731	1422423	281949	260721	753071				110393		347615
	GF203	GESOS	GF203	GF204	GF200	GF202	GF204		GF204	GF204		GF204	GF203	GF201		GF202	GF201			GF202	GF201	GF204	GF201	GF202	GF203				GF201		GF200

692.7969 -1.5940364	997.7.00		695.6689	692.6083 -1.1219267	692.5914		692.4097 -2.0395461	•			692.166 -1.2786312	692.166 -1.2786312		692.036 1.39925037	691.8334	691.7843 -1.4113847	691.6057 1.07519886	691.5818	691.4644 -1.6753826		691.4161	691.1113		690.9543	690.8564	690,6837 -1,1314258	690.4895 1.87918366		D.	690.187 -1.2252238
COL15A1		DKFZP564M2423	KIAA0993	KIAA1078			GALT				ASCL1	ASCL1		PDE4D		GPR65	KIAA0102				SHOC2			STCH		NPY1R			IN HBB	
collagen, type XV, alpha 1	ESIS	DKFZP564M2423 protein	KIAA0993 protein	KIAA1078 protein	EST	galactose-1-phosphate	uridylyltransferase	ESTS	ESTs	achaete-scute complex	(Drosophila) homolog-like 1 achaete-scute complex	(Drosophila) homolog-like 1 phosohodiesterase 4D, cAMP-	specific (dunce (Drosophila)- homolog phosphodiesterase	E3)	ESTs	G protein-coupled receptor 65	KIAA0102 gene product	EST	ESTs	suppressor of clear, C.	elegans, homolog of	ESTs	stress 70 protein chaperone,	microsome-associated, 60kD	ESTs	neuropeptide Y receptor Y1	ESTs	inhibin, beta B (activin AB beta	polypeptide)	ESTs
Hs.83164	HS. 1819	Hs.165998	Hs.198135	Hs.23585	Hs.116273		Hs.75641	Hs,31511	Hs.193423		Hs.1619	Hs.1619		Hs.172081	Hs.173749	Hs.131924	Hs.77665	Hs.120378	Hs.99528		Hs.104315	Hs.192398		Hs.106369	Hs.269275	Hs.169266	Hs.265642		Hs.1735	Hs.191419
4A464342 Hs.83164	HS. I 819	4A487070 Hs.22615	4A149198 Hs.13393	AA190785 Hs.42821	AA628862 Hs.116273		4A857212 Hs.75641	AA453441 Hs.31511	AA287964 Hs.64988		AA441935 Hs.96944	AA441935 Hs.1619		AA481397 Hs.89407	Hs.31208	Hs.131924	AA487265 Hs.77665	AA719362 Hs.120378	4A460331 Hs.99528		AA037031 Hs.61594	AA780745 Hs.121037		Hs.118980	4A150298 Hs.62640	Hs.89604	Hs.50152		Hs.1735	Hs.19026
AA464342	174367	AA487070	AA149198	AA190785	AA628862		AA857212	AA453441	AA287964		AA44193	AA44193		AA481397	H27554	T86932	AA487265	AA719362	AA460331		AA037031	AA78074		H85557	AA150298	R19478	N67323		W44338	R00928
809901	2/1067	841195	504575	627343	1033983		1435029	788225	701461		774082	774082		746321	162753	115277	841501	1292733	795773		472103	867751		222025	491478	33045	286608		323599	124730
GF200	GFZUZ	GF202	GF201	GF202	GF204		GF203	GF203	GF203		GF200	GF200		GF200	GF201	GF202	GF200	GF204	GF202		GF204	GF204		GF201	GF201	GF200	GF202		GF204	GF200

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-2.3930522	-2.1222438	-1.2859259	-1,4409633		1.42820407	-1.2952801				-2.6913935	-2.4502098			-1.0359151	-1.2821861		-1.5160922				-1.7306878						-1.1118923	1.21618238
690.0587	690.0046	689.9127	689.5563		689.53	689.5101				689.4527	689.4081			689.3607	689.1845		689.1031	689.0115		688.9874	688.9823	688.5651		688.5079	688.3679		688.1648	687.9512 687.9265
	KIAA0669				RP2						ARP			DXS9879E	KIAA0546		IDS	GRP		SACM2L	LOC51293						ATP1A3	GC20
ESTs	<iaa0669 gene="" p="" product<=""></iaa0669>	EST	EST	etinitis pigmentosa 2 (X-linked	ecessive)	ESTs	Homo sapiens map 17q24;	5.13cR from GATA41C05	epeat region, complete	sedneuce	Arginine-rich protein	ONA segment on	chromosome X (unique) 9879	expressed sequence	<iaa0546 p="" protein<=""></iaa0546>	duronate 2-sulfatase (Hunter	syndrome)	gastrin-releasing peptide	suppressor of actin mutations	2, yeast, homolog-like	8D6 antigen	ESTs	ESTs, Weakly similar to !!!! ALU SUBFAMILY J	WARNING ENTRY !!!! H.sapiens]	ESTs	ATPase, Na+/K+ transporting,	alpha 3 polypeptide	translation factor sui1 homolog GC20 ESTs
Hs.108377	Hs.52526	Hs.112687	Hs.122087		Hs.44766	Hs.13073				Hs.6482	Hs.75412			Hs.18212	Hs.26764		Hs.172458	Hs.1473				Hs.128371		Hs.33944	Hs.108198		Hs.274371	Hs.21756 Hs.32587
H72878 Hs.108377	W60983 Hs.124735	AA609314 Hs.112687	AA779223 Hs.122087		W00899 Hs.44766	AA621302 Hs.13073				H23162 Hs.108009	R91550 Hs.75412			AA480035 Hs.18212	AA432112 Hs.26764		AA017170 Hs.36240	AA026118 Hs.1473		AA454836 Hs.5717	AA434403 Hs.106196	AA628225 Hs.116219		W86002 Hs 33944			AA775957 Hs.33016	AA488391 Hs.21756 AA699882 Hs.117348
214059	339235	1031588	452672		296180	744632				52315	196501			754046	784163		361570	469306		809961	770879	1055677		416128	417404		970271	843008 462409
GF203	GF202	GF202	GF203		GF200	GF202				GF202	GF200			GF200	GF202		GF203	GF201		GF201	GF203	GF204		GE201	GF201		GF203	GF202 GF204

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Horno sapiens cDNA FLJ11219 fls, done s.40337 PLACE1008122 687,5929	Human DNA sequence from clone 2614% on chromosome 6q21-22. 1. Contains the 9 part of the gene for a novel organic cation transporter (BAC ORF RG331POS), the DDO gene for D-aspartate oxidase (EC 1.4.3.1), ESTS, STSs, GSSs	s. 191996 and two putative CpG islands PDD19 CPG 97.3439 -1.0212913 s.28615 PDD19 protein PDD19 CPG 97.3471 -1.5964087 SCEC46 (S. cerevisiae) Telated	99		ESTs ESTs nuclear receptor subfamily 5,	8.183123 group A, member 2 NR5A2 696.7178 ESTs, Weakly similar to PYRUVATE CARBOXYLASE 8.47649 PRECURSOR [M.musculus] 686.6681 precursor specific beta-1-	0	
no sapiens cDNA 11219 fis, clone CE1008122	nan DNA sequence from e 261K5 on chromosom 1-22.1. Contains the 3' p te gene for a novel organ on transporter (BAC ORI 331PG3), the DDO gene paratrate oxides (EC 3.1), ESTs, STSs, GSSs	two putative CpG island 319 protein 324 (S. cerevisiae) relate	e family, member B s coglycan, delta (35kD	oprotein) A0992 protein s	's 's ear receptor subfamily 5	up A, member 2 s, Weakly similar to RUVATE CARBOXYLAS ECURSOR [M.musculus;	oprotein 5 othetical protein pase 8, apoptosis-related	eine protease rs
FLJ1 Hs.40337 PLA		Hs.191996 and Hs.25615 YDD SEC	Hs.7239 gene Hs.179756 EST sarc dyst	Hs.151899 glyo Hs.258812 KIA/ Hs.189917 EST		Hs.183123 grou EST PYR Hs.47649 PRE	Hs.251850 glyo Hs.91973 hypo	Hs.203961 EST
R54073 Hs.6394		AA707336 Hs.121731 R41217 Hs.21656	AA991931 Hs.7239 AA629035 Hs.119228	AA234982 Hs.44029 AA479270 Hs.108588 W93382 Hs.59446	AA609647 Hs.112740 AA678087 Hs.118387	N59115 Hs.91310 AA101777 Hs.47649	N48620 Hs.93960 N26714 Hs.43846	AA448468 Hs.19949 AA778432 Hs.5858
41495		451511 29430	1613449 744014	666829 / 754250 / 415095 /	_ `	246872 1	279319 266250	782488 379346
GF201		GF203 GF202	GF204 GF204	GF200 GF202 GF201	GF202 GF203	GF201 GF204	GF202 GF201	GF200 GF204

1.1210609	1.08997706	-1.4220268	-1.2561729		-1.2064888	-1.02802	-2.4179649	-1.2244285		1.12035575	-2,2922711	
686.3414	686.1603 686.1271	686.1014	685.9383		685.9034	685.7162	685.6731 685.5385	685.3215	685.2143	685.1195 685.0831	685.0082	684.9863 684.8627
	UBE1L DKFZP564M2423		EIF4B				MAPK1		P14	EIF3S5 KIAA0374		AHCYL1 LOC51582
ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H sapiens]	ubiquiur-acuvaurig enzyme E1, like DKFZP564M2423 protein	ESTs, Weakly similar to WNT- 1 PROTO-ONCOGENE PROTEIN PRECURSOR [H.sapiens]	eukaryotic translation initiation factor 4B	Homo sapiens cDNA FLJ11021 fis, clone PLACE1003704, weakly similar to SPLICING FACTOR.	ARGININE/SERINE-RICH 4 ESTs, Weakly similar to	THIOREDOXIN [H.sapiens] mitogen-activated protein	kinase 1 ESTs	ESTs	protease inhibitor 4 (kallistatin) P14 eukaryotic translation initiation factor 3, subunit 5 (epsilon,	47kD) svntaohilin	ESTs S-adenocylhomocycteine	hydrolase-like 1 antizyme inhibitor
Hs.70404	Hs.16695 Hs.165998	Hs.29764	Hs.93379		Hs.81648	Hs.98712	Hs.66151 Hs.174104	Hs.49459	Hs.159628	Hs.7811 Hs.100837	Hs.124013	Hs.4113 Hs.223014
Hs.70404	Hs.16695 Hs.44639	AA236986 Hs.29764	Hs.21801		Hs.114241	AA431210 Hs.98712	AA120887 Hs.103766 AA416740 Hs.109104	Hs.49459	AA628410 Hs.76705	AA455151 Hs.33060 AA872045 Hs.100837	AA703432 Hs.124013	AA454718 Hs.4113 AA676515 Hs.109931
H61037	N23454 N34863	AA236986	R68102		N50738	AA431210	AA120887 AA416740	N68171	AA628410	AA455151	AA70343	AA454718 AA676518
208769	250883 276574	687972	138374		283723	782171	491012 731376	292230	1032774	809881	450136	809758 882571
GF200	GF201 GF202	GF202	GF200		GF203	GF202	GF201 GF202	GF200	GF204	GF202	GF203	GF201 GF201

1.097248	-1.325753 -1.5419986	-1.9986965	-2.6023392	-1.3816608	1.02908462 1.26561442 -1.4425789	1.00836781	-1.9962308	1.17527573 1.78956555	-2.3188518
684.5737 684.5687 684.3053	683.871 683.8259	683.5305	683.3162	683.2722 683.0201	682.9164 682.5725 682.477 682.4297	682.3566	681.9835	681.9112 681.7775 681.6852 681.6766	681.6201
FUBP1	TFG SYNGR1		PSK-1	.DB1	IF116 ARL1 KIAA0668	CREBBP			AF060862
íi é	standard symbol and name) synaptogyrin 1 Shows cDNA Homo sapiens mRNA; cDNA DKFZp564E153 (from clone	DKFZp564E153) Homo sapiens mRNA; cDNA DKFZp564D246 (from clone DKFZp564D246)	type I transmembrane receptor (seizure-related protein)	Homo sapiens cDNA FLJ20684 fis, clone KAIA3469 LIM domain binding 1 interferon, gamma-inducible		drome) for	KIAA1173 protein, partial cds ESTs, Weakly similar to !!!! ALU CLASS B WARNING	ENTRY !!!! [H.sapiens] ESTs ESTs FSTs	netical protein
Hs.118962 Hs.100134 Hs.43129	Hs.250897 Hs.6139	Hs.8769 Hs.11673	Hs.6314	Hs.7734 Hs.26002	Hs.155530 Hs.242894 Hs.14665 Hs.5898	Hs.23598	Hs.27566	Hs.165411 Hs.11910 Hs.121398 Hs.184164	Hs.71791
90	R60847 RG.53 W90588 Hs.59284	N94344 Hs.55036 AA706901 Hs.11673	AA426408 Hs.6314	R49329 Hs.106084 AA421335 Hs.26002	AA491191 Hs.75783 N36233 Hs.113612 H06282 Hs.14665 AA709037 Hs.82290	AA023014 Hs.23598	N38888 Hs.27566	N66845 Hs.49271 T68887 Hs.11910 AA778529 Hs.121398 AA425386 Hs.29555	AA400188 Hs.71791
299360 488155 254315	42076 418159	309447	752802	38213 739230	824602 272750 44092 506550	364329	279979	295604 82236 1048861 773308	742776
GF201 GF201 GF202	GF200 GF202	GF203 GF203	GF202	GF203 GF203	GF200 GF203 GF202 GF204	GF200	GF203	GF200 GF202 GF204	GF202

	Atty Docket No. 2172	-2.0092199	1.06528424	1.23893382	-1.5808329	-1.7188341	-2.7453495		1.10469548	-1.4645932	1.06881261
	Atty	681.6006	681.5663	681.4587	681.4544 681.4313	681.3882 681.2372	681.1375 681.0972	680.8737	680.822 680.7977 680.346	680.3107 680.1938 680.1859 680.0777	680.0511
		RBM9		HSD17B3						SYN1	GIOT-4
DOMOVYON DYNYM	APPENDIX A	RNA binding motif protein 9 Homo sapiens homeobox	protein (HOX-1.3) gene, complete cds	dehydrogenase 3 Homo sapiens mRNA; cDNA	DKFZp762M127 (from clone DKFZp762M127) ESTs ESTs, Moderately similar to	H.sapiens]	notio seperis inniva, cura DKFZp761E0711 (from clone DKFZp761E0711) ESTs ESTs, Weakly similar to homolog of Drosophila discs	large protein, isoform 2 [H.sapiens]	ESTs, Weakly similar to KIAA0801 protein [H.sapiens] EST ESTs Horno sapiens paired	mesodem nomes box i (PMX1), mRNA synapsin I ESTs ESTs	GIOT-4 for gonadotropin inducible transcription repressor-4
		Hs.5011	Hs.37034	Hs.477	Hs.22483 Hs.194485	Hs.221760 Hs.53031	Hs.110095 Hs.95663	Hs.66295	Hs.95321 Hs.63237 Hs.43230	Hs.30528 Hs.225936 Hs.13328 Hs.46476	Hs.197219
		AA451903 Hs.24764	AA706301 Hs.37034	AA437291 Hs.477	W93688 Hs.22483 R11217 Hs.108495	T48293 Hs.56537 N35250 Hs.53031	AA598632 Hs.110095 AA446658 Hs.95663	AA865202 Hs.66295	H55893 Hs.95321 AA055969 Hs.63237 N24581 Hs.43230	AA663309 Hs.55395 H48153 Hs.75099 AA449703 Hs.13328 N45114 Hs.46476	AA599140 Hs.112508
	k et al.	786673	1155071	758222	357298 129447	74051 271926	897868	1459105	204083 377644 267241	853367 178950 785928 282884	950497
	Westbrook et al.	GF202	GF203	GF200	GF201 GF203	GF202 GF201	GF203 GF202	GF204	GF200 GF202 GF201	GF203 GF201 GF203 GF201	GF202

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GF202	731115	AA417280 Hs.98215	Hs.98215	Hs.98215	ESTS		679.7529	-1.3133483
GF203 GF203 GF201	435524 152270 417067	AA701375 H04757 W87385	AA701375 Hs.120439 H04757 Hs.117592 N87385 Hs.47435	Hs.120439 Hs.117592 Hs.47435	nomo sapiens manos, conse DKFZp434E1212 (from clone DKFZp434E1212) ESTs		679.7445 679.568 679.5289	1.22564501
GF201	781017	AA446027 Hs.1395	Hs.1395	Hs.1395	early growth response 2 (Krox- 20 (Drosophila) homolog) TIA1 cytotoxic granule-	EGR2	679.0867	
GF203	187029	R82978	Hs.24042	Hs.239489	associated RNA-binding protein	TIA1	679.0667	-1.2497035
GF201 GF202	345616 730398	W72431 AA469939	W72431 Hs.103169 AA469939 Hs.105323	Hs.82226 Hs.105323	glycoprotein (ransmernorane) nmb ESTs	GPNMB	678.9702 678.9489	-1.0363855
GF204	768263	AA424993 Hs.73680	Hs.73680	Hs.73680	ESTs, Weakly similar to KIAA0750 protein [H.sapiens]		678.9107	
GF203	269606	N26769	Hs.79396	Hs.79396	N-metriyipurine-DivA glycosylase	MPG	678.8824	-1.3518405
GF200	146123	R79082	Hs.79005	Hs.79005	protein tyrosine phosphatase, receptor type, K	PTPRK	678.6672	-1.4137174
GF200	730410	AA469965 RG.62	AA469965 RG.62	Hs.1765	lymphocyte-specific protein tyrosine kinase	ГСK	678.6533	-1.0954659
GF204	461454	AA705022	AA705022 Hs.120806	Hs.269562	ESTs		678.2753	10000
					Homo sapiens cDNA FLJ10956 fis, clone PLACE1000420, weakly similar to 7,8-DIHYDRO-8- OXOGUANINE TRIPHOSPHATASE (EC			
GF201 GF202 GF203	203008 347730 767991	H54263 W84891 AA418828	H54263 Hs.102106 W84891 Hs.58664 AA418828 Hs.43273	Hs.144407 Hs.169440 Hs.43273	3.1.6) ESTs ESTs		678.1737 678.1209 678.0337	1.18159724 -1.6029012

1.29078573 1.47483158	-1.7576315				-2.1220962 1.51440472	00000	1.15626888	1.26229411	-1.5641162	1.34117375		-1.1847209 -1.6395497	-1.305607
677.8973 677.8323 677.8261	677.6554	677.6461	677.5466 677.5466 677.52		677.4316 677.3768	677.3583	6/7.2823	677.2336	677.1968 677.1719	677.0573	676.9918	676.673 676.5912	676.4858 676.3244
KIAA1007		22 E	YWHAZ		PAX5			MMD	MAGEA4	MAP3K4	VAMP2		FABP3
3 1007 protein	none receptor	Interactor 8 tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation		sox gene 3 (b-cell specific activator	protein) F ESTs	ESTs	ESTS monocyte to mecrophade		melanoma antigen, family A, 4 MAGEA4 EST	mitogen-activated protein kinase kinase kinase 4	vesicle-associated membrane protein 2 (synaptobrevin 2) 1 Homo sapiens clone 25052	mRNA sequence ESTs fatty acid binding protein 3,	muscle and heart (mammary- derived growth inhibitor) ESTs
	2 2	Hs.6685	Hs.75103 Hs.116829 Hs.194071		Hs.22030 Hs.111725	Hs.221535	Hs.24078	Hs.79889	Hs.37107 Hs.124723	Hs.32353	Hs.194534	Hs.165570 Hs.269550	Hs.49881 Hs.267705
AA132874 Hs.24989 722212 Hs.23361 469819 Hs.81461	AA428179 Hs.98542 AA235974 Hs.87517	AA425650 Hs.7525	AA485749 Hs.104960 AA634374 Hs.116829 N20577 Hs.42872		55 Hs.22030 29 Hs.111725	_	44 Hs.24078	AA487643 Hs.79889	AA857809 Hs.37107 N49581 Hs.124723	AA293860 Hs.32353	79 Hs.91589	R41560 Hs.13547 AA701361 Hs.119235	AA044307 Hs.49881 N52272 Hs.32675
\		773208 AA42!	811166 AA48574 743818 AA63437 264105 N20577		129613 R16555 115205 T86429	_	133150 R26444	841331 AA48	1475476 AA857809 277707 N49581	727229 AA290	136676 R35079	29841 R41560 435493 AA70136	486394 AA04430 245877 N52272
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676.3085	676.1451	676.1095	676.0374			675 9688		675.954	675.7026	675.6035	675.5212	675.4291		675.3088	675.2514		675.0524	675.0204	674.8281	674.8111			674.8064	674.7664	674.7373	674.5586		674.276 674.0488	
	EIF4B		IL7R						RNAHP	FLJ20485		BSG			NOL										ACT	FOX		АЅЪН	
ESTs eukarvotic translation initiation	factor 4B	ESTs	interleukin 7 receptor	Homo sapiens cDNA FLJ10347 fis, clone	NT2RM2001035, highly similar	to CCH4-ASSOCIATED	ESTs, Moderately similar to	HHLA3 protein [H.sapiens]	RNA helicase-related protein	hypothetical protein	ESTs	basigin	ESTs, Moderately similar to	HN1 [M.musculus]	nucleolin	ESTs, Weakly similar to !!!! ALU CLASS B WARNING	ENTRY !!!! [H.sapiens]	ESTs	ESTs	ESTs	Homo sapiens cDNA	FLJ11174 fis, clone	PLACE1007367	ESTs	activator of CREM in testis	lysyl oxidase	Homo sapiens mRNA; cDNA DKFZp564D246 (from clone	DKFZp564D246) aspartate beta-hydroxylase	
Hs.58972	Hs.93379	Hs.261362	Hs.237868			He 996318		Hs.226046	Hs.8765	Hs.98806	Hs.13911	Hs.74631		Hs.109706	Hs.79110		Hs.110965	Hs,238797	Hs.22902	Hs.269120			Hs.24359	Hs.27186	Hs.5460	Hs.102267		Hs.11673 Hs 121576	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
Hs.58972	AA678315 Hs.119654	_	4A485865 Hs.1732			AA419609 He 17035		4A664149 Hs.10597	Hs.110440	4A609161 Hs.112657	Hs.13911	AA436440 Hs.74631		AA035430 Hs.109706	AA476294 Hs.79110		4A421037 Hs.110965	Hs.106364	Hs.22902	Hs.49161			AA779293 Hs.24359	Hs.27186	AA889787 Hs.125905	Hs.81993		Hs.102361 Hs.117755	2
W87394	AA678315	AA14776	AA48586			444196		AA66414	T56281	AA60916	R06119	AA4364		AA03543	AA47629		AA42103	N70848	R45404	N66550			AA77928	H22932	AA88978	W70343		H97000	2000
417094	430948	589967	840460			759634		855496	78353	1031402	124891	756533		471568	770704		739244	299609	35311	278761			453083	52026	1460824	345849		249949	2
GF202	GF203	GF202	GF201			GESUS	5	GF204	GF201	GF202	GF200	GF201		GF204	GF202		GF203	GF201	GF203	GF201			GF204	GF201	GF204	GF201		GF201	3

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	-1.0415872	-1.05426118	-2.5010838 -1.7106029 -1.0406094	-1.0159084	-1.2207661
673.786 673.786 673.6172 673.5728	673.512 673.3478 673.3478	673.333 673.1105 672.8428 672.8428	672.592 672.3367 671.9491 671.9205 671.6703	671.2663 671.2663 671.2065	671.0496 671.0051 670.918 670.8723
LOC51322 TARBP1	MAN2A2 KYNU	COAMO		FALZ	DIO2 NPTXR CDO1
hypothetical protein ESTs TAR (HIV) RNA-binding protein 1 ESTs mannosidase, alpha, class 2A,	member 2 kynureninase (L-kynurenine hydrolase) ESTs	ESTs ESTs ESTs ESTs, Weakly similar to BRX protein [M.musculus] intercellular adhesion molecule	ESTs ESTs ESTs ESTs p53-induced protein chromoseme condensation 1 ESTs, Highty similar to leucine rich-repeat protein	[M.musculus] fetal Alzheimer antigen ESTs, Weakly similar to tuffelin [M.musculus] delodinase, iodothyronine.	type II neuronal pentraxin receptor ESTs cysteine dioxygenase, type I
Hs.70333 Hs.164502 Hs.151518 Hs.121592	Hs.182923 Hs.169139 Hs.98497	Hs.159306 Hs.159306 Hs.119488	Hs.592733 Hs.58280 Hs.203514 Hs.187615 Hs.74427 Hs.84746	Hs.126085 Hs.99872 Hs.50841	Hs.154424 Hs.91622 Hs.28886 Hs.3229
AA633545 Hs.70333 R53431 Hs.22256 N62244 Hs.77048 N74507 Hs.121592	AA682490 Hs.116693 H87471 Hs.81771 AA425166 Hs.98497	N26908 HS.43872 T92418 HS.16829 AA702220 HS.119488	M78169 Hs.58280 H77361 Hs.39743 AA426026 Hs.86089 H12189 Hs.74427 AA291398 Hs.84746	AA778089 Hs.126085 AA700730 Hs.113108 AA036952 Hs.50841	AA018134 Hs.42263 R52651 Hs.91622 H85465 Hs.107134 AA497111 Hs.3229
856504 39824 287745 291724	450645 252515 768993	257249 118078 447480	130201 346899 233589 757246 48285 724615	379709 435350 472081	362694 40014 249707 823562
GF204 GF204 GF201 GF204	GF203 GF201 GF203	GF202 GF202 GF204	GF201 GF204 GF202 GF200 GF200	GF204 GF203 GF204	GF200 GF204 GF201 GF200

	-1.5653171	-1.2427535 1.59317391 -1.493302	1.90810314	-1.3803988 1.32357409 -1.2712176
	670.8008 670.7609 670.7592 670.6587	670.6494 670.5009 670.3812 670.2587 670.1256	670.098	669.9213 669.9122 669.6724
	KIAA0999	CDC4L		 PAX8 YDD19
Human DNA sequence from done 109F14 on chromosome done 109F14 on chromosome 6p21.221.3. Condains the attendatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL 10A gene, a PUTATIVE ZNATIVE ZNATIVE ZNATIVE ZNATIVE ZNATIVE Carea, and the PPARID to LIKE cene, and the LIKE cene, and the PPARID to LIKE cene, and the LIKE ce	Peroxisome Proliferato ESTs KIAA0999 protein ESTs ESTs, Highly similar to	SECRETOGRANIN III PRECURSOR [M.musculus] ESTs ESTs cell division cycle 4-like EST	Homo sapiens cDNA FLJ11200 is, clone PLACE1009622, weakly smilar to MATERNAL EFFECT PROTEIN STAUFEN Homo sapiens mRNA', cDNA DKFZp654M0763 (from clone DKFZp654M0763)	ESTs, Highly similar to TRAF4 associated factor 1 [H.sapiens] paired box gene 8 YDD19 protein ESTs
	Hs.203846 Hs.82567 Hs.4278 Hs.78200	Hs.22215 Hs.89257 Hs.112496 Hs.62354 Hs.60215	Hs.96870 Hs.8175	Hs.181466 Hs.73149 Hs.25615 Hs.118180
	AA156787 Hs.118718 W86630 Hs.32765 AA418042 Hs.18999 AA460299 Hs.78200	AA634158 Hs.22215 AA283942 Hs.89257 AA598943 Hs.112496 AA041499 Hs.62354 AA007502 Hs.60215	AA452829 Hs.20967 AA664020 Hs.8175	T91225 Hs.112307 AA405891 Hs.73149 T50075 Hs.9089 N68504 Hs.118180
	502311 416627 767747 795746	858401 700574 898038 376516 429333	788549	111812 742101 70202 294066
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669.6553	669.6371	669.623	669.5417	669.4915		669.3326	668.9959	668.9684	668.6176		668.5266	668.4391	668.1555	668.1318	668.1317	667.9126	667.8517		667.8198
		XRCC4	DKFZP56401863	PAFAH1B1	_		MITF	PEDF	ADA			LOC51296		HMG2L1			KIAA1012		
ESTs ESTs, Weakly similar to Similar to S.cerevisiae	(H.sapiens) X-ray repair complementing	hamster cells 4	DKFZP56401863 protein	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit (45kD)	ESTs, Weakly similar to weakly similar to ANK repeat	orf7 protein [C.elegans] microphthalmia-associated	transcription factor	pigment epithelium-derived factor	adenosine deaminase	Homo sapiens cDNA FLJ10803 fis, clone	NT2RP4000833	peptide transporter 3	ESTS	high-mobility group protein 2- like 1	ESTs	ESTs	KIAA1012 protein	ESTs, Weakly similar to E- SELECTIN PRECURSOR	[H.sapiens]
Hs.98612	Hs.104613	Hs.150930	Hs.173074	Hs.77318		Hs.14337	Hs.166017	Hs.173594	Hs.1217		Hs.8173	Hs.237856	Hs.35096	Hs 92260	Hs.30622	Hs.72063	Hs.42959		Hs.271350
1276641 AA776775 Hs.98612	AA425545 Hs.104613	Hs.21523	HS.44401 HS.11814	AA775445 Hs.77318		Hs.113078	Hs.82000	AA463946 Hs.17353	AA683578 Hs.1217		Hs.8173	4A994205 Hs.11388	Hs.23188	He 92260		4A150435 Hs.72063	4A479887 Hs.112297		Hs.24712
AA77677	AA42554	R14027	N32309 N52763	AA77544		R11236	N66177	AA46394	AA68357		N59078	AA99420	N91101	W42451	AA48641	AA15043	AA47988		R33858
1276641	768965	26811	259896 283382	878178		129392	278570	810290	505881		246800	1631132	292939	323074	842882	491435	772888		136246
GF204	GF202	GF200	GF203	GF203		GF200	GF203	GF201	GF203		GF203	GF204	GF200	CE201	GF202	GF201	GF202		GF203

-1.2142181	-1.5083047						-2.0240897		1.22219098		4 22210000	22219090	1.33080487	-1.6060687			-1.8933794		1.22927295	1.00542835	
		27 92	. 2	9	5	,							•		=			88			
665.6284	665.3544	665.3372	665.2802	665.1306	665.1245		665.1201 664.9945		664.8183		004000	664.5867	664.4913	664.4582	664,4071		664.3817	664.3638	664.3621	664.2841	664.2081
	2		œ																		
	CFIM25		GPNMB			I	BTRC							WS-3					ERO1L	TINF2	
Homo sapiens mRNA for KIAA1406 protein, partial cds pre-mRNA cleavage factor Im	(25kD) ESTs, Weakly similar to	ZK757.1 [C.elegans] FSTs	glycoprotein (transmembrane)	Splicing factor, arginine/serine- rich, 46kD	eukaryotic translation initiation factor 4B	beta-transducin repeat	containing ESTs	Homo sapiens mRNA for lentin recentor dene-related	protein	Homo sapiens mRNA for	lepuil leceptol genericated	protein ESTs	ESTs	novel RGD-containing protein WS-3	ESTs	Homo sapiens cDNA FLJ10909 fis, clone OVARC1000091, weakly	FACTOR C1	ESTs	ERO1 (S. cerevisiae)-like TERE1 (TRE1)-interacting	nuclear factor 2	ESTs
Hs.23076	Hs.9605	Hs.193811 Hs 125446	He 82926	Hs.155160	Hs.93379		Hs.226434 Hs.13132		Hs.23581		10000	Hs.23581 Hs.169854	Hs.24601	Hs.39913	Hs.269679		Hs.20597	Hs.125043	Hs.25740	Hs.7797	Hs.120379
AA160606 Hs.95915	AA031770 Hs.97914	H53968 Hs.119356	A4425450 Hs 82226	Hs 94339			AA705262 Hs.18375 AA235343 Hs.13132		Hs.54515		100	Hs.23581 Hs.106184	_		Hs.130842		AA488367 Hs.20597	Hs.55427	AA186804 Hs.25740	Hs.7797	AA778851 Hs.120379
AA16060	AA03177	H53968	440548	W92120	AA77584		AA23534		H51066		000	H51066 W84638	R33193	AA451781	W80510		AA48836	W86391	AA1868(H96734	AA7788
592707	470846	202799	773330	415288	878517		461628 687638		194182		000	194182 356883	135777	788745	415549		843163	415891	625875	251682	452916
GF202	GF200	GF204	G 201	GF201	GF204		GF204 GF203		GF200		0	GF200	GF200	GF200	GF204		GF202	GF201	GF202	GF202	GF204

Hs.1087 Hs.104072 Hs.104072 Hs.127828 Hs.1380 Hs.1380 Hs.68877 Hs.68877 Hs.90402 Hs.90402 Hs.193042 Hs.193042 Hs.193042 Hs.193042 Hs.193042 Hs.193042 Hs.193042 Hs.193043 Hs.132997 Hs.193044 Hs.13299 Hs.13291 Hs.21321				MOSCAC GOZZEGED APPENDIX A		Atty	Atty Docket No. 2172
Hs. 1087 Serine/throonine kinase 2 STK2 664.1947							
Hs. 127828 Protein (G protein), gamma 7 GNG7 G63.8628 Hs. 127828 protein (G protein), gamma 7 GNG7 G63.7621 Hs. 1390	AA496013 Hs.1087	280	Hs.1087	serine/threonine kinase 2	STK2	664.1947	1.21950078
Hs.127828 gradin in tracellor, gammary GNG7 G83.7821 protestome (protein), gammary GNG7 protestome (protein), gammary GNG7 hs.68877 22 macropaln) subunit, beta type, amacropaln) subunit, beta type, controllor, gammary GNG8 Hs.68877 polypeptide Hs.7225 Ras-associated protein Rap1 LOC51277 G63.322 Hs.9042 frame 1 CPRA Hs.87150 containing mRNA G210rf4 G63.323 Hs.87150 containing mRNA G220rf4 G63.0854 Hs.18032 ESTs Hs.4944 EST Hs.4944 EST Hs.69590 pyruvate kinase, liver and RBC PKLR G62.8333 Hs.59490 pyruvate kinase, liver and RBC PKLR G61.8054 Hs.31281 DKFZp564E1383) (from clone Hs.51321 DKFZp564E1383) (from clone Hs.51321 Homo sapiens cDNA FS.7940 (1GFII mRNA-binding protein 3 KOC1 G61.8054 Hs.31286 ESTs Hs.09881 HEMBA-tootxof7 Hs.51970 linked Hs.109881 HEMBA-tootxof7 Hs.21970 linked Hs.11970 linked Hs.177192 ESTs	AA191404 Hs.104072	34072	Hs.104072	ESTS		663.8628	-1.6262639
Hs.1390 2 Ordertrome b-245, alpha bit. 458877 PSMB2 PSMB2 663.36011 Ps.68877 polyhochrome b-245, alpha bit. 458877 polyhochrome b-245, alpha chromosome 21 open reading CYBA 663.382 Arrange and CYBA 663.382 Arrange and CYBA 1 LOC51277 663.382 Hs.9042 Frame 1 CACIN/CIGTGI) repeat- CACIN/CIGTGI, repeat- CACIN/	AA701654 Hs.119692	9695	Hs.127828	protein (G protein), gamma 7 proteasome (prosome, marropain) subunit bata tuna	GNG7	663.7621	-2.5896364
Hs.68877 polypeptide CYBA 663.3421 Hs.47225 Rax-associated protein Rap1 LOC51277 663.3421 Hs.9042 frame 1 C21ord 663.328 Hs.9042 ESTs 663.0942 Hs.19322 ESTs 663.0942 Hs.19324 EST 662.0944 Hs.13229 ESTs 662.0947 Hs.42997 EST FST 662.0947 Hs.42997 EST Homo sapiens mRNA, cDNA Hs.21321 DKFZp54E1363 (from clone Hs.4324 EST Hs.49424 EST Hs.49424 EST Hs.4344 EST Hs.4344 EST Hs.49424 EST Hs.49424 EST Hs.49424 EST Hs.49424 EST Hs.49434 Hs.71361 GST Hs.49434 Hs.49434 EST Hs.49434 EST Hs.49434 EST Hs.49434 EST Hs.49434 EST Hs.49434 GST Hs.4944 GST Hs.49444	T98663 Hs.11	6554	Hs.1390	2	PSMB2	663.6011	1.19261275
18,0867/ Physphoge Construction Constructio		į	11000	cytochrome b-245, alpha	400	0000	1
Hs. 9042 Irane 1 C210rd 683.253 Hs. 19361 ESTs C3 C310rd 683.253 Hs. 19361 C4CA/D/I/GT6)n repeat 683.0842 Hs. 18322 ESTs 60-0ontlaining mRNA 683.0858 Hs. 180948 EST 683.0854 Hs. 128997 EST Hono sapiens mRNA; cDNA DNFZp564E1383 (from done Hs. 21321 DNFZp564E1383) Hs. 95990 pyruvate kinase, liver and RBC PKLR 662.3827 Hs. 95990 pyruvate kinase, liver and RBC PKLR 662.3427 Hs. 31286 ESTs 662.3421 Hs. 13314 ESTs 662.3421 Hs. 13081 Hs. 14000307 Hs. 21970 linked protein), gamma 3, gNO3LG 661.3034	1161830 AA8/6021 Hs.688// 283080 N51304 Hs.47225	7225	HS.68877 HS.47225	polypeptide Ras-associated protein Rap1	CYBA LOC51277	663.332	-1.2809022
Hs. 9942 frame 1 C2 tort4 663.253 Hs. 193613 ESTs concluded AdAZBR11 (CAC)n/(GTG)n repeat-Hs. 19322 ESTs containing mRNA 663.0654 Hs. 19322 ESTs containing mRNA 663.0658 Hs. 18924 EST 662.3247 Hs. 29997 EST 662.38779 Hs. 29990 pyruvate kinase, liver and RBC PKLR 662.3427 Hs. 59990 pyruvate kinase, liver and RBC PKLR 662.3427 Hs. 59990 IGF-II mRNA-binding protein 3 KOC1 661.3554 Hs. 31281 GETS 662.3421 Hs. 31381 HeMAA-binding protein 3 KOC1 661.3554 Hs. 31480 ESTs 661.3630 Guanine nucleotide binding protein 3 kOC1 661.3031 Hs. 21970 linked 16 protein), gamma 3, GNG3LG 661.3031 Hs. 21970 linked 16 protein), gamma 3, GNG3LG 661.3091 Hs. 21970 linked 16 protein), gamma 3, GNG3LG 661.3091				chromosome 21 open reading			
Hs. 193613 ESTS 663.0842 Hs. 87150 containing mRNA Hs. 19222 ESTS Hs. 152924 ESTS Hs. 152937 EST Hs. 49424 EST Hs. 21321 DKFZp564E1363) Hs. 21321 DKFZp564E1363) Hs. 29990 pyruvate kinase, liver and RBC PKLR 662.0866 Hs. 13314 ESTS Hs. 3940 IGF-II mRNA-binding protein 3 KOC1 661.8554 Hs. 31286 ESTS Hs. 108881 HEMBA voloxior Hs. 21970 linked protein), gamma 3, gMG3LG 661.3031 Hs. 1177192 ESTS	1256714 AA876148 Hs.125326	125326	Hs.9042	frame 1		663.253	
Hs.87150 containing mRNA (ACD)M(GTG)in repeat- (ACD)M(GTG)M(GTG)in repeat- (ACD)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(GTG)M(AA677703 Hs.114686	14686	Hs.193613	ESTs		663.0942	
Hs. 87150 containing mRNA 683.0854 Hs. 19322 ESTs Hs. 19322 ESTs Hs. 19324 EST Hs. 26947 Hs. 26947 Hs. 26940 EST Hs. 24944 EST How saplens mRNA; cDNA Hs. 21321 DKFZp564E1383) Hs. 29590 pyruvate kinase, liver and RBC PKLR 662.4507 Hs. 29590 pyruvate kinase, liver and RBC PKLR 662.4507 Hs. 31240 (1GF-II) mRNA-binding protein 3 KOC1 661.8554 Hs. 31286 Hs. 31400 ESTs Hs. 31286 Homo saplens cDNA Hs. 109881 HELMOT Sit soone Hs. 109881 HELMOT Sit soone Hs. 197192 ESTs Hs. 21970 GROSSOT GROSSOT GROSSOT GROSSOT GROSSOT Hs. 31970				Human clone A9A2BB11			
Hs. 19922 ESTs Hs. 19924 KIAA0729 protein KIAA0729 683.0558 Hs. 19924 EST Hs. 49424 FST Hs. 49424 FST Hs. 49424 FST Homo sapiens mPlNA; cDNA Hs. 21321 DKFZp654E1383 (from clone) Hs. 21321 DKFZp654E1383 (from clone) Hs. 13314 ESTs Hs. 7344 ESTs Hs. 7346 IGF-II mFlNA-binding protein 3 KOC1 661.9554 Hs. 31286 ESTs Hs. 108881 HEMBA roocan's GNG3LG Hs. 1970 Igt is, clone protein (G protein), gamma 3, GNG3LG Hs. 1970 Ilriked Hs. 1970 Ilriked Hs. 1971 ESTs Hs. 1972 ESTS HS. 1973	635836 A A A A A A B A A A A A A A A A A A A	20503	Hs 87150	containing mBNA		663 0854	
Hs. 19894 KIAA0729 protein KIAA0729 662.9247 Hs. 158997 EST 682.9833 Hs. 48424 EST 682.9833 Hs. 48424 Homo sapiens mRNA; cDNA 682.8833 DKT2p564E1363) Hs. 21321 DKT2p564E1363) Ks. 95990 pyruvate kinase, liver and RBC PKLR 662.4507 Hs. 13314 ESTs 662.4207 Hs. 31286 ESTs 661.9554 Hs. 108881 HeMAA-binding protein 3 KOC1 661.9554 Hs. 108881 HeMAA-binding protein 3 KOC1 661.8034 Hs. 1970 GF-II mRNA-binding protein 3 KOC1 661.8034 Hs. 21970 GF-II mRNA-binding protein 3 KOC1 661.8034 Hs. 21970 Inked 16 protein), gamma 3, GNG3LG 661.3091 Hs. 1971 BEST 661.3102		9322	Hs 19322	ESTS		663.0558	-1.7249898
Hs.125997 EST 662.8933 Hs.49424 EST 662.8933 Hs.49424 EST 662.873 Homo sapiens mRNA; cDNA Hs.21321 DKFZp54E1383) Hs.59590 pyruvate kinase, liver and RBC PKLR 662.4507 Hs.31286 ESTs 661.8574 Hs.31286 Homo sapiens cDNA Hs.31288 Hs.31286 Hs.3240 (1GF-II mRNA-binding protein 3 KOC1 661.8554 Hs.31288 Hs.31286 Homo sapiens cDNA Hs.108881 Hs.Man 400307 Hs.21970 guanine nucleotide binding protein (G protein), gamma 3, gNG3LG 661.3031 Hs.21970 linked	AA430050 Hs.19542	9542	Hs.180948	KIAA0729 protein	KIAA0729	662.9247	-1.1696311
Hs.49424 EST Hono sapiens mRNA; cDNA Hono sapiens mRNA; cDNA DK72p564E1383 (from done Hs.21321 DK72p564E1383) Hs.95990 pyruvate kinase, liver and RBC PKLR 662.3421 Hs.13314 ESTs Hs.71286 ESTs Hs.71920 GF-II mRNA-binding protein 3 KOC1 661.9554 Hs.108881 HEMBA 1000307 guanine nucleotide binding protein (G protein), gamma 3, GNG3LG 661.3091 Hs.21970 linked Hs.177192 ESTs GR2.362 661.3091 GR3.362 661.3091 GR3.362 661.3091 Hs.21970 linked Hs.177192 ESTs	1460827 AA889798 Hs.125997	125997	Hs.125997	EST		662.8933	
Henro saplens mFINA; cDNA Hes.21321 DKFZp564E1383 (from done Hs.95990 pyruvate kinase, liver and RBC PKLR 662.3421 Hs.13314 ESTs 662.3421 Hs.73440 IGF-II mFINA-binding protein 3 KOC1 661.8727 Hs.31286 ESTs 661.8727 Hs.108881 HEMBA roosay FLJ101012 fis, clone protein (G protein), gamma 3, GNG3LG 661.3091 Hs.1970 linked 661.2102	N68000 Hs.	Hs.49424	Hs.49424	EST		662.8779	-1.1758562
Hs.91321 DKFZp564E1383) 682.4507 Hs.95990 pyruvate kinase, liver and RBC PKLR 662.3421 Hs.73314 ESTs 662.0866 Hs.731286 ESTs 661.9554 Hs.31286 ESTs 661.9554 Hs.31286 Hs.71012 Its, clone Hs.108881 HEMBA1000307 guanine nucleotide binding protein (3 protein) gamma 3, Hs.21970 linked BSTs 661.3091 Hs.21970 linked 661.3091				Homo sapiens mRNA; cDNA DKFZp564E1363 (from clone			
Hs. 99900 pyruvate kinase, liver and RBC PKLR 682.3421 Hs. 13314 ESTs 682.0866 Hs. 79440 IGF-II mRNA-binding protein 3 KOC1 661.9554 Hs. 31286 ESTs 661.9574 Hs. 108881 HEMBA 1000307 guanine nucleodide binding protein (G protein), gamma 3, Hs. 21970 lirked binding general 3, 1177192 ESTs 661.3091	AA486770 Hs.21321	1321	Hs.21321	DKFZp564E1363)		662.4507	1.21570931
Hs.7940 (GF-II mRNA-binding protein 3 KOC1 661.9554 Hs.31286 ESTs CANA-binding protein 3 KOC1 661.9727 Hs.108881 HEMBA1000307 Gylanine nucleotide binding protein (G protein), gamma 3, Hs.21970 linked BSTs 661.3091 Hs.77192 ESTs 661.3091	H77542 Hs. R62461 Hs.	Hs.117731 Hs.13314	Hs.95990 Hs.13314	pyruvate kinase, liver and RBC ESTs	PKLR	662.3421 662.0866	-2.3210483 -1.3688748
Hs.31286 ESTS 661.8727 H mon sapiens cDNA FLJ1001'2 lis, glone Hs.108881 HEMBA1000307 661.8034 guamine nucleodide binding protein (G protein), gamma 3, Hs.21970 linked CFSTS 661.3091 Hs.177192 ESTS 661.2102	AA187143 Hs.79440	79440	Hs.79440	IGF-II mRNA-binding protein 3	KOC1	661.9554	-1.0770967
Hs.108881 HEMBA1000307 661.8034 guaranne nucleodide binding protein (G protein), gamma 3, Hs.21970 linked GNG3LG 661.3091 Hs.177192 ESTs 661.2102	H14830 Hs.3	1286	Hs.31286	ESTs Homo sapiens cDNA FLJ10012 fis. clone		661.8727	-1.079876
Hs.21970 inked GNG3LG Hs.177192 ES1s	AA460521 Hs.108881	108881	Hs.108881	HEMBA1000307 guanine nucleotide binding protein (G protein). gamma 3.		661.8034	-1.3431447
	AA456571 Hs.21970 AA046067 Hs.62921	1970	Hs.21970 Hs.177192	linked ESTs	GNG3LG	661.3091 661.2102	

		-1.6356496								-1.3465823		1.01727811										-1.1791635							-1.7595816			2.79103595		-1.6777383
		660.9815	660.9353	660.931				660.8944	9669.099	660.6328		660.6141	660.5784	660.5413					660.5341			660.4423	660.4067	660.1845	660.1175		660.0947	660.0916	659.7722	659.7386		659.5077	659.4892	659.4841
		PROSC	AN.					PPP3CA				COPA							LAMC2				USP1						CHM-I	PRPH		LOC51596	DKFZF434C171	
ozolino outhotoco	transcribed (bacterial	homolog)	nucleoside phosphorylase	ESIS	protein phosphatase 3	(formerly 2B), catalytic subunit,	alpha isotorm (calcineurin A	alpha)	ESTs	EST	coatomer protein complex,	subunit alpha	ESTs	ESTs	laminin, gamma 2 (nicein	(100kD), kalinin (105kD),	BM600 (100kD), Herlitz	junctional epidermolysis	pnllosa))	Homo sapiens cDNA	FLJ10352 fis, clone	NT2RM2001152	ubiquitin-specific protease 1	ESTs	ESTs	ESTs, Highly similar to NY-	REN-45 antigen [H.sapiens]	ESTs	chondromodulin I precursor	peripherin	divalent cation tolerant protein	CUTA	DKFZP434C171 protein	ESTs
		Hs.210749	Hs.75514	Hs.43586				Hs.272458	Hs.11924	Hs.22517		Hs.75887	Hs.226313	Hs.57843					Hs.54451			Hs.100914	Hs.35086	Hs.95734	Hs.83722		Hs.239155	Hs.117592	Hs.97932	Hs.37044		Hs.107187	Hs.209100	Hs.192993
		W86106 Hs.32376		N49979 Hs.43586				AA121266 Hs.34641	AA035494 Hs.11924	R42061 Hs.22517		N62180 Hs.117679	_	W63785 Hs.57843					AA677534 Hs.54451			AA701866 Hs.100914	T55607 Hs.9922	AA133778 Hs.95734	T67223 Hs.83722		AA448160 Hs.5624	W88747 Hs.18636	AA461485 Hs.97932	AA975388 Hs.37044		AA457543 Hs.118373	\sim	R93984 Hs.128742
		416202	269890	282787				490178	471755	30428		289822	234172	342208					460403			434782	73596	503541	99999		782766	417804	796659	1556056		838732	549867	276126
		GF203	GF201	GF201				GF201	GF204	GF203		GF203	GF204	GF201					GF201			GF203	GF201	GF201	GF201		GF201	GF201	GF203	GF204		GF202	GF204	GF202

-1.0200423	1.08854572	1.78999386	1.23400584 1.64848579 -1.0528744 -1.0166993 -1.241718	-1.3648785	-1.0358808
659,4504	659.1583 659.1493	658.863 658.8071 658.5994 658.4462 658.4113	658.3924 658.2028 658.2028 658.1235 658.0732 658.0571	657.3174 657.3174 657.2367 657.2236	657.1217 657.0246
KDR		KIAA0180	NET1A VPS26	SEC61G KCNJ13	PSAP DSG1
kinase insert domain receptor (a type III receptor tyrosine Minase) Homo sapiens cDNA FLJ1147 fis, clone PLACE 1006878, weakly similar to Homo sapiens mRIA for type II membrane	protein, clone:HP10328 ESTs ESTs, Weakly similar to cDNA EST yk375c3.5 comes from	this gene [C.elegans] ESTs ESTs KIAA0180 protein ESTS	protein (nonogene) protein (nonogene) vacuolar protein sorting 26 (yeast homolog) ESTs ESTs ESTs	ESTS is Sectification invaridy-rectifying potassium invaridy-rectifying channel, subfamily J, member 13 ESTs prosaposin (variant Gaucher disease and variant metachromatic	leukodystrophy) desmoglein 1
Hs.12337	Hs.173203 Hs.108920	Hs.69192 Hs.194563 Hs.178067 Hs.178292 Hs.55533	Hs.25155 Hs.67052 Hs.13852 Hs.22085 Hs.99596 Hs.6783	Hs.4212 Hs.9950 Hs.11364 Hs.247124	Hs.78575 Hs.2633
AA026831 Hs.12337	Hs.100983 Hs.108920	AA988574 Hs. 69192 AA668647 Hs. 103301 AA453260 Hs. 98179 T91958 Hs. 90981 AA283029 Hs. 55533		Hs. 4212 Hs. 9950 Hs. 11364 Hs. 124258	N72215 Hs.50201 AA041388 Hs.110416
AA02683	R82733 N21368	AA98857 ⁴ AA668647 AA453260 T91958 AA283029	R24543 AA064946 T99617 R16983 AA463509	R51357 W96107 T63998 R51988	N72215 AA041388
469345	149742 265522	1602018 859534 795347 112131 713286	131867 529147 123354 129777 797009 772944	39306 358456 79808 40063	291255 376423
GF200	GF200 GF202	GF204 GF204 GF201 GF200 GF203	GF200 GF202 GF200 GF202 GF202 GF201	GF202 GF200 GF201 GF201	GF201 GF202

1.45564368	1.10176905	1.06681879	1.30328407	1.5413853	1.3612407		1.16618255	
656.9872 656.8415 656.794	656.7207 656.7003 656.5182	656.5142 656.509	656 5085	656.4528 656.3803	656.2862 656.1572	655.8682	655.7484	655.668
PIR	KIAA0916 KIAA0823	MAN2C1		ITGA8			REG1A TM9SF2	RFC2
ESTs, Moderately similar to mSin3A associated polypeptide p30 [H.sapiens] ESTs Pirin	ESTs, Weakly similar to T15B7.2 [C.elegans] KIAA0916 protein KIAA0893 protein	mannosidase, alpha, class 2C, member 1 ESTs	ESTs, Weakly similar to Glutamate/lysine rich second exon shows similarity to rat neurofilament triplet M protein IC elegens	[C:elegaris] integrin, alpha 8 FSTs	EST ESTS ESTs Weakly similar to	putative type III alcohol dehydrogenase (D.melanogaster) regenerating islet-derived 1 alpha (pancreatic stone purotein pancreatic thread	protein) transmembrane 9 superfamily member 2	replication factor C (activator 1) 2 (40kD) Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
Hs.38750 Hs.112198 Hs.79259	Hs.114062 Hs.151411 Hs.45719	Hs.26232 Hs.115779	He 79451	HS.91296 Hs.42338	Hs.49872 Hs.70903	Hs.184261	Hs.1032 Hs.28757	Hs.139226 Hs.6776
AA034062 Hs.38750 772562 Hs.12576 H69334 Hs.38842		- 69	A 150 / 84 10 70 / 51	48.150484 HS.72451 R87964 HS.91296 H97033 Hs.42338		N70632 Hs.11553	AA625655 Hs.1032 AA479252 Hs.28757	AA663472 Hs.116908 AA974173 Hs.6776
429942 A 22144 T 234237 H			K00E00			299274 N	745343 A 753917 A	860000 A
GF201 GF201 GF200	GF201 GF203	GF200 GF203	000	GF202 GF200	GF202 GF202 GF202	GF201	GF201 GF200	GF204 GF204

<u>.</u>	
keta	
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Westbrook et al.	k et al.				APPENDIX A		Attry	ATTY DOCKET INO. ZI 726/3
GF203	245838	N55326	Hs.47951	Hs.184134	ESTs		655.5819	-2.3776704
GF201	755689	AA496438	AA496438 Hs.1497	Hs.1497	retinoic acid receptor, gamma ubiquitin-activating enzyme E1 (A1S9T and BN75 tencerature sensitivity	RARG	655.4931	
GF200 GF203	898262 726679	AA598670 AA398331	AA598670 Hs.2055 AA398331 Hs.97612	Hs.2055 Hs.97612	complementing) ESTs	UBE1	655.4811	1.35628097
GF203	282094	N48258	Hs.46645	Hs.46645	ESTs Homo sapiens mRNA; cDNA DKFZp434K1323 (from clone		655.2468	1.05944335
GF201 GF202	811138	AA48573(AA412067	AA485730 Hs.21346 AA412067 Hs.98117	Hs.21346 Hs.98117	DKFZp434K1323); partial cds ESTs ESTs, Weakly similar to	•	655.037	-1.0757313
GF201	377610	AA055833	AA055833 Hs.58152	Hs.58152	anagen-specinic protein mKAP13 [M.musculus]		654.9767	
					Homo sapiens cDNA FLJ11290 fis, clone PLACE1009622, weakly similar to MATERNAL			
GF201	487860	AA045462	AA045462 Hs.21146	Hs.96870	EFFECT PROTEIN STAUFEN ESTs, Weakly similar to unknown protein		654.9022	
GF200	199251	R95780	Hs.35460	Hs.221867	[R.norvegicus]		654.8975	1.0423694
GF204	844955	AA77354	AA773544 Hs.4205	Hs.4205	Homo sapiens cDNA FLJ20383 fis, clone KAIA2948 dynein, cytoplasmic, light		654.8173	
GF203	703800	AA27831	AA278319 Hs.44251	Hs.194625	intermediate polypeptide 2 Homo sapiens mRNA for	DNCLI2	654.7416	-1.1197666
GF203	725629	AA29372	AA293728 Hs.125134	Hs.125134	KIAA1172 protein, partial cds adenovirus 5 E1A binding		654.6378	-1.8210872
GF201	971382	AA68305	AA683058 Hs.108547	Hs.3238	protein hyaluronan-mediated motility	BS69	654.5424	
GF200	128947	R10284	Hs.72550	Hs.72550	receptor (RHAMM)	HMMR	654.3623	1.05038376

-1.3817954	-1.4193827	1.96365885	-1.4138811	-1.1334265	1,29833854		-2.246686					-1.4332236					1.21644534	-1.9566277	-1.8428777
654.1938	654.1669 654.079 653.6407	653.4984 653.3738	653.3539	653.3148	653.2147	653.1788	653.1674	653.1279		653.0643	653 0352	652.9867		652.9446	652.8386		652.5309	652.4718 652.4453	652.4271 652.4197
	CREME9	RPL7A	LOC54104	ZNF143							ARPP-19				FXR2		GFER	втғз	PTPRB
ESTs, Weakly similar to KIAA1006 protein [H.sapiens] cytokine receptor-like	molecule 9 ESTs BB1	ribosomal protein L7a EST	hypothetical protein zinc finger protein 143 (clone	pHZ-1)	EST FSTs Weakly similar to	unknown [H.sapiens]	EST	ESTs	Homo sapiens mRNA for	KIAA1342 protein, partial cds	eyene Anna prosprioprocent, to	ESTs	ESTs, Weakly similar to ZINC FINGER PROTEIN 33A	[H.sapiens] fracile X mental retardation.	autosomal homolog 2	growth factor, erv1 (S. cerevisiae)-like (augmenter of	liver regeneration)	basic transcription factor 3 ESTs	protein tyrosine phosphatase, receptor type, beta polypeptide PTPRB ESTs
Hs.99291	Hs.7120 Hs.88373 Hs.78768	Hs.99858 Hs.117063	Hs.12871	Hs.154095	Hs.121260	Hs.238756	Hs.25067	Hs.34782		Hs.8059	He 7951	Hs.153958		Hs.58338	Hs.52788		Hs.27184	Hs.101025 Hs.93764	Hs.123641 Hs.188965
AA452801 Hs.99291	AA215643 Hs.16181 AA863050 Hs.88373 AA453593 Hs.7735	R00595 Hs.18907 AA677528 Hs.117063	H05934 Hs.12871	AA443659 Hs.89430	AA757932 Hs.121260	AA774478 Hs.111136	R49116 Hs.25067	AA130042 Hs.34782		H23524 Hs.31988	A A O 46500 Lic 7051	N45313 Hs.46507		W73793 Hs.58338	R25403 Hs.113329		AA465021 Hs.27184	AA609731 Hs.110538 AA016234 Hs.93764	Al022531 Hs.123641 AA676865 Hs.16811
788524	683721 1455524 795216	123441	43461	783836	396252	399240	38803	503851		51799	407444	283312		344135	133179		810063	1031903 359285	1650998 460143
GF203	GF203 GF204 GF201	GF200	GF202	GF200	GF203	GF204	GF203	GF201		GF201	1000	GF202	<u> </u>	GF201	GF204		GF200	GF202 GF201	GF204 GF203

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	-1.0092068	-1 4067577	10.000	-2.2584437				1.2803759			-1.8366779							1.38561629					-1.0147005
652.2979	652.2685	651 9064	1000:100	651.788			651.7004	651.5219	651.5073	651.459	651.2803		651.2802	651.1172		651.0311	650.9458	650.8018	650.7126	650.7048		650.6924	620.6669
		A D D C A	† 1	, АТF5				KIAA0828		SSI-1	KIAA0781					FZD1	TNF		KIAA1311			ALDH1	ITSN1
ESTs, Moderately similar to rhotekin [M.musculus] Homo sapiens mRNA; cDNA	DKFZp4340119)	actin related protein 2/3	complex, subum 4 (20 ND)	activating transcription factor 5 ATF5 Human DNA sequence from clone RP4-676J13 on chromosome 6q14. Contains	the 3' end of the gene for flavohemoprotein b5+b5R	cytochrome b-type NAD(P)H oxidoreductase, ESTs, STSs	and GSSs	KIAA0828 protein	ESTs	JAK binding protein	KIAA0781 protein	Homo sapiens clone 23700	mRNA sequence	ESTs	frizzled (Drosophila) homolog	1 ************************************	cinerfamily member 2)	ESTs	KIAA1311 protein	ESTs	aldehyde dehydrogenase 1,	soluble intersectin 1 (SH3 domain	protein)
Hs.58215	Hs.22051	00000	HS. 148570	Hs.9754			Hs.5741	Hs.4984	Hs.116135	Hs.50640	Hs.42676		Hs.66187	Hs.17697		Hs.94234	He 2/1570	Hs.124979	Hs.61441	Hs.5241		Hs.76392	Hs.66392
R85466 Hs.107770	AA191336 Hs.22166	000000000000000000000000000000000000000	AA865878 HS.104730	T90841 Hs.90997			4A400321 Hs.5741	199883 Hs.4984	AA626236 Hs.116135	AA485355 Hs.104474	190161 Hs.64592		R41730 Hs.66187	T95862 Hs.17697		N70776 Hs.94234	A A 6 9 0 6 9 7 7	138425 Hs.124979	AA131769 Hs.61441	AA682392 Hs.5241		AA664101 Hs.76392	AA496795 Hs.66392
180018 F	627272		1456962	112371			743367	Ξ	745512 /	811006 /	240914 H		31818 F	120423		298134	700377			461770		855624 /	897652
GF204	GF202	L	GF203	GF200			GF201	GF203	GF204	GF201	GF200		GF201	GF204		GF201	70000	GF203	GF201	GF204		GF201	GF200

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1.36704325	-1.5408897	-1.4375362	-1.1808296 1.55912941 -1.2917054	-2.3168155	-1.0180939	-1.3885892 1.00225845	-1.2344987	1.03179194	-1.096215 1.3131255	1.15480029
650.54 650.5194	650.5096 650.4289	650.3394 650.3027	650.2564 650.235 650.0881 649.7087	649.7056 649.566	649.539	649.4434 649.4299	649.3717	649.0075	648.9281 648.9176	648.816
SAG			DKFZP5641052	KIAA0411 PTTG1				KIAA0419	D8S2298E	CORO2B
S-antigen; retina and pineal gland (arrestin) ESTs ESTs Moderately similar to PETINOPA ASTOMAL! IKF	FROTEIN 1 [H.sapiens] EST ESTS, Highly similar to NADP-DEPENDENT LEUKOTRIENE B412-		DKFZP5641052 protein EST ESTs ESTs	411 gene product ry tumor-transforming 1 Moderately similar to r to protocadherin-3	[H.sapiens]	ESTs, Weakly similar to KIAA0940 protein [H.sapiens] ESTs	09510	product one 25085	mRNA sequence reproduction 8 coronin, actin-binding protein.	28
Hs.32721 Hs.169927	Hs.269217 Hs.125450	Hs.114670 Hs.121776	Hs.5364 Hs.210105 Hs.86071 Hs.126123	Hs.7977 Hs.252587	Hs.266470	Hs.106292 Hs.179864	Hs.107213 Hs.271639	Hs.236828	Hs.9167 Hs.153678	Hs.24907
AA057232 Hs.32721 R20628 Hs.21373	H85528 Hs.83815 AA883353 Hs.125450	N76331 Hs.114670 AA883375 Hs.121776	AA452831 Hs.5364 V70203 Hs.49805 AA443846 Hs.86071 AA905833 Hs.126123	AA598665 Hs.7977 AA430032 Hs.7487	W72881 Hs.58254	R56234 Hs.106292 AA701444 Hs.117145	AA481403 Hs.107213 N95076 Hs.107861	્ય	W69271 Hs.36181 AA465570 Hs.82076	N92783 Hs.24907
381287 A. 26297 R.	221928 Hi 1460257 A		788555 A 296468 N 784100 A 1505279 A		345262 W	40965 Ri 435055 A	~ _	•	343760 W 814214 A	303199 N
GF200 GF204	GF203 GF204	GF200 GF204	GF203 GF202 GF202 GF204	GF202 GF201	GF202	GF202 GF203	GF203 GF201	GF202	GF203 GF200	GF203

-1.7379099	-1.1214081	1.41031894	-1.3608398	-1.2860501	-1.0311514 -1.1047138 -1.8243364 1.05630802	-1.2176855	2.04707317	1.40836534 -1.2789037 -1.1249379
648.8101	648.7747 648.5408	648.5048 648.4796	648.47 648.4213	648.2416 648.2164 648.135 648.1292 648.0966	648.0891 647.9679 647.7487 647.5447	647.4966	647.4584	647.2595 647.243 647.0637 646.9901
		FBW3	HCLS1	BMI1 DKFZp762K0911 LOC51316	KIAA0029	ASCL1 ASCL1	PRRG1	LOC51240
ESTs ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING FNTRY !!!!	[H.sapiens] ESTs FSTs. Weakly similar to MAD	PROTEIN [H.sapiens] F-box protein Fbw3	substrate 1 ESTs murino laukemia viral (hmi-1)	oncogene homolog hypothetical protein hypothetical protein ESTs	KIAA0029 protein ESTs ESTs ESTs	Corsophila) homolog-like 1 achaete-scute complex (Drosophila) homolog-like 1 profiles-rich Glad (G-like	polypeptidamine acid, polypeptida ESTs, Weakly similar to hypothetical protein [H.sapiens]	ESTs hypothetical protein ESTs ESTs
Hs.46693	Hs.192915 Hs.103218	Hs.42053 Hs.24307	Hs.14601 Hs.124636	Hs.431 Hs.5807 Hs.107139 Hs.271711 Hs.44166	Hs.268053 Hs.278383 Hs.57637 Hs.19569	Hs.1619 Hs.1619	Hs.40637 Hs.72318	Hs.182980 Hs.7870 Hs.118002 Hs.23368
N48590 Hs.46693	AA460366 Hs.99201 AA678094 Hs.103218	H95253 Hs.42053 AA463476 Hs.24307	AA424575 Hs.14601 AA857110 Hs.124636	AA608856 Hs.123994 AA775157 Hs.125175 AA150263 Hs.107139 H90907 Hs.114196 W94009 Hs.44166	0	AA441935 Hs.96944 AA441935 Hs.1619	N30161 Hs.40637 AA159900 Hs.72318	AA283609 Hs. 88503 AA437132 Hs. 7870 AA682863 Hs. 118002 H70815 Hs. 23368
279278	796084 430715	234348 811803	767183 1434924	1048586 868736 491644 240990 357531	825271 50175 206341 124822	774082	268188	713347 757384 450402 214077
GF202	GF202 GF204	GF204 GF203	GF200 GF204	GF202 GF204 GF201 GF201	GF202 GF202 GF203 GF203	GF200 GF200	GF201 GF202	GF203 GF204 GF203 GF200

	1.27382495	1.09603306				1.10049564	-2.7506934		-1.3348961						-1.3152417		1.31713759		1.0446905	
646.7552 646.7379	646.6808	646.5784 646.5309	646.4897	646.333		646.3168	646.2078	646.1827	646.1743		646.1136		645.9653		645.935		645.9196	645.7393	645./3/3	645.5272
H2AFL		PER3		FCGR2B					KIAA0475		NDUFB9		DYRK2				SRPR	PHAP1		
H2A histone family, member L H2AFL ESTs ESTs, Weakly similar to predicted using Genefinder	[C.elegans]	period (Drosophila) homolog 3 PER3 ESTs	ESTs	Fc fragment of IgG, low affinity IIb, receptor for (CD32)	chromosome 1 specific	transcript KIAA0493	ESTs	ESTs	KIAA0475 gene product	NADH dehydrogenase (ubiquinone) 1 beta	subcomplex, 9 (22kD, B22)	dual-specificity tyrosine-(Y)-	kinase 2	ESTS, Weakly similar to !!!! ALU SUBFAMILY SQ	WARNING ENTRY IIII	signal recognition particle	receptor ('docking protein') putative human HLA class II	associated protein I	ESTS	ESIS
Hs.28777 Hs.6845	Hs.64783	Hs.12592 Hs.59332	Hs.165335	Hs.278443		Hs.251108	Hs.85944	Hs.172971	Hs.5737		Hs.15977		Hs.173135		Hs 227505		Hs.75730	Hs.179902	Hs.5997	Hs.191198
N50797 Hs.37641 AA496030 Hs.6845	AA702104 Hs.64783	AA447743 Hs.43548 W90735 Hs.59332	AA453485 Hs.97885	106 Hs.119428		R34603 Hs.24822	0	N46849 Hs.42403	AA419200 Hs.5737		Al025126 Hs.15977		429 Hs.26236		200 Hs 16547		AA598621 Hs.75730	AA496539 Hs.54476	7	R05945 Hs.119631
283919 N50797 759184 AA49603	384257 AA70	813639 AA4 418248 W90	795358 AA4	138369 R68106		136557 R34(1631762 Al02		50884 H18429		118049 T92200		898242 AA5			124948 R05
GF201 GF204	GF203	GF203 GF202	GF201	GF201		GF200	GF203	GF201	GF203		GF204	i	GF204		GESUS	5	GF200	GF201	GF202	GF204

-1.1083207	1.43638132	1.08954993	-2.6484316 1.33088837 1.01593112	-1.1319361	-1.6253903 -1.6314503 -1.133593	-1.0156171	-1.01561/1 -1.1565564 -1.5013597	1.13898873
645.4764	645.3955	645.3249 644.892	644.5715 644.496 644.4876	644.4743 644.4531	644,4148 644,3702 644,3584 644,2765 643,8503		643.8062 643.696 643.6744 643.2506 643.249	643.2401 643.2108
TFG		PSCD2 KIAA0537		KIAA1311	РАРРА DKFZP434B0923	MSF	MSF NN8-4AG	
TRK-fused gene (NOTE: non- standard symbol and name) Homo sapiers mRNA; cDNA	DKFZp38611524 (from clone) DKFZp58611524) pleckstrin homology, Sec7 and collection domains 2	t	NT2RP4002071 EST ESTs	Homo sapiens cDNA FLJ20425 fis, clone KAT02707 KIAA1311 protein pregnancy-associated plasma	protein A hypothetical protein ESTs ESTs	megakaryocyte stimulating actor megakaryocyte stimulating	actor retinoic acid responsive EST ESTs	ESTs, Weakly similar to KIAA0591 protein [H.sapiens] ESTs
Hs.250897	Hs.274368 I	Hs.200598 H	Hs.17283 Hs.124705 Hs.102367	Hs.71040 Hs.61441	Hs.75874 Hs.97266 Hs.98306 Hs.260930 Hs.167708		Hs.218791 Hs.54413 Hs.48584 Hs.235534 Hs.168955	Hs.132756 Hs.269139
Hs.118891	Hs.119516	Hs.8517 Hs.12836	AA194019 Hs.29216 H66442 Hs.38508 AA180237 Hs.102367	Hs.66954 Hs.62917	Hs. 79712 Hs. 97266 Hs. 98306 Hs. 48694 Hs. 93953	AA280514 Hs.100096	AA280514 Hs.80749 AA334704 Hs.54413 NG2618 Hs.48584 R36212 Hs.70203 AA868028 Hs.126093	Hs.103182 Hs.49964
R60846	W81562	AA465031 Hs.8517 AA774839 Hs.12836	AA194019 Hs.29216 H66442 Hs.38508 AA180237 Hs.10236	AA063624 Hs.66954 AA046116 Hs.62917	W84789 Hs.79712 AA704401 Hs.97266 AA418743 Hs.98306 N63032 Hs.48694 N48050 Hs.93953	AA280514	AA280514 Hs.80749 AA934704 Hs.54413 N62618 Hs.48584 R36212 Hs.70203 AA868028 Hs.12609	W86466 W01511
42076	347687	810092 970743	665668 229651 611481	366009 376664	415828 450962 767843 278874 281659	712641	712641 1572526 288892 136855 1461158	416611 294445
GF200	GF200	GF200 GF204	GF202 GF200 GF202	GF201 GF202	GF201 GF203 GF203 GF201 GF202	GF200	GF200 GF204 GF202 GF200 GF200	GF201 GF200

ESTs, Moderately similar to

					ARL-6 interacting protein-6			
GF202	877634	AA488176 Hs.24650	Hs.24650	Hs.24650	[M.musculus]		643.1218	1.76057173
GF204	745351	AA625667 Hs.22612	Hs.22612	Hs.22612	ESTS, Wearly Silling to NT- REN-25 antigen [H.sapiens] Homo sapiens mRNA for		643.1105	
GF200	294133	1 66266N	Hs.7742	Hs.161700	KIAA1133 protein, partial cds tumor rejection antigen (gp96)		643.0325	1.45441071
GF204	26519	R20669	Hs.56785	Hs.82689	1	TRA1	643.0262	
GF202	128131		Hs.20417	Hs.140576	ESTs		643.0038	-1.4631622
GF200	740476	AA478043 Hs.80645	Hs.80645	Hs.80645	interferon regulatory factor 1	IRF1	642.9299	1.01644456
GF204	1292588	AA719056 Hs.97647	Hs.97647	Hs.97647	ESTs		642.8406	
					ESTs, Highly similar to HKL1			
GF202	1070015	AA599717 Hs.107823	Hs.107823	Hs.107823	[H.sapiens]		642.7672	-1.2247251
GF204	1292070	AA707536 Hs.121732	Hs.121732	Hs.189013	ESTs		642.7361	
					Homo sapiens cDNA			,
					FLJ10697 fis, clone			
					NT2RP3000527, weakly			
					similar to ZINC FINGER			
GF201	51255	H18646 Hs.31586	Hs.31586	Hs.104557	PROTEIN 43		642.7084	
GF203	487499	AA045115 Hs.24758	Hs.24758	Hs.24758	ESTs		642.6954	-2.2796234
GF204	434877	AA701249 Hs.124213	Hs.124213	Hs.271511	ESTs		642.6346	
					O-6-methylguanine-DNA			
GF204	1588791	AA978354 Hs.1384	Hs.1384	Hs.1384	methyltransferase	MGMT	642.5175	
GF200	843426	AA489498 Hs.103102	Hs.103102	Hs.171501	ubiquitin specific protease 11	USP11	642.373	-1.3690498
GF200	843426	AA489498 Hs.7832	Hs.7832	Hs.171501	ubiquitin specific protease 11	USP11	642.373	-1.3690498
					TATA box binding protein (TBP)-associated factor, RNA			
GF200	252185	H87496	Hs.62444	Hs.153022	polymerase I, C, 110kD	TAF1C	642.1797	-1.1602976
					Homo sapiens mRNA; cDNA DKFZp564P013 (from clone			
GF204	1609748	AA991579 Hs.97263	Hs.97263	Hs.278231	DKFZp564P013)		642.1343	
					Homo sapiens cDNA FLJ20259 fis, clone			
GF201	73188	T57196	Hs.9956	Hs.9956	COLF7443		642.1128	

		-1.0144397	1.01390266	-1.6452573					-1.097916		-1.097916		-1.4854445			-1.6205861									-1.4587679				-1.6790168		1 2002001	1.605657.1-	-1.06/3035		-1.3520446
	641.9073	641.8105	641.6155	641.5786	641.486		641.4286		641.3113		641.3113	641.2111	641.1902			641.1502	641.1304				641.1047		641.0667	641.0641	640.865			640.6619	640.3691		000000000	040.2020	640.2743	640.1956	640.1903
			KIAA0104				AKAP3		GPD1		GPD1	CTSG											COPEB	DKFZP56611024					ARL2						CLCN3
Homo sapiens clone LCHN	mRNA sequence	ESTs	KIAA0104 gene product	ESTs	ESTs	A kinase (PRKA) anchor	protein 3	glycerol-3-phosphate	dehydrogenase 1 (soluble)	glycerol-3-phosphate	dehydrogenase 1 (soluble)	cathepsin G	ESTs	ESTs, Weakly similar to	ACTIN, CYTOPLASMIC 2	[H.sapiens]	ESTs	ESTs, Weakly similar to	TERATOCARCINOMA-	DERIVED GROWTH	FACTOR 1 [H.sapiens]	core promoter element binding	protein	DKFZP566I1024 protein	EST	Homo sapiens mRNA; cDNA	DKFZp434C2016 (from clone			ESTs, Weakly similar to Kelch	mour containing protein	[H.Sapleris]	ESTs	ESTs	chloride channel 3
	Hs.12461	Hs.100960	Hs.75574	Hs.130518	Hs.35089		Hs.98397		Hs.25478		Hs.25478	Hs.100764	Hs.183974			Hs.98764	Hs.121729				Hs.127179		Hs.4055	Hs.78605	Hs.46575			Hs.17110	Hs.154162		0000	HS.3826	Hs.240934	Hs.271773	Hs.174139
	AA029331 Hs.16412	N51577 Hs.100960	AA521243 Hs.75574	AA609199 Hs.112661	N50845 Hs.35089		AA626349 Hs.98397		AA192547 Hs.99897		AA192547 Hs.119601	W92603 Hs.110186	AA005358 Hs.60115			AA431801 Hs.98764	AA779788 Hs.121729				AA962534 Hs.127179		5	N46240 Hs.102610	N46007 Hs.46575			R38943 Hs.13546	AA700172 Hs.8967			ž		W95051 Hs.16324	AA461332 Hs.87195
	366763	280444	827144	1031448	280954		745086		628418		628418	357681	429202			782559	1034547				1602193		360436	279091	277679			24958	452780			565849	220394	415281	796341
	GF201	GF203	GF200	GF202	GF201		GF204		GF200		GF200	GF201	GF202			GF202	GF204				GF204		GF201	GF201	GF202			GF204	GF203		0	GF202	GF203	GF201	GF200

-1.2707641	1.45043923	-1.2745597	-1.0865967 1.03514953 -1.3254446	-1.2940303	-1.3007013	-1.0423617	-1.0423617	-1.0471344	-2.0120035	-1.5726599	-1.3283618	:	1.04544913			1.18161064	-1.5222756	-1.2215815
640.0768	639.9932 639.6474	639.6273	639.6003 639.5764 639.4581	639.4514 639.4264	639,3568	639.3339	639.3339	639.2936	639.1828	639.0491	638.6692	638.6446	638.5332		638.5137	638.3811	638.3414	638.3401
LIMS1			RAB7 KIAA0864	WARS		MAC30	MAC30						KIAA0947					
LIM and senescent cell antigen-like domains 1 Homo sapiens mRNA; cDNA	DKFZp761G151); partial cds ESTs	ESTs, Weakly similar to c-type lectin DCL1 [M.musculus]	oncogene family KIAA0864 protein ESTs	tryptophanyl-tRNA synthetase WARS ESTs Homo sapiens cDNA FI.11004 fis clone	HEMBA1000076	hypothetical protein	hypothetical protein	ESTs	ESTs	EST	ESTs	ESTs	KIAA0947 protein	DKFZp564D0472 (from clone	DKFZp564D0472)	EST	ESTs	ESTs
Hs.112378	Hs.35453 Hs.41407	Hs.267006	Hs.237955 Hs.84883 Hs.143495	Hs.82030 Hs.98685	Hs 43946	Hs.199695	Hs.199695	Hs.10338	Hs.57876	Hs.60389	Hs.190555	Hs.17244	Hs.5070		Hs.208414	Hs.71601	Hs.178603	Hs.42732
AA504265 Hs.83987	T96924 Hs.17925 H90477 Hs.41407	N26083 Hs.108994	AA496780 Hs.99794 AA489609 Hs.84883 AA020000 Hs.78221	AA664040 Hs.82030 AA432144 Hs.98685	W31717 Hs 111742		_	6	W67536 Hs.57876	AA010383 Hs.60389	AA703553 Hs.128968	AA005290 Hs.17244	AA149527 Hs.5070		AA878558 Hs.125391	AA137180 Hs.71601	AA007344 Hs.43949	H99774 Hs.42732
825416	121136 241475	268979	897626 897563 363575	855786 781489	320794	292388	292388	773573	343174	430255	450233	428824	588368		1492404	502744	429263	263839
GF203	GF201 GF200	GF202	GF200 GF200 GF200	GF201 GF202	GESUS	GF200	GF200	GF202	GF202	GF202	GF203	GF201	GF202		GF204	GF202	GF202	GF202

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-2.1573937		1.0567608	1.01450347	-1.1359758		-1.2193784	-1.2639306	
638.323	638.2728	638.1975	638.1342	638.1117	638.0007	637.699 637.6951	637.669	637.5548
			PIP5K1B		TIF1GAMMA	ADAM9 DKFZP586G1517	CRHR1	
ESTs, Weakly similar to Weak similarly with non-histone chromosomal protein HMG-1 (C.elegans) Human DiNk sequence from chromosoma 2241.33 -13.33 contains the MAPK12 gene from incigen activated protein kinase 12 (SAPKs), the MAPK12 gene from fingen activated protein kinase 12 (SAPKs), the MAPK12 gene for mitogen activated protein kinase 12 (SAPKs), the MAPK11 gene for mitogen activated protein kinase 12 (SAPKs), the	(PRKM11), gene KIAA0315, the gene for a novel protein s	chain 3 mRNA, complete cds phosphatidylinositol-4-	House Sahilase, 1950 I., beta Homo sapiens mRNA; cDNA	DKFZp564K0222) transcriptional intermediary	factor 1 gamma a disintegrin and metalloproteinase domain 9	(meltrin gamma) DKFZP586G1517 protein	Control of the Property of the Ports of the	[H.sapiens]
Hs.10487	Hs.26593	Hs.158295	Hs.78406	Hs.6375	Hs.168005	Hs.2442 Hs.44155	Hs.79117 Hs.165077	Hs.113613
Hs.10487	AA485381 Hs.26593	AA196486 Hs.85849	Hs.49742	Hs.14079	AA001635 Hs.125057	Hs.2442 Hs.100383	Hs.79117 Hs.37579	Hs.117470
N72879	AA485381	AA196486	N69781	N67366	AA001635	H59231 H80063	H07088 H58702	R43553
291539	811025	628336	287411	286503	428109	204257 249070	44692 206288	32794
GF202	GF201	GF200	GF202	GF202	GF204	GF201 GF203	GF200 GF203	GF204

1.09553785 1.10109988 1.00739961 -1.1582801	-1.086745 -1.3624949 -1.5603271 -1.774632		-1.4175953 -1.0669724
637.5018 637.4495 637.4465 637.2871 637.2205 637.2073	637.0663 637.0069 636.9308 636.7311	636.6878 636.4554	636.3128 636.2289 636.0641 635.7626 635.5977
DCX PLOD3	PSIME3	CLTA	WASPIP
doublecortex; lissencephaly, X- linked (doublecortin) ESTs procollagen-lysine, 2- oxoglutarate 5-dioxygenase 3 1 ESTs ESTs ESTS ESTS	Homo sapiens cDNA FLJ20434 fis, clone KAT03803 ESTs Froteasome (prosome, macropaln) activator subunit 3 (PA28 gamma; Ki)	clathrin, light polypeptide (Lca) CLTA ESTs	Human DNA sequence from 12645 on chromosome 1268.21-36.33. Contains three novel genes (ore with DnaJ domains), the gene for KIAAG469 and the HKR3 gene for GLI-Kruppel family member for GLI-Kruppel family member HKR3. Contains ESTs, STSs, GSSs, three Cybb islands, genomic marker D wiskotit-Aldrich syndrome protein interacting protein EST ESTS
Hs.34780 Hs.32250 Hs.153357 Hs.96499 Hs.44940 Hs.31302	Hs.33020 Hs.94229 Hs.152978 Hs.152978	Hs.104143 Hs.18963	Hs.26938 Hs.128695 Hs.112863 Hs.275702 Hs.120346
AA676864 Hs.34780 N30152 Hs.32250 AA905976 Hs.128784 AA525337 Hs.96499 N39092 Hs.44940 H15050 Hs.31302	N31946 Hs.33020 N70072 Hs.94229 AA486324 Hs.85054 T96913 Hs.91145	AA055475 Hs.28799 AA705374 Hs.18963	AAB57119 Hs.26938 AA459654 Hs.95123 AA620460 Hs.112863 AA776778 Hs.120346
896968 268157 1505469 685081 276512 48363	272034 297919 840517 121409	377545 462116	1434923 795544 951102 417920 1276651
GF203 GF201 GF204 GF203 GF202 GF202	GF203 GF200 GF200 GF202	GF204 GF204	GF204 GF202 GF202 GF202 GF204

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	-1.1027287 -1.2473301	-1.0166118	-1.0166118	1.00685653				-1.1526773		-1.2065739				1.14280356						-1.2793937				1.07527488	1.20971722		-1.0331992	1.03000164		-1.3743852	
	635.5656 635.5435	635.3598	635.3598	635.2941		1	635.0757	634.9376	634.9049	634.7985				634.6791	634.5377					634.3692		634.3533		634.3475	634.2773	634.2371	634.0396	633.9366	633.9348	633.9093	
	LOC51690 SEC13L1	GPD1	GPD1	WDR5			I GM3	UROD		TK1												SAE1		BICD1	LOC51632	DKFZP586G1624			KPNB2		
U6 snRNA-associated Sm-like	protein LSm7 SEC13 (S. cerevisiae)-like 1	glycerol-3-phosphate dehydrogenase 1 (soluble)	glycerol-3-phosphate dehydrogenase 1 (soluble)	WD repeat domain 5	transglutaminase 3 (E	polypeptide, protein-glutamine-	gamma-glutamyltransterase) uroporphyrinogen	decarboxylase	ESTs	thymidine kinase 1, soluble	ESTs, Highly similar to	phosphatidylserine-specific	phospholipase A1 deltaC	[H.sapiens]	ESTs	Homo sapiens cDNA	FLJ11344 fis, clone	PLACE1010870, moderately	similar to ZINC FINGER	PROTEIN 91	SUMO-1 activating enzyme	subunit 1	Bicaudal D (Drosophila)	homolog 1	CGI-76 protein	DKFZP586G1624 protein	EST	ESTs	karyopherin (importin) beta 2	ESTs	
	Hs.70830 Hs.227949	Hs.25478	Hs.25478	Hs.13889			Hs.2022	Hs.78601	Hs.109851	Hs.105097				Hs.226675	Hs.58092					Hs.30503		Hs.250747		Hs.164975	Hs.184325	Hs.125262	Hs.47108	Hs.104106	Hs.168075	Hs.85629	
	AA402875 Hs.70830 AA496784 Hs.104111	AA192547 Hs.99897	AA192547 Hs.119601	AA421266 Hs.13889			N90882 Hs.82139	4A424441 Hs.78601	AA434409 Hs.55574	AA778098 Hs.105097					W70282 Hs.58092					AA400229 Hs.30503		AA620917 Hs.65973		4A504478 Hs.24912	701340 Hs.25480	AA916726 Hs.126757	V50733 Hs.47108	4A195651 Hs.104106	W32511 Hs.100348	AA188785 Hs.85629	
	741842 <i>H</i> 897636 <i>H</i>	628418	628418	-			301735 N	760148						_	344837					743224 F		1055607 /		825325 /	124116 F	1473682 /	283703 N	665148 /	321492	626199	
	GF203 GF200	GF200	GF200	GF202			GF201	GF200	GF201	GF203				GF200	GF201					GF202		GF204		GF203	GF200	GF204	GF202	GF203	GF201	GF202	

					DG8GYY88 DYDHD1			
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GF201	882548	AA676484 Hs.74451	51 Hs.74451	1451	calpain, small polypeptide	CAPN4	633.8997	
GF200	233071	H75632 Hs.91468		Hs.160417	transmembrane protein 2 killer cell lectin-like recentor	TMEM2	633.7969	-1.3228059
GF201	415086	W93370 Hs.282		Hs.258850	subfamily C, member 3	KLRC3	633.6768	
				!	ESTs, Weakly similar to		070000	4700054
GF203	199505	R97503 Hs.30443 AA418388 Hs 75844		Hs.30443 Hs.75844	KIAAU/9/ protein [H.sapiens] ESTs		633.5701	1.17315739
202 10	200	2000		-	splicing factor 3b, subunit 2,			
GF201	857661	AA633757 Hs.75916		Hs.75916	145kD	SF3B2	633.4225	100001
GF202	783959	AA447383 Hs.58248		Hs.58248	ESIS		633.4136	-1.3303784
GF200	783645	AA46565 Hs.89905		Hs.180789	mRNA, 3' end of cds		633.3131	1.33840004
GF202	731284	AA416692 Hs.98266		Hs.191597	ESTs		633.253	-1.398258
GF202	364896	AA024494 Hs.61199		Hs.61199	ESTs		633.1997	-1.3172133
GF202	301842	N91175 Hs.109653	- 8	4s.109653	ESTs		633.0914	-1.2568573
					ESTs, Highly similar to elastic			
GF204	23119	R38653 Hs.100877		Hs.100877	titin [H.sapiens] mucosal vascular addressin		632.9839	
GF201	859807	AA668527 Hs.102598		Hs.102598	cell adhesion molecule 1	MADCAM1	632.9821	
GF201	771023	AA427978 Hs.17419		Hs.268636	ESTs		632.9572	
GF202	288675	N62401 Hs.48531		Hs.48531	EST		632.8915	1.1480168
					ESTs, Weakly similar to transformation-related protein			
GF202	484701	AA037619 Hs.109731		Hs.109731	[H.sapiens]		632.8862	-1.2781301
					polymerase (RNA) II (DNA directed) polypeptide I			
GF203	378502	AA777192 Hs.47062		Hs.47062	(14.5kD)	POLR2I	632.8516	-1.3525534
GF202	949967	AA600207 Hs.8045		045	ESTs		632.8415	-1.3275664
GF202	279577	N48899 Hs.46551		Hs.46551	EST		632.6364	-1.101516
GF204	743859	AA634436 Hs.115185	_	4s.115185	ESTs		632.5977	
GF204	41332	_		Hs.26608	ESTs		632.4988	
GF201	47626	H11325 Hs.21659	_	4s.21659	ESTs		632.3985	

1.52254165	-1.0322044			1.2829659 -1.5288926			-1.3047939	1.13271746			1.15443807
632.2578 632.2084	632.1649 632.0146	631.9974	631.8692	631.7233 631.6819 631.6102	631.5764	631.3657	631.3239 631.2775	631.2682	631.1423	630.9879	630.7617
	SRM160	SPOCK		MYL5		PDXK	BUB1B	DKFZP586I1023	POLG2		STAT1
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.saplens] ESTs ESTs ESTRandard nuclear matrix protein (olenty of prolinos 101-	like) ESTs sparc(osteonectin, cwcv and kazal-like domains	can) Similar to !!!! SX	[H.sapiens] myosin, light polypeptide 5,	regulatory ESTs	ESTs pyridoxal (pyridoxine, vitamin	B6) kinase budding uninhibited by benzimidazoles 1 (yeast	homolog), beta ESTs	DKFZP58611023 protein polymerase (DNA directed),	gamma 2, accessory subunit ESTs, Moderately similar to hypothetical protein	[H.sapiens]	signal transducer and activator of transcription 1, 91kD
Hs.110187 Hs.116140	Hs.18192 Hs.17661	Hs.93029	Hs.262847	Hs.170482 Hs.22579	Hs.120858	Hs.38041	Hs.36708 Hs.26563	Hs.111515	Hs.30541	Hs.131768	Hs.21486
AA639719 Hs.110187 AA626254 Hs.116140	AA976063 Hs.18192 AA707325 Hs.17661	AA699317 Hs.93029	W04713 Hs.54805	AA464121 Hs.73939 R51836 Hs.22579	AA707615 Hs.120858	AA158035 Hs.38041	AA488324 Hs.36708 R56880 Hs.26563		Al023804 Hs.30541	1031717 AA609584 Hs.131768	AA486367 Hs.21486
433300	1558411 451489	433666	320455	810671 39147	1292121	590640	842968	180902	1642634	1031717	840691
GF203 GF204	GF204 GF203	GF201	GF201	GF200 GF203	GF204	GF201	GF202 GF204	GF200	GF204	GF204	GF200

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GF202 GF200 GF204	283665 207107 1034738	N52930 H48677 AA780190	N52930 Hs.47579 H48677 Hs.117774 A4780190 Hs.50328	Hs.161465 Hs.128783 Hs.50328	ESTs ESTs ESTs Homo sapiens mRNA; cDNA DKF7n4341, 2015 (from clone		630.5898 630.5804 630.5788	-2.075189 -1.559573
GF201	758293	AA404239	AA404239 Hs.83349	Hs.14838	DKFZp434L2015); partial cds		630.4815	
GF200	727192	AA293819	4A293819 Hs.89713	Hs.172674	cells, cytoplasmic 3	NFATC3	630.4532	-1.3100501
GF201	382564	W0Z4U3 AA069372	W0Z4U3 HS.16139 AA069372 Hs.96028	HS.226414 Hs.96028	forkhead box D1	FOXD1	630.3751	000000000000000000000000000000000000000
GF204	145136	R77434	777434 Hs.29643	Hs.29643	ESTs		630.3704	
GF202 GF202	951108 795265	AA620466 AA454018	AA620466 Hs.67928 AA454018 Hs.99251	Hs.67928 Hs.99251	ESTs ESTs		630.3275 630.1774	-1.4673653 -1.6752055
GF202	1055137	AA621367	4A621367 Hs.119683	Hs.119683	ESTs		630.1514	-1.2186598
					Human mRNA for ornithine			
					decarboxylase antizyme, OHF		0,00	1000
GF200	841617	AA487681	4A487681 Hs.71303	Hs.125078	1 and ORF 2		630.1316	-1./03515/ -1.5692748
3	2000	4	10.00.61	100000	NADH dehydrogenase			
					(ubiquinone) flavoprotein 2			
GF203	1486260	AA922326	AA922326 Hs.51299	Hs.51299	(24KD)	NDUFV2	630.0582	-1.2487768
GF201	809951	AA454823	AA454823 Hs.26425	Hs.26425	ESTs		629.9897	
GF204	360547	AA015978	4A015978 Hs.104523	Hs.171937	ESTs		629.9618	
					ESTs, Weakly similar to ORF2			
GF204	155702	R72068	Hs.28813	Hs.28813	[M.musculus]		629.9563	
GF200	195487	R92163	Hs.47123	Hs.175979	ESTS		629.837	1.21444866
					Homo sapiens clone 2502/			
GF201	51344	H21040	Hs.6434	Hs.6434	mRNA sequence		629.8013	
					Human MHC class II HLA-DQ- heta mRNA (DB7 DQw2)			
GF204	1631863	A1004331	A1004331 Hs.73933	Hs.73933	complete cds		629.7717	
GF204	361082	AA017215	AA017215 Hs.60764	Hs.60764	ESTs		629.7216	
GF204	32776	R43522	Hs.11325	Hs.11325	ESTs		629.6826	
GF203	666451	AA232939		Hs.6763	KIAA0942 protein	KIAA0942	629.658	-1.8144663
GF203	209118	H63518	Hs.19977	Hs.19977	ESTs		629.6558	-1.2304623
GF204	1292505	AA719240	4A719240 Hs.120370	Hs.120370	ESTs		629.5665	

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-1.2251286			-2.0666194	1 244 4001		-1.4265494	2.06577291		1.0933488	1.22395546	-1.6361408			-1.0874069	1.05074758			1.20882438	-2.1922713
629.151	629.1085	628.9244	628.8698	628.7714	200 1320	628.7125	628.687		628.6409	628.563	628.3882		628.3365	628.2781	628.0613	627.8672		627.6849	627.6381 627.543
e PTPRB		ALOX12	SDHC		0		ACOX1			ARCF1			E2F5					N1	
protein tyrosine phosphatase, receptor type, beta polypeptide PTPRB ESTs, Moderately similar to unnamed HERV-H protein	[H.sapiens]	arachidonate 12-lipoxygenase ALOX12 succinate dehydrogenase	membrane protein, 15kD	ESTs	Novel human gene mapping to chomosome 13, similar to rat	RhoGAP	acyl-Coenzyme A oxidase	ESTs, Weakly similar to cleft lip and palate transmembrane	protein 1 [H.sapiens]	family F (OABP) member 1	ESTs	E2F transcription factor 5,	p130-binding	ESTs	EST	EST	LIV-1 protein, estrogen	regulated ESTs, Moderately similar to !!!! ALU SUBFAMILY J WABNING FNTRY !!!!	[H.sapiens] ESTs
Hs.123641	Hs.271896	Hs.1200	Hs.3577	Hs.82169	US.100040	Hs.13649	Hs.167835		Hs.11282	He 12013	Hs.112389		Hs.2331	Hs.10490	Hs.112731	Hs.21345		Hs.79136	Hs.16341 Hs.104792
Hs.10623	Hs.43951	Hs.1200	4A062805 Hs.3577	AA496937 Hs.82169	4,4463/14 TIS.103003	AA256386 Hs.13649	Hs.76493		AA480894 Hs.11282	He 12013			AA455521 Hs.2331	Hs.10490	AA609605 Hs.112731	Hs.21345		Hs.79136	AA917483 Hs.16341 AA417285 Hs.104792
H18633	N72852	T97276	AA0628	AA4969	AA465/	AA2563	H65659		AA4808	T70122	AA6096		AA4555	R69333	AA6096	R40945		H29407	
51041	291459	121454	366132	897511	840444	682045	210862		814584	80046	1031845		809828	142076	1031737	28474		52933	1533611 731140
GF200	GF201	GF201	GF202	GF204	GFZ0Z	GF202	GF200		GF203	CESOO	GF202		GF201	GF200	GF202	GF204		GF200	GF204 GF202

-1.7794693	-2.2512465	1.16442732 -1.3961227	-1.2012491		-1.2457972 1.58040529		-1.1348347	-1.1348347	-1.7612368		-1.9395444
626.1863 625.9922	625.9792	625.7895 625.7822	625.5565 625.5565	625.4855	625.0268 624.9222		624.8021	624.8021	624.7395	624.6545 624.4603 624.3522 624.3331	624.3322
adns	IGFBP3	KIAA0063		LOC51303	POLR2A KIAA1020		ST13	ST13	СНD3	AK1 KIAA0288	
sudD (suppressor of bimD6, Aspergillus nidulans) homolog ESTs	insulin-like growth factor binding protein 3 ESTs, Weakly similar to	unknown [D.melanogaster] KIAA0063 gene product	ESTs ESTs FK506 binding protein	precursor polymerase (RNA) II (DNA directed) polypeptide A	(220kD) KIAA1020 protein	suppression of tumorigenicity (13 (colon carcinoma)	interacting protein) suppression of tumorigenicity 13 (colon carcinoma) (Hsp70-	nteracting protein) chromodomain helicase DNA	binding protein 3 EST, Weakly similar to Zn- alpha2-glycoprotein	H.sapiens] adenylate kinase 1 nistone deacetylase A ESTs	ESTs, Moderately similar to KIAA0909 protein [H.sapiens]
st Hs.209061 A: Hs.33756 E	in Hs.77326 bi	-	Hs.102947 E Hs.31797 E FI	Hs.24048 pr	Hs.171880 (2 Hs 109445 K	. <i>o</i> , —	Hs.119222 in st	Hs.119222 in	Hs.25601 bi	Hs.228711 [F Hs.76240 at Hs.91400 hi Hs.103334 E	E Hs.91532 K
T54144 Hs.109901 AA677037 Hs.117025	AA598994 Hs.16275	4A460847 Hs.23038 T63072 Hs.3094	AA479063 Hs.102947 H49519 Hs.31797	7 Hs.24048	AA479052 Hs.90331 T69475 Hs.48329		s Hs.119222	S Hs.75971	AA778077 Hs.25601	AA677165 Hs.117039 W23690 Hs.81736 AA996024 Hs.91400 AA017213 Hs.103334	2 Hs.91532
	AA5989		-	N72137		3	H65676	H65676			H71092
69184	897727	796281 79229	754033 178860	291097	740130		210887	210887	379708	454317 327635 1606829 361069	211800
GF201 GF203	GF202	GF202 GF200	GF203 GF201	GF201	GF200	5	GF200	GF200	GF203	GF204 GF201 GF204 GF204	GF200

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		-1.4740061		-1.0781031	-1.1979341	1.63394231	1.14815077		-1.5728416	-1.47016				-1.0266484			-1.6723504	-1.2848552	-1.0785067	1.14359836		-2.1881152	-1 5130009	20000
	624.3098	624.1761	624.1106	624.0916	624.0571	623.8962	623.7751		623.7391	623.6718	623.4781		623.2935	623.2914		623.0425	622.986	622.9157	622.7994	622.7924		622.7275	622.5407	622.4507
										7														
e ≘ e s										OSR1													76P	
Human DNA sequence from clone 431H6 on chromosome 16. Contains a rovel gene with some homology to mouse HN1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains	ESTs and GSSs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs, Weakly similar to	unknown [H.sapiens]	oxidative-stress responsive 1	ESTs	ESTs, Highly similar to CGI-	121 protein [H.sapiens]	EST	Homo sapiens clone 23918	mRNA sequence	ESTs	ESTs	EST	ESTs	ESTs, Highly similar to CGI-	149 protein [H.sapiens] gamma tubulin ring complex	protein (76p gene)	ESTs
	Hs.172035	Hs.269284	Hs.58992	Hs.206219	Hs.18987	Hs.21955	Hs.6093		Hs.105189	Hs.95220	Hs.22510		Hs.26706	Hs.48374		Hs.108894	Hs.42975	Hs.134542	Hs.102728	Hs.120759		Hs.189658	Hs.20621	Hs.61241
	AA045658 Hs.100421	4A176688 Hs.29	4A700126 Hs.58992	452534 Hs.16072	4A236798 Hs.18987	Hs.21955	Hs.6093		4A489670 Hs.105189	Hs.117752	Hs.22510		AA009629 Hs.114742	Hs.48374		Hs.12411	Hs.42975	Hs.106459	Hs.102728	Hs.120759		AA232208 Hs.31260	AA464952 Hs.105064	AA025006 Hs.61241
	AA04565	AA17668	AA70012	H52534	AA23679	R42227	T59940		AA48967	R95128	R44082		AA00962	N59381		H29625	N21299	T95396	N62332	R93409		AA23220	AA46495	AA02500
	489208	280609	435808	202209	669379	29594	79431		824329	198690	33408		429784	290083		52974	265478	120516	287866	197102		666362	810082	365336
	GF201	GF202	GF204	GF200	GF203	GF203	GF203		GF203	GF202	GF201		GF204	GF202		GF201	GF202	GF200	GF202	GF202		GF202	GF201	GF201

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APPENDIX A Homo sapiens cDNA

1 09101077	1.02191077	-1.1/21012	1.15994341							1.27506309	-1.5638956		-1.0938012		-1.0329597							-1.3388281			-1.5381631	7	-1.192234		
0770 0440	022.0440	022.020	621.9152			621.9104	621.8599	621.8144	621.7659	621.2057	620.9014		620.6901		620.6851	620.663					620.562	620.5616	620.5513	620.4333	620.4045	620.2396	620.1953	620.039	
			CD53			PPP2R2B		FGL2		KIAA0310	DKFZP566E144				STAF50							COL4A5	NRP2		FXC1	IL13RA1	O O O	KIAA0304	
FLJ10842 fis, clone	NIZHP4001343	SIS	CD53 antigen	protein phosphatase 2	(formerly 2A), regulatory subunit B (PR 52), beta	isoform	ESTs	fibrinogen-like 2	ESTs	KIAA0310 gene product	DKFZP566E144 protein	Homo sapiens cDNA Fl. 110511 fis. clone	NT2RP2000656	stimulated trans-acting factor	(50 kDa)	ESTs	Homo sapiens cDNA	FLJ20797 fis, clone	COL00256, highly similar to	AF151824 Homo sapiens CGI-	66 protein mRNA collagen, type IV, alpha 5	(Alport syndrome)	neuropilin 2	ESIS	fracture callus 1 (rat) homolog FXC1	interleukin 13 receptor, alpha 1 IL13RA1	ESI	KIAA0304 gene product	
000000-11	HS.260238	HS.15548	Hs.82212			Hs.7688	Hs.61847	Hs.2659	Hs.125568	Hs.5716	Hs.7527		Hs.106768		Hs.68054	Hs.62713					Hs.6406	Hs.169825	Hs.17778	Hs.117802	Hs.54943	Hs.250911	Hs.113114	Hs.92236	
		H01425 HS.15548	AA132090 Hs.82212			H15677 Hs.101416	AA121313 Hs.61847	H56349 Hs.2659	AA884326 Hs.125568	AA454812 Hs.5716	H83283 Hs.37907		R26684 Hs.123112		AA083407 Hs.68054	AA136022 Hs.62713					AA459901 Hs.91879	AA029997 Hs.82578	_	R98962 Hs.117802	N27437 Hs.53057	H16589 Hs.117648	AA/008/1 Hs.113114	AA625915 Hs.92236	
,			504226			49303	490232	203732	1466904	809944	199175		132476		549146	502568					809422	470001		200868	268240			744980	
000	GF203	GF200	GF200			GF201	GF201	GF201	GF204	GF200	GF203		GF203		GF200	GF201					GF201	GF203	GF201	GF204	GF203	GF204	GF203	GF201	

-1.4281366	1.12983374 -1.4219193 -1.1780413	-1.1195055 -2.5023621				-2.1229097 1.04444483	1.11547698	1.36467613	1.36467613
620.0231 619.9754	619.8804 619.8427 619.8039 619.6775	619.6763 619.6725	619.6437	619.6417	619.6298	619.5923 619.4878	619.2233	619.1176	619.1176
SPP2	ОСВР		KCNN4	SNA11	HUNK	RFX5	SFRS7		
secreted phosphoprotein 2, 24kD ESTs Homo sanians clone 24665	∢ .	DKFZp434132) EST potassium intermediate/small conductance calcium-activated channel, subfamily N, member		_	normonally upregulated neu iumor-associated kinase H egulatory factor X, 5 (influences HLA class II	expression) R ESTs solicing factor, arginine/serine-		protein Homo sapiens mRNA for leptin receptor gene-related	protein
96 Hs.12230 24 Hs.103296 Ei	Hs.90063 m Hs.112668 Ei Hs.22550 Ei Hs.180933 Cj	Hs.137556 D Hs.48560 Ei ρς α	Hs.10082 4	Hs.31945 si sr Hs.48029 zi	ns. Hs.109437 tu re (ii	Hs.166891 e: Hs.118422 E	Hs.184167 riv H	Hs.23581 pl	Hs.23581 pi
N54053 Hs.12230 AA009593 Hs.103296	AA457517 Hs.90063 AA609232 Hs.112668 R59990 Hs.22550 T60082 Hs.9571	AA707714 Hs.19481 N62532 Hs.48560	AA778857 Hs.122069	AA873339 Hs.31945 AA464983 Hs.48029	Hs.10344	AA418216 Hs.77997 AA682671 Hs.118422	Hs.556	Hs.54515	Hs.23581
N54053 AA009593	AA457517 AA609232 R59990 T60082	AA707714 N62532	AA778857	AA873339 AA464983	T58129	AA418216 AA682671	H54020	H51066	H51066
247241 365517	838478 1031489 42387 76308	412911	452909	1471821 810119	79240	767753 450877	202904	194182	194182
GF203 GF201	GF202 GF202 GF203 GF201	GF203 GF202	GF204	GF204 GF201	GF201	GF200 GF203	GF200	GF200	GF200

Auty Doored No. 2 17 24	-1.2790989		-2.6003773	-1.2243001	-1.9249825	-1.3778138		-1.5202805	-1.1786731	71686110.1				-1.1915933	1 11118672		-1.1918657	-2.0658218	-1.2730984	4 4700500	-1.4/00393	
And a	618.9603 618.948 618.9418 618.8782	618.8475	618.8425	618.8411	618.826	618.8121	618.735	618.6231	618.507	618.474	018.4292		618.3527	618.194	617 9446	617.9228	617.8218	617.8149	617.7172	1	517.512	
	KIAA0965		KIAA0368	CAPN2		ČHR.		LOC51720	CHIT1				GNAI2									
APPENDIX A	ESTs KIAA0965 protein ESTs ESTs	ESTs, Highly similar to zona- pellucida-binding protein	KIAA0368 protein	calpain, large polypeptide L2 Homo sapiens mRNA for	KIAA1138 protein, partial cds	growth hormone receptor Homo sapiens mRNA for	FLJ00007 protein, partial cds retinoid x receptor interacting	protein	chitinase 1 (chitotriosidase)	ESTs	ESIS	guanine nucleotide binding protein (G protein), alpha	inhibiting activity polypeptide 2 GNAI2	ESTs	mony sapiens clone 23003	FSTs	ESTS	ESTs	ESTs	ESTs, Highly similar to CGI-62	protein [H.sapiens]	
	Hs.47368 Hs.184523 Hs.43791 Hs.268654	190091	Hs.3852	Hs.76288	Hs.115726	Hs.125180	Hs.59563	Hs.7889	Hs.91093	Hs.14706	Hs.23450		Hs.77269	Hs.7076	0000	Hs 97883	Hs.57664	Hs.14238	Hs.147710		Hs.118821	
	AA883675 Hs.47368 N93455 Hs.54951 W67292 Hs.43791 R00403 Hs.18759	37000 -11 474004 44	AA4004/4 hs.396/3 AA916908 Hs.3852	AA102454 Hs.76288	AA608832 Hs.112600	AA775738 Hs.125180	AA045079 Hs.59563	AA482294 Hs.7889	T94272 Hs.91093	_	N32274 Hs.108312		AA071330 Hs.77269	H13439 Hs.7076		197215 HS.15014	AA486731 Hs.57664	AA700706 Hs 14238	AA460333 Hs 49608	2	N25899 Hs.34726	
k et al.	1466621 307304 343387 123196	00000	1473773	549728	1030613	378565	487824	824701	119384	124020	272632		530139	148838	00000	1202860	841207	434990	795777		258451	
Westbrook et al.	GF204 GF201 GF201 GF200		GF201 GF203	GF200	GF202	GF203	GF204	GF203	GF200	GF200	GF201		GF201	GF203		GF200	GE 201	GF203	GESUS	5	GF203	

-1.345463	-1.0856374		-1.6432627		1.00866513 -1.4125028 -1.7079022 -1.3702553	1.23369322	1.0210839
617.2631	616.962 616.962	616.7704	616.7535		616.5974 616.5709 616.5684 616.5381	616.4501 616.4424 616.4401 616.4051	616.3919
DLD	AGA TARDBP		AGOPA		ERCC5 DKFZP586I1023	PIGB	
ditydrolpoamide defydrogenase (E3 component of pyrwate defydrogenase complex, 2- xox-gitarate complex, branched chain keto acid defydrogenase complex)	es Is aspartyglucosaminidase TAB DNA binding protein ESTs, Weakly similar to extochrome c-like polypebtide	[H.sapiens] ESTs, Weakly similar to Ydr386wp [S.cerevisiae]	KIAA1303 protein, partial cds coatomer protein complex, subjunit alpha	excision repair cross- complementing rodent repair deficiency, complementation group 5 (xeroderma pigmentosum,	(Cockayne syndrome)) ESTs EST DKFZP58611023 protein	phosphaticymostici gycan, class B ESTs ESTs	ESTS, Weakly Sittlind to TALT [H.sapiens]
	Hs./1825 Hs.207776 Hs.193989	Hs.24597 Hs.125104	Hs.20677		Hs.20849 Hs.20812 Hs.48012 Hs.111515	Hs.247118 Hs.131818 Hs.60887 Hs.182171	Hs.24572
AA453879 Hs.74635	AA156234 Hs. 71825 V51521 Hs.111661 V69283 Hs. 7786	R33082 Hs.24597 AA258031 Hs.125104	AA401378 Hs.20677		N62586 Hs.48576 R19310 Hs.20849 N57483 Hs.48012 AA019335 Hs.118455	N51166 Hs.82506 N91797 Hs.94450 AA634250 Hs.60887 AA699620 Hs.114864	Hs.24572
AA453679	AA156234 N51521 N69283	R33082 AA258031	AA401378		N62586 R19310 N57483 AA019335	N51166 N91797 AA634250 AA699620	R32959
813648	505339 281476 293576	135752 703386	742698		292463 130043 277327 363081	281465 307174 868441 436420	135352
GF200	GF202 GF201 GF200	GF201 GF204	GF202	3	GF200 GF200 GF202 GF203	GF200 GF202 GF204 GF204	GF203

	-1.295561		-1.4727274	-1.4343965							1.27066356						-1.4349616		1.1902161		1.3483399			1 1057664	-1.133/004		-1.8171428	-2.00sr co
	614.113		614.0504	613.9498		613.9409	613.8597				613.8244		613.8087		613.5767	613.4639	613.3373	613.2501	613,0452	612.9713	612.9537		612 9525	640 047E	012.34/0		612.7881	012.010
						RAD23B					GGH		NR1H2		MBD1			FLJ11235	KARS				EDAC) i			SFTPA1	NIMAUSO
Homo sapiens cDNA FLJ10299 fis, clone NT2RM2000013, moderately similar to DNA-DIRECTED RNA POLYMERASE III 128 RNA POLYPEPTIDE (EC	2.7.7.6)	Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone	DKFZp586E1624)	ESTs	RAD23 (S. cerevisiae)	homolog B	ESTs	gamma-glutamyl hydrolase	(conjugase,	folylpolygammaglutamyl	hydrolase)	nuclear receptor subfamily 1,	group H, member 2	methyl-CpG binding domain	protein 1	EST	ESTs	hypothetical protein	lysyl-tRNA synthetase	ESTs	ESTs	Rap1 guanine-nucleotide-	exchange factor directly	TOT-	ESIS	surfactant, pulmonary-	associated protein A1	NAAUSSO protein
	Hs.197642		Hs.94030	Hs.117864		Hs.178658	Hs.42380				Hs.78619		Hs.100221		Hs.6211	Hs.125957	Hs.28242	Hs.97268	Hs.3100	Hs.12396	Hs.26034		0570	200	HS.85445		Hs.177582	HS.22982
	Hs.26641		Hs.94030	Hs.117864		Hs.13912	Hs.42380				AA455800 Hs.78619		AA629265 Hs.100221		4A459922 Hs.6211	AA889411 Hs.125957	AA485676 Hs.125177	AA883950 Hs.97268	AA486374 Hs.3100	Hs.114661	Hs.26034		A A A E 2 4 00 U 0 0 5 7 0	2000	AA181233 HS.85445		AA487385 Hs.76474	AASSSSS HS.S// 15
	R96520		N52362	H71242		N55067	N59377				AA455800		AA62926		AA45992	AA88941	AA485676	AA883950	AA486374	W69799	R42112		V A 45 2 4 0 5	001011	AA18123		AA48738	AAGAAZD
	199644		284497	214624		245452	290082				809588		744052		795647	1468082	811101	1467641	842818	344191	29585		705302	10000	624347		841507	726481
	GF203		GF202	GF202		GF201	GF201				GF200		GF201		GF201	GF204	GF203	GF204	GF200	GF204	GF203		5000	22.0	GF202		GF200	GF 203

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APPENDIX A

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1.24675355		-1.0278084 -1.9575659 -1.3841787	4 -1.6999504
612.4751 612.2658 612.1624 611.808 611.7582	611.7569 611.7038 611.6824 611.6131	611.557 611.4829 611.4533 611.4079 611.2745	611.0834
LAT	TRIP3 DAP10 ISLR DAP	NICE-1 KIAA0653 MADH1	DNHBL
Homo sapiens mFNA for hypothetical protein, clone 2746033 ESTs EST linker for activation of T cells ESTs thurnful hormone recentor thurnful hormone recentor	inferration 3 DNAX-activation protein 10 immunoglobulin superfamily containing leucine-rich repeat ESTs death-associated protein	NICE-1 protein ESTs KIAA063 protein MAD (mothers against Adecapentaplege, Drosophila) homolog 1 Human mRNA for SB classII histocompatibility artigen alpha-chain	Human DNA sequence from clone RP11-3921.4 on chromosome Zqq13,22-13.33. Contains (part of) up to six movel genes or pseudogenes, the gene for a novel forthead protein similar to FOXD4 (forthread box D4, FREAC5), the gene for a novel proper protein similar to foxD4 forthead box D4, FREAC5), the gene for a novel phosphoglucomutase like dynein, heavy chain beta-like
Hs.8179 Hs.31539 Hs.116208 Hs.83496 Hs.26580	Hs.2210 Hs.117339 Hs.102171 Hs.59115 Hs.75189	Hs.110196 Hs.143752 Hs.14155 Hs.79067 Hs.914	Hs.7535 Hs.16520
AA634427 Hs.8179 AA886333 Hs.31539 AA628188 Hs.116208 W74254 Hs.83496 R56813 Hs.26580		W96216 Hs.110166 AA609057 Hs.112638 AA476212 Hs.14155 R83757 Hs.79067 AA634028 Hs.914	AA485713 Hs.7535 AA486418 Hs.7535
743860 1492967 1055827 346360 41329	824906 462536 236333 703798 814381	358599 1031280 771314 187614 868332	840442 842896
GF203 GF204 GF201 GF201 GF204	GF200 GF200 GF200 GF200 GF200	GF202 GF202 GF201 GF203 GF203	GF201 GF202

-1.9254371	-1.5702153	-1.0516713	-2.2809861	1.27825563	1.02994631	-1,4751136 1,34294152 -1,5515364 -1,1408223
610.8697	610.5658 610.4163	610.3903 610.3341 610.2919	610.2316 610.0162 610.0066 609.9934	609.8564 609.8066 609.6948 609.692 609.6291 609.6094	609.5111 609.5082 609.4106	609.3926 609.2925 609.2607 608.8238
		SMN1 MRG15	KIAA0663	MRJ RFP KRT18		EEF1A1 CIR CXADR
ESTs, Weakly similar to F25B5.3 [C.elegans] ESTs EST, Weakly similar to granule cell marker protein	[M.musculus] ESTs survival of motor neuron 1,	telomeric ESTs MORF-related gene 15 Homo sapiens mRNA; cDNA DKFZp434C0917 (from clone	DKFZp434C0917); partial cds ESTs KIAA0663 gene product ESTs MBJ gene for a member of the	DNAJ protein family ret finger protein Keratin 18 ESTS EST EST ESTS, Weakly similar to	rypotherical protein H.sapiens] ESTs ESTs, Highly similar to CGI-15 protein [H.sapiens] enkarvotic translation	elongation factor 1 alpha 1 ESTs CBF1 interacting corepressor coxsackie virus and adenovirus receptor
Hs.237536 Hs.209424	Hs.117078 Hs.97111	Hs.77306 Hs.241334 Hs.6353	Hs.22934 Hs.194040 Hs.17969 Hs.69169	Hs. 181195 Hs. 142653 Hs. 65114 Hs. 14221 Hs. 157002 Hs. 214783	Hs.35254 Hs.23198 Hs.10117	Hs.181165 Hs.46895 Hs.89421 Hs.79187
AA420965 Hs.26871 AA021134 Hs.61081	AA677682 Hs.117078 AA412283 Hs.97111	AA004858 Hs. 103282 AA425105 Hs. 33781 190438 Hs. 111905	AA634199 Hs.22934 T66849 Hs.12957 N57577 Hs.102704 AA886876 Hs.69169	AA496106 Hs.3845 AA489067 Hs.106031 AA664179 Hs.65114 AA68954 Hs.1221 AA885466 Hs.12651 T68844 Hs.11901	AA418724 Hs.35254 R42836 Hs.23198 Al000311 Hs.10117	AA443702 Hs.29835 N49109 Hs.46895 R53406 Hs.89421 N31467 Hs.79187
731227 AA 364100 AA	460459 AA 731457 AA	428928 AA 768569 AA 110872 T90	868112 AA 66341 T6 279999 N5 1493243 AA	757147 AA 824788 AA 85521 AA 433663 AA 1466402 AA 82171 T6	767801 AA 31237 R4 1613955 AIC	784028 AA 279806 N4 154093 R5 265680 N3
GF202 GF203	GF204 GF202	GF201 GF203 GF201	GF204 GF200 GF201 GF204	GF202 GF204 GF201 GF203 GF204 GF201	GF203 GF203 GF204	GF202 GF202 GF200 GF200

			APPENDIX A		000	0
	AA455058 Hs.48965	Hs.48965	ESTs Fc fragment of lqG, receptor,		608.6492	-2.001952
~ _	AA430668 Hs.110804 H61082 Hs.14743	Hs.160741 Hs.14743		FCGRT	608.3928 608.3693	-2.6799257
			PTPRF interacting protein,	č	900 2616	0 0057049
•	4A459403 Hs.99483	HS.13320/	pinding protein I (liprin beta I) PPFIBFI		608.2313	1 22 25 55 55
	2	Hs.161815	isoulis sociator	NCD	608.1634	-1.4430004
	14/312 HS./6014	TS.09090		15	607.8685	1 8034497
		Hs.14158	≡ e	CPNE3	607.8235	-1.7159214
	_	Hs.220647	ESTs		607.8126	1.83248708
			Homo sapiens cDNA			
_	N49604 Hs.32356	Hs.32356	FLJ20628 fis, clone KAT03903		607.7405	
_	R61821 Hs.91916	Hs.91916	mRNA sequence		607.6895	1.25893931
	9	Hs.170328		MSN	607.658	-1.2945425
			gap junction protein, beta 1, 32kD (connexin 32, Charcot- Marie-Tooth neuropathy, X-			
	N62394 Hs 2679	Hs 2679		GJB1	607.4954	
	_	Hs.46932	ESTs		607.4549	-1.1847555
			ition factor II,			
	AA115919 Hs.9348	Hs.169921	i, pseudogene 1 Homo sapiens cDNA	GTF2IP1	607.4049	1.19152747
			FLJ20153 fis, clone COL08656, highly similar to AJ001381 Homo sapiens			
	N95358 Hs.43754	Hs.109805	mutated allele		607.3721	1.01815975
	4		ESTs		607.2875	
		Hs.276	ESTS		9996'909	-2.6771218

	1.09379953	1.29427083	1001000	-1.668/93/					-1.34126	-1.4976156	1.97169934					-1.0405896	-1.7739754	-1.786125	1.15270555	-1.5731741	-1.5731741			1.06344369			-2.0917119	
606.8467	606.6577	606.5652	606.5003	606.4829	606.4014	606.3198			606.2507	606.2479	606.071		606.0635	605.923		605.8997	605.8962	605.8935	605.7289	92.209	605.6776		605.5448	605.5368		605.433	605.4172	
	SMP1	CDKN3		PCTK1										CST6		PIGF				STHM	STHM		CASQ2					
ESTs, Weakly similar to ubiquitin hydrolyzing enzyme I H.sapiens]	prane protein 1 ndent kinase CDK2-associated	specificity phosphatase)		IRE protein kinase 1	ESTs H.saniens gene from PAC	106H8, similar to Dynamin	Homo sapiens mRNA for G3a	protein (G3a gene, located in the class III region of the major	ristocompatibility complex)	ESTs	ESTs	Homo sapiens clone 25196	ence		ıtidylinositol glycan,		ESTs	EST	ESTs	sialyltransferase S	sialyltransferase S	calsequestrin 2, cardiac		ESTs	ESTs, Highly similar to ARF STPase-activating protein	GIT2 IH. sapiens]	EST	
E! uk Hs.41381 IH	 				Hs.269194 E	Hs.56175 10	Ĩ	₽#	Hs.247129 hi	_	Hs.129907 E	_	Hs.4285 m	Hs.83393 c)		ςı.		Hs.99583 E	Hs.93828 E	Hs.107573 si	Hs.107573 si		-	Hs.28102 E	шс	He 80279	,,	
AA628246 Hs.116227	AA402766 Hs.4961	AA284072 Hs.84113	4A663551 Hs.116914	4A283125 Hs.75679	4A004447 Hs.108153	W81520 Hs.56175			V74679 Hs.84509	V71648 Hs.118192	4A058586 Hs.129907		753544 Hs.4285	W72895 Hs.83393		180865 Hs.81647	4A699943 Hs.17892	AA461314 Hs.99583	47333 Hs.114410	AA497051 Hs.10937	AA497051 Hs.118009		83	H05731 Hs.28102		A ASZSONR Hs 120822	AA479962 Hs 105645	100001
1055775 AA6			_	_	428946 AA0	347725 W81			298702 N74	_	380823 AA0		40159 R53			230360 H80		796319 AA4	_	823590 AA4	823590 AA4		· ·	43706 H05		455185 AAG		
GF204	GF200	GF200	GF204	GF200	GF201	GF201			GF203	GF202	GF203		GF204	GF201		GF200	GF203	GF202	GF203	GF200	GF200		GF201	GF203		CESON	50210	3

	011000	1.33046416		-1.7996652	1.20452125	-1.3069446	-1.7501931	-1.1210204				-1.1381588	-2.1102624			-1.1855626	1.53565102	-1.4089763				-1.3022497				1.15272856		-1.1845655	-2.0455197		-1.3899035	-1.2172289		
605.3592		605.3364	605.3344	605.2772	605.2435	605.232	605.1366	605.0397	604.9511		604.9177	604.8864	604.8281			604.8017	604.6179	604.609	604.5247	604.5199	604.4572	604.4078			604.3878	604.3157	604.3065	604.2827	604.2729	604.1608	604.149	604.027	604 0104	1000
DKFZP564B0769			coxec	KIAA1067							P28							DKFZP586P0123								KIAA0957			KIAA0690				DAIDHO	ארטואע
DKFZP564B0769 protein	H.sapiens DNA for cyp related	pseudogene cytochrome c oxidase subunit	Vic	KIAA1067 protein	EST	ESTs	ESTs	ESTs	EST	dynein, axonemal, light	intermediate polypeptide	ESTs	ESTs	Homo sapiens mRNA; cDNA	DKFZp434L1021 (from clone	DKFZp434L1021); partial cds	ESTs	DKFZP586P0123 protein	ESTs	ESTs	ESTs	ESTs	ESTs, Highly similar to 13kD	differentiation-associated	protein [H.sapiens]	KIAA0957 protein	ESTs	EST	KIAA0690 protein	ESTs	ESTs	ESTs	relifiation in the second of t	N
He 18368	200	Hs.166079	Hs.74649	Hs.243901	Hs.112635	Hs.180295	Hs.107992	Hs.13740	Hs.120373		Hs.33846	Hs.127365	Hs.129885			Hs.5392	Hs.89029	Hs.6285	Hs.106645	Hs.269179	Hs.60291	Hs.98681			Hs.44163	Hs.30991	Hs.105727	Hs.99749	Hs.60103	Hs.127275	Hs.260750	Hs.4210	11. 01107	Hs.95197
AA426051 Hs 44981	10044500	AA873089 Hs.104117	AA025630 Hs.57915	N63987 Hs.19436	C	R15922 Hs.100860		T70541 Hs.13740	2		AA447593 Hs.33846	N50661 Hs.127365	AA708327 Hs.129885			AA436378 Hs.5392	AA282541 Hs.89029	AA398306 Hs.6285	AA286902 Hs.106645	W90726 Hs.59329	R67318 Hs.60291	AA432134 Hs.98681			AA994811 Hs.44163	N68497 Hs.6717	AA504273 Hs.105727	AA459358 Hs.99749	AA460229 Hs.60103	AA626261 Hs.127275	N20833 Hs.42893	N40968 Hs.4210		AA447978 Hs.95197
757245	13/243	1325751	366238	289494	1031278	53331	208599	108265	1292694		782688	280785	392641			752813	712976	726822	701450	418054	140907	781492			1635110	294040	825413	814501	796508	745547	265042	279824		782730
F0630	40215	GF203	GF201	GF203	GF202	GF203	GF203	GF200	GF204		GF201	GF203	GF203			GF202	GF203	GF203	GF204	GF201	GF201	GF202			GF204	GF200	GF204	GF203	GF203	GF204	GF202	GF203		GF201

Westbrook et al.	k et al.				APPENDIX A		Atty	Atty Docket No. 21726
GF203	823878	AA490474 Hs.61539	Hs.61539	Hs.61539	ESTs		603.9781	1.17637408
GF204 GF202 GF204	460180 731299 377987	AA676938 Hs.11701: AA421005 Hs.11199 AA788874 Hs.64859	AA676938 Hs.117015 AA421005 Hs.111993 AA788874 Hs 64859	Hs.117015 Hs.191603 Hs.64859	ESTs, Weakly similar to alpha-1(XVIII) collagen [M.musculus] ESTs ESTs		603.9601 603.7593 603.5071	-1.1045807
GF200	345430	W72473	Hs.85701	Hs.85701	phosphoinositide-3-kinase, catalytic, alpha polypeptide	PIK3CA	603.2911	-1.0354302
GF200 GF202	113300	T83829 Hs.102507	Hs.102507 Hs.71233	Hs.203920	homolog 5 ESTs	DLG5	603.203 603.0742 603.0548	1.1592234 -1.0973295
GF200	460034 789376	AA453335 Hs.13046	AA453335 Hs.13046	Hs.13046	thioredoxin reductase 1 biliverdin reductase B (flavin	TXNRD1	602.9871	1.12961769
GF203 GF201	1420370 428005	AA857035 Hs.76289 AA001718 Hs.14351	Hs.76289 Hs.14351	Hs.76289 Hs.189711	reductase (NADPH)) ESTs Homo sapiens cDNA	BLVRB	602.6113 602.455	1.05688647
GF203	814682	AA481060 Hs.10248	Hs.10248	Hs.10248	FLJ20167 fis, clone COL09512		602.3157	-1.5779488
GF202 GF203	681917	AA256132 Hs.97847 AA703383 Hs.12077	AA256132 Hs.97847 AA703383 Hs.120779	Hs.173880 Hs.191088	accessory protein ESTs	IL1RAP	602.2404 602.2392 602.0386	-1.1926183 -1.1247007
GF203 GF203 GF203	767706 268726 452563	AA417956 N24002 AA778846	AA670637 HS.117742 AA417956 HS.40782 N24002 HS.88527 AA77846 Hs.131806	Hs.40782 Hs.88527 Hs 185233	ESTS ESTS ESTS		602.0677 602.0677 601.9926 601.9732	1.03208418 -1.4034656 -1.0354953
GF200	229580	H66611	Hs.105255	Hs.209099	ESTs, Weakly similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]		601.8188	-1.5113046
GF202	343515	W69127	Hs.3449	Hs.274411	related protein RAZ1	SDP1	601.8007	1.36865737
GF200	299085	W05553	Hs.20993	Hs.20993	ESTS, Trighing Similar to National REN-2 antigen [H.sapiens] Homo sapiens clone 24723		601.7339	-1.0793683
GF201	269246	N26645	Hs.77080	Hs.58220	mRNA sequence		601.5682	

-1.0197138	-1.4563753		-1.0446973		-1.2917704	-1.8151932			1.93545796	-1.4210391	-1.1651209	-1.4731802			1.93627658	-2.2824276		-1.1469797	-1.6306791	-1.1103551	-1.4182144	-1.5750451	-1.6282755		1.10126181	-1.1312442				1.10679804
601.502 601.4595	601.3485 600.9945		600.8971		600.7354	600.6924		600.5093	600.4108	600.3832	600.2679	600.2507	600.2488	600.2337	600.1892	600.1428	600.0994	600.0831	8600.009	600.0024	599.9163	599.8693	599.7375		599.6457	599.5906			599.4396	599.4178
UGT2B7	HNRPH1		HMG17L3		EBAG9				KIAA0101		USP10			DKFZP434N014									KIAA0732		SFRS3	KIAA0355			SNRPG	
UDP glycosyltransferase 2 family, polypeptide B7 ESTs	neterogeneous nuclear ribonucleoprotein H1 (H) ESTs	high-mobility group (nonhistone chromosomal)	protein 17-like 3	estrogen receptor-binding	fragment-associated gene 9	ESTs	Homo sapiens clone 23551	mRNA sequence	KIAA0101 gene product	ESTs	ubiquitin specific protease 10	ESTs	ESTs	DKFZP434N014 protein	EST	ESTs	ESTs	ESTs	ESTs	ESTs	EST	ESTs	KIAA0732 protein	splicing factor, arginine/serine-	rich 3	KIAA0355 gene product	small nuclear	ribonucleoprotein polypeptide	g	ESTs
Hs.10319 Hs.8172	Hs.245710 Hs.118314		Hs.236774		Hs.9222	Hs.180799		Hs.184019	Hs.81892	Hs.99641	Hs.78829	Hs.112674	Hs.204619	Hs.93836	Hs.63171	Hs.48984	Hs.120762	Hs.105661	Hs.58521	Hs.105667	Hs.240272	Hs.143654	Hs.20185		Hs.167460	Hs.186840			Hs.77496	Hs.99387
A1000188 Hs.10319 AA453804 Hs.72044	AA463446 Hs.115579 AA626333 Hs.118314		R17124 Hs.63272		T50699 Hs.9222	AA495947 Hs.41222		W72559 Hs.102933	W68220 Hs.81892	AA465368 Hs.99641	AA465611 Hs.78829	AA609251 Hs.112674	T40725 Hs.8295	N40917 Hs.93836	AA055236 Hs.63171	N64455 Hs.48984	H51377 Hs.107373	AA485360 Hs.105661	AA460230 Hs.58521	AA485451 Hs.105667	N92293 Hs.54771	T80848 Hs.67982	AA424887 Hs.20185		AA598400 Hs.4118	AA446737 Hs.23841			AA133577 Hs.77496	AA455052 Hs.99387
1636606 813754	811770		31873		78217	768460		345329	342640	814099	814792	1031509	61044	277134	377440	294381	179443	810993	796510	811063	307995	109314	768199		950092	784104			586895	812243
GF204 GF203	GF203 GF204		GF200		GF200	GF203		GF201	GF200	GF203	GF200	GF202	GF201	GF201	GF202	GF203	GF201	GF202	GF203	GF202	GF202	GF200	GF203		GF200	GF200			GF201	GF203

1.95438715 32832203 1.16603602 -1.2301178 -1.1657625 -2.0093952 1.1947405 -1.0694188 -1.3552103 -1.1780293 -1.1737003 599.3813 597.5313 597.3476 597.1232 599.2587 598.9334 598,4099 398.3826 598.3802 597,1705 598.6641 598.2406 598.0668 597.7384 97.5758 597.2825 597.854 597.798 598.803 597.881 GUCY1A3 SLC2A3 NAPTB SFRS3 GPX3 GDI2 PARTICLE RECEPTOR BETA splicing factor, arginine/serineprotein IT1 mRNA, partial cds ESTs, Weakly similar to CGIjuanylate cyclase 1, soluble, 3DP dissociation inhibitor 2 ESTs, Moderately similar to ESTs. Moderately similar to Human clone 23773 mRNA Homo sapiens clone 25107 etracycline transporter-like complex 3, beta 2 subunit glutathione peroxidase 3 SIGNAL RECOGNITION Homo sapiens unknown SUBUNIT [M.musculus] ransporter), member 3 adaptor-related protein 39 protein [H.sapiens] solute carrier family 2 protein [M.musculus] facilitated glucose mRNA sequence seguence (plasma) alpha 3 ESTS ich 3 STS ESTS ESTS **∃STs** STS EST. EST 4s.130699 Hs.172153 Hs.127310 Hs.167460 4s.245322 Hs.107637 Hs.116771 4s.190347 Hs.56845 Hs.12152 Hs.48692 Hs.83724 Hs.75295 4s.86256 4s.12320 4s.36185 Hs.21022 Hs.22353 Hs.4220 1s.7594 Hs.127310 Hs.115114 Hs.117503 Hs.116771 4A621478 Hs.112991 AA705058 Hs.120901 AA620485 Hs.62273 AA778530 Hs.48692 Hs.113821 Hs.56845 AA279150 Hs.22353 R95693 Hs.12152 AA191294 Hs.82333 Hs.62130 AA206454 Hs.86256 AA004675 Hs.75802 Hs.12320 AA009778 Hs.36185 Hs.21022 AA283947 Hs.89260 R69790 R45279 H19242 R92806 H11692 H22346 173794 H99317 R37351 048865 1055278 626793 645670 141762 173554 704026 197176 262542 428789 461489 429820 700563 198904 951241 34464 51011 26443 22851 47510 GF200 GF202 GF204 GF202 3F201 GF204 GF203 GF202 GF202 GF204 GF200 GF203 3F201 GF204 GF200 GF203 GF204 GF203 3F201

Atty Docket No. 21726/95	-1.360902 -1.1998139	1.66993792 -2.1258033 -1.1612089	1.27605013				1.07736395	-1.9953871	-1.7618803	-1.7230972	
Atty	597.1171 596.9177 596.7233	596.6674 596.5756 596.3633	596.3099 596.2958	596.1387	596.0317	595.897	595.828	595.8102	595,7692	595.7324 595.6133 595.6053	595.5773 595.4764 595.3714
	KIAA0476	SUCLG2 EMP3	LOC51784	CPN1		PABPC4	C150RF3		DGKZ	XPR1	
APPENDIXA	ESTs ESTs KIAA0476 gene product	succinate-CoA ligase, GDP- forming, beta subunit SUCL(ESTs epithelial membrane protein 3 EMP3	sterile-alpha motif and leucine zipper containing kinase AZK ESTs	carboxypepindase IV, polypeptide 1, 50kD ESTs, Weakly similar to	(H.sapiens)	poly(A)-binding protein, cytoplasmic 4 (inducible form) PABPC4	frame 3 Homo sapiens mRNA; cDNA	DKFZp761C169 (from clone DKFZp761C169); partial cds diacylolycerol kinase zeta	(104KD)	xenotropic and polytropic retrovirus receptor ESTs	ESTs, Moderately similar to transcription repressor protein PRDI-BF1 [H.sapiens] ESTs
	Hs.22325 Hs.184192 Hs.6684	Hs.247309 Hs.50220 Hs.9999	Hs.115175 Hs.250722	Hs.2246	Hs.169001	Hs.169900	Hs.75847	Hs.71252	Hs.89981	Hs.227656 Hs.94554 Hs.250426	Hs.116328 Hs.244624 Hs.221497
	AA044106 Hs.22325 R06745 Hs.19782 W81135 Hs.106399	N90368 Hs.118130 W02401 Hs.50220 W73810 Hs.9999	H17034 Hs.106558 AA699589 Hs.119447	AA679422 Hs.2246	N48708 Hs.5701	H18434 Hs.113815	N54914 Hs.75847	R82825 Hs.107468	AA262204 Hs.89981	AA453474 Hs.100525 AA426110 Hs.94554 H71320 Hs.102210	AA629337 Hs.116328 W69805 Hs.6125 N72882 Hs.43260
k et al.	486374 126509 347035	292612 295590 344272	50477 433491	432210	279399	50987	244637	148960	686164	795185 757392 230016	743699 344210 291558
Westbrook et al.	GF203 GF200 GF201	GF200 GF200 GF203	GF202 GF204	GF201	GF201	GF204	GF200	GF203	GF200	GF201 GF202 GF201	GF204 GF204 GF201

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GF202	288961	N62712	Hs.109246	Hs.226223	KIAA0618 gene product Human clone 23719 mRNA	KIAA0618	595.3116	-1.999741
GF201	773373	AA425722	4A425722 Hs.80305	Hs.80305	eouenbes		595.1595	
GF204	858779	AA779063	AA779063 Hs.122686	Hs.122686	ESTs		594.9459	
GF204	970480	AA776174	4A776174 Hs.130320	Hs.110613	KIAA0220 protein	KIAA0220	594.9407	
					microtubule-associated protein			
GF203	647397	AA199717	4A199717 Hs.6995	Hs.101174	tan	MAPT	594.8378	-2.086489
GF201	346538	W74418	Hs.55410	Hs.55410	ESTs		594.8221	
GF201	282500	N49853	Hs.79202	Hs.21895	plexin B3	PLXNB3	594.6418	
GF204	23228	R38662	Hs.12354	Hs.12354	ESTs		594.6077	
					ESTs, Highly similar to			
GF204	261699	H99123	Hs.117980	Hs.117980	KIAA0187 [H.sapiens]		594.5305	
GF201	347183	W80666	Hs.46824	Hs.46824	ESTs		594.4318	
					integrin cytoplasmic domain-			
GF200	815534	AA456882	AA456882 Hs.11992	Hs.173274	associated protein 1	ICAP-1A	594.3684	1.51263508
GF203	753404	AA410396	AA410396 Hs.76591	Hs.76591	KIAA0887 protein	KIAA0887	594.3667	-1.30304
GF203	452708	AA779251	AA779251 Hs.122583	Hs.122583	ESTs		593.9907	1.13514776
GF201	397495	AA701081	AA701081 Hs.113541	Hs.114169	KIAA0416 protein	KIAA0416	593.9077	
					5-methyltetrahydrofolate-			
					homocysteine			
GF201	666169	AA233650	AA233650 Hs.82283	Hs.82283	methyltransferase	MTR	593.8728	
GF203	283748	N50742	Hs.4257	Hs.4257	ESTs		593.8469	1.39626213
GF202	772441	AA405558	AA405558 Hs.66378	Hs.66378	ESTs		593.8209	-1.4589361
GF203	436121	AA701996	AA701996 Hs.109722	Hs.169228	delta (Drosophila)-like 1	DLK1	593.8064	-1.377351
					Homo sapiens cDNA			
					FLJ10813 fis, clone			
GF203	785663	AA449085	4A449085 Hs.106210	Hs.106210	NT2RP4000979		593.7121	-1.3505069
GF201	810700	AA457688	AA457688 Hs.106963	Hs.106963	ESTs		593.6342	
GF201	278956	N66653	Hs.94181	Hs.94181	ESTs		593.4518	
GF204	1456701	AA864861	AA864861 Hs.122607	Hs.122607	B-cell CLL/lymphoma 9	BCL9	593.4355	
					nuclear factor I/X (CCAAT-			
GF201	130046	R19306	Hs.77816	Hs.35841	binding transcription factor)	NFIX	593.3673	
					TO COOL TO SAPIENT THE NAME OF THE PARTY OF		0000	
GF201	811100	AA485665	AA485669 Hs.86541	HS.59563	FLJUUUUV protein, partial cds		280.0380	

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-1.9077112		-1.1966022		-1.3981515	.00558104	-1.5876523	-1.0126652		-1.2407702		1.32488975		1.11393591	1.2984147					-1.0107554	
,	9				•									8		2		96		
593.29	593.1279	593.0963	593.0081 592.9909	592.9611	592.8484	592.7516	592.6636		592.563	592.4297	592.3227		592.17	592.0908		591.9615		591.9596	591.864 591.8585	
		UBE3A	TAF2I CNIL				HAN11							STRIN		RPS5P1		MAFG	HOXC4	
illar to !!!!	illar to sapiens] e E3A us E6-	tein re BNA						o CGI-83				cDNA	5			,	urotic	ein G		
rately sin MILY SQ ENTRY !!	rately sim rotein [H.: tein ligase Illoma viru	nding pro	II, I, 28KD				protein	y similar t	tpiens]			ns mRNA	1726)	. <u>:</u>	otein S5	<u>.</u>	Joaponel a (avian)	mily, pro	2	
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]	KIAA0891 protein [H.sapiens] KIAH0891 protein [H.sapiens] ubiquitin protein ligase E3A (human papilloma unus E6-	syndrome) TATA box binding protein	polymerase II, I, 28kD cornichon-like	ESTs	ESTs	ESTs	WD-repeat protein	ESTs, Highly similar to CGI-83	protein [H.sapiens]	ESTs	ESTs	Homo sapiens mRNA; cDNA	DKFZp434J1726)	STRIN protein	ribosomal protein S5	pseudogene 1	v-maf musculoaponeurotic fibrosarcoma (avian)	oncogene family, protein G	ESTs homeo box C4	
E K P E	SEES	g % T E	8.8	ES	ES	ES	×	S	brc	ES	ES	운 건	ăă	ST	Ð	šd	∑ €	9	낊 운	
Hs.13179	Hs.22466	Hs.180686	Hs.83126 Hs.201673	Hs.40178	4s.133456	ds.9905	Hs.154397		Hs.118554	Hs.120852	4s.47448		Hs.17992	Hs.180403		Hs.237225		Hs.252229	Hs.152385 Hs.116050	
유	НS	¥	운 운	웊	£	£	£		웃	£	£		±	£		£			옷 옷	
Hs.13179	AA455107 Hs.22466	Hs.79408	N92711 Hs.83126 AA521110 Hs.18120	AA411607 Hs.40178	Hs.20811	Hs.9905	AA725641 Hs.118960		AA435999 Hs.86214	AA705436 Hs.120852	Hs.47448		Hs.17992	AA461508 Hs.112144		AA039547 Hs.72803		Hs.108926	Hs.17781 Hs.50895	
	55107 1		11 1	1607		47	5641		32999	5436			F97183	1508		39547 1				
H94903	AA46	R85213	N92711 AA52111	AA41	R19189	T55547	AA7		AA43	AA70	N52158		1471	AA46		AAO		N21609	T96309 W07690	
230196	809848	180520	306444 826341	754654	129925	73526	1343768		730741	462192	284408		121220	795831		376217		266037	121028 300866	
GF200	GF201	GF200	GF201 GF204	GF203	GF200	GF202	GF203		GF202	GF204	GF202		GF200	GF202		GF201		GF201	GF201 GF200	

1.52411392 -1.4383152 -2.0211647 -1.1186475 -1.2682324591.6146 591.3452 591.3347 591.2515 591,2443 591.2072 591.1713 591.1077 590.9879 591.8302 591.7463 591,4399 591.4169 591.1921 591,4297 TAF-172 CASP10 ADTAB ALEX3 EHD3 SPS caspase 10, apoptosis-related OKFZp434N2116 (from clone chromosome 22 Contains the <!AA0563 protein [H.sapiens]</p> KIAA1209 protein, partial cds Homo sapiens mRNA; cDNA ranscription factor 2). NAGA Homo sapiens mRNA; cDNA DKFZp434G227 (from clone Human DNA sequence from acetylgalactosaminidase), a ESTs, Moderately similar to complex 2, alpha 2 subunit **TBP-associated factor 172** egulatory element binding genes for SREBF2 (sterol Homo sapiens mRNA for EH domain containing 3 gene similar to neuronal-SYNTHETASE; Human selenium donor protein adaptor-related protein SELENOPHOSPHATE clone CTA-250D10 on pseudogene similar specific septin 3, a DKFZp434N2116) systeine protease DKFZp434G227) ALEX3 protein alpha-N-ESTS ESTs ESTS Hs.124027 Hs.180930 Hs.181205 Hs.172788 Hs.8073 Hs.97794 Hs.109111 Hs.19121 Hs.14232 4s.92290 4s.51965 4s.87125 4s.46679 Hs.5353 4s.7378 AA777774 Hs.109111 AA884668 Hs.121607 AA488081 Hs.26508 Hs.14244 AA417699 Hs.14232 AA400412 Hs.97794 Hs.10474 AA862722 Hs.19121 AA443602 Hs.46679 AA985084 Hs.56397 Hs.76234 4s.92290 Hs.5353 AA666390 Hs.8073 AA479351 Hs.7378 W85892 N54456 R22052 N70181 180712 1616181 448575 469115 1468655 859253 743275 416099 746204 245174 753907 298021 241481 130777 840702 771274 GF202 GF200 GF203 GF201 GF200 GF204 GF204 GF204 **GF202** GF204 GF204 GF204 GF201 3F201 3F201

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GF203	397649	AA708275 Hs.120103	Hs.95871	ESTs ESTs, Weakly similar to reverse transcriptase		590.7128	1.04589858
GF201	134997	R31793 Hs.78226	Hs.121585	[H.sapiens]		590.7026	
GF202	767422	AA417919 Hs.48291	Hs.48291	specific, rod, delta Homo sapiens mRNA; cDNA DKFZp7610051 (from clone	PDE6D	590.577	-1,4589461
GF203	897276	AA677650 Hs.110443	Hs.110443	DKFZp7610051) similar to S68401 (cattle)		590.5583	-2.2985093
GF201 GF201	34442 505054	R44985 Hs.22920 AA149802 Hs.37925	Hs.22920 Hs.37925	glucose induced gene ESTs	HS1119D91	590.4245 590.3755	
GF203	796496	AA460224 Hs.22964	Hs.180859	containing) subunit A 1 Homo saniens mBNA for	KATNA1	590.3456	-1.6152179
GF202 GF202	742695 1035457 683129	AA400297 Hs.23410 AA621665 Hs.113004 AA214542 Hs 104177	Hs.23410 Hs.208957 Hs.104177	NICE-5 protein EST FST		590.3168 590.3074 590.2441	-1.1055669 -1.6203848 -2.2428551
GF204	32772	R43519 Hs.98118	Hs.102469	putative nuclear protein CGG triplet repeat binding	LOC51307	590.2123	
GF204	897189	AA676974 Hs.86041	Hs.86041	protein 1 Homo sapiens mRNA; cDNA DKFZp434B1813 (from clone	CGGBP1	590.191	
GF203 GF202	205497 731084	H57857 Hs.12646 AA421481 Hs.98134	Hs.12646 Hs.126866	DKFZp434B1813); partial cds ESTs A kinasa (PBKA) anchor		590.1415 590.1216	-2.6790202 -1.1460119
GF203	195751	R89082 Hs.12835	Hs.12835	protein 2 (17.12.) aromotoprotein 2 (17.12.) aromotoprotein 2 (17.12.) ELJ10242 fis, clone HEMBR1000630	AKAP7	589.8495	-1.1290992
GF204	1506477	_	Hs.1592	CDC16 (cell division cycle 16, S. cerevisiae, homolog)	CDC16	589.7479	
GF203 GF203	703820	AA278326 Hs.35445 AA448660 Hs.49349	Hs.35445 Hs.49349	Glucosidase II [H.sapiens] beta-site APP-cleaving enzyme	BACE	589.6353	2.09594152
3							

				APPENDIX A			
GF201 GF204	809857	AA455128 Hs.62743 AA778609 Hs.120316	Hs.52515 Hs.120316	transducin (beta)-like 2 ESTs	TBL2	589.5291 589.4775	
				met proto-oncogene (hepatocyte growth factor			
GF202	626841	AA191433 Hs.81688	Hs.81688	receptor)	MET	589.4478	-1.7660412
GF202	292531	N62652 Hs.109366	Hs.109366	ESTs		589.2711	-1.3256551
GF204	233910		Hs.268902	ESTs		589.0922	
				frizzled (Drosophila) homolog			
GF200	133114	R26355 Hs.24032	Hs.19545	4	FZD4	588.938	1.12551534
GF201	428492		Hs.60140	ESTs		588.8835	
				ESTs, Weakly similar to Kelch			
				motif containing protein			
GF201	771013	AA427873 Hs.22471	Hs.181341	[H.sapiens]		588.8517	
GF200	768324	AA424807 Hs.23488	Hs.23488	KIAA0107 gene product	KIAA0107	588.8232	-1.5929817
				ESTs, Weakly similar to IP63			
GF204	435619	AA703191 Hs.8772	Hs.241231	protein [R.norvegicus]		588.8033	
GF200	85497	T71879 Hs.2253	Hs.2253	complement component 2	C5	588.7111	-1.1168004
GF201	340641		Hs.39987	ESTs		588.7031	
GF202	246614		Hs.118064	ESTs		588.5809	-1.3669462
GF201	503520	īΰ	Hs.57873	ESTs		588.3931	
GF204	1473118	AA873542 Hs.126247	Hs.163323	ESTs		588.1935	
GF201	504431	AA151245 Hs.66199	Hs.66199	ESTs		588.1225	
				Homo sapiens mRNA; cDNA			
				DKFZp434M035 (from clone			
GF203	752770	AA417895 Hs.17834	Hs.17834	DKFZp434M035)		587.9821	1.03045517
GF201	376574	AA041482 Hs.42502	Hs.42502	ESTs		587.7503	
				Homo sapiens cDNA			
				FLJ11309 fis, clone			
GF201	284621	N64801 Hs.47265	Hs.28005	PLACE1010076		587.7314	
GF204	1292468	AA718933 Hs.98177	Hs.180192	ESTs		587.7225	

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APPENDIX A

1.38374447 -1.9452412 -1.1986418 -1.4921866 -1.7725705 587.7156 587.6129 587.5796 587.4148 587.1923 587.1737 587.7047 587.6789 587.5587 587.5528 587,4671 587.4652 RANBP6 LGALS4 PDCD4 5 Fc fragment of IgG, low affinity chromosome 20 Contains part Human DNA sequence from Homo sapiens partial mRNA Homo sapiens clone 23904 contains CCA trinucleotide ESTs, Weakly similar to !!!! ectin, galactoside-binding, or choline dehydrogenase locus D20S101) similar to Homo sapiens mRNA full of a novel gene similar to synthetase, a novel gene repeat), a gene similar to programmed cell death 4 length insert cDNA clone la, receptor for (CD32) glutamyftranspeptidase RAN binding protein 6 MARNING ENTRY !!!! EUROIMAGE 248114 uridine phosphorylase soluble, 4 (galectin 4) Jone RP1-18C9 on ALU SUBFAMILY J acetyl-coenzyme A mRNA sequence (chdh gene) [H.sapiens] Gamma-HMG2 ESTS STS 4s.100997 4s.100407 4s.115472 4s.167496 Hs.180030 Hs.131668 Hs.250175 Hs.59584 Hs.78864 4s.77573 Hs.8963 4s.5302 AA700367 Hs.117066 Hs.115472 Hs.113353 Hs.100756 R9840 Hs.19802 AA827468 Hs.87699 AA634109 Hs.78864 AA779148 Hs.59584 AA487608 Hs.67364 AA099568 Hs.77573 4A489790 Hs.4976 AA130579 Hs.5302 705810 R32025 90606H 1422496 134430 868380 125311 839566 240988 452635 839081 460504 586685 489677 26522 GF202 GF201 GF204 GF200 GF204 GF204 GF202 GF204 GF203 GF201 GF204 GF203

	-1.003137	1.27449228	1.03430756	-2.7908758				1.31421318	1.11024342			1.15518731	1,44692469		-2.1968019	1.04241236	-1.0376018			-1,3835995		-1.5187984
	587.1487 587.1052	586.6581	586.5056	586.418 586.3215	586.171	586.0838		585.9909	585.9011		585.8797	585.8745	585.7387		585.7185	585.6024	585.479	585.4751		585.3594		585.2655
				MMP14		KIAA0916		KIAA0204					MYO5B									
Homo sapiens mRNA; cDNA DKFZp761A072 (from clone	DKFZp761A072) ESTs Homo sapiens clone 23579	mRNA sequence Homo sapiens cDNA FLJ10345 fis. clone	NT2RM2000984 matrix metalloproteinase 14	(membrane-inserted) EST	ESTs	ESTS KIAA0916 protein	Ste20-related serine/threonine	kinase	ESTs	ESTs, Weakly similar to 17.9 KD MEMBRANE PROTEIN	C21ORF4 [H.sapiens] ESTs. Weakly similar to p60	katanin [H.sapiens]	myosin VB	ESTs, Weakly similar to	KIAA0339 [H.sapiens] Homo sapiens HSPC183	mRNA, complete cds	ESTs	ESTs	ESTs, Weakly similar to ubiquitin conjugating enzyme	[H.sapiens]	Homo sapiens cDNA FLJ20345 fis, clone	HEP13723
	Hs.46743 Hs.6994	Hs.170226	Hs.247452	Hs.2399 Hs.61141	Hs.25750	HS.15/212 Hs.151411		Hs.105751	Hs.7980		Hs.221785	Hs.100861	Hs.172506		Hs.112586	Hs.274417	Hs.10903	Hs.58670		Hs.168232		Hs.20558
	AA412051 Hs.28741 AA670305 Hs.6994	Hs.83466	AA775774 Hs.6544	N33214 Hs.2399 AA022466 Hs.61141	4A432256 Hs.25750	AA904803 Hs.130099 AA488899 Hs.38316		W17289 Hs.100301	AA476584 Hs.7980		AA009671 Hs.20650	H96095 Hs.12171	AA401349 Hs.97412		AA608769 Hs.112586	4A464612 Hs.126940	AA432083 Hs.10903	Hs.58670		Hs.106616		Hs.20558
	AA41205 AA67030	W68711	AA77577.	N33214 AA02246	AA43225	AA48889		W17289	AA47658		AA00967	H96095	AA40134		AA60876	AA46461	AA43208	W84432		R30957		R70925
	729957 878330	342685	878231	270505	782314	1504447		302031	785365		429737	250822	743143		1030635	812988	784146	356629		134172		142647
	GF202 GF204	GF202	GF203	GF201	GF201	GF204 GF204	; ;	GF200	GF203		GF201	GF203	GF202		GF202	GF203	GF202	GF204		GF200		GF200

1.01218486 -1.4708898 -1.4736733	1.14660829-1.7640891	1.166805	1.098290/ -1.3565581	1,47048214
585.2311 585.2048 585.186 585.175 585.171	585.0073	584.8845 584.8796 584.7277 584.7277	584.6085 584.5989 584.5166 584.5063 584.4219	584.1871 584.1505 584.0867 584.0493 583.9761
CAST	DKFZP58611023 KIAA0554	FADD OXTR	TSFM	DPH2L1
Homo sapiens clone 24665 mRNA sequence EST calpastatin ESTs ESTs	DKFZP58611023 protein KIAA0554 protein Fas (TNFRSF6)-associated	via death domain ESTs oxyltocin receptor ESTs ESTs Homo sapiens cDNA FLJ10896 ils, clone NT2RP5003461, weakly	smilar to RLR1 PROTEIN ESTS ESTS ESTS ESTS Ts translation elongation tactor, mitochondrial diphriat toxin resistance protein required for	(Saccharomyese)-like 1 wingless-type MMTV integration site family member 2 mirovascular endothelial differentiation gene 1 ESIs ESIs, Weakly similar to dL29K1.2 [H.sapiens]
Hs.90063 Hs.139077 Hs.247043 Hs.102314 Hs.102314	Hs.11515 Hs.168350	Hs.86131 Hs.108194 Hs.2820 Hs.8352 Hs.41423	Hs.16411 Hs.298312 Hs.238809 Hs.116768 Hs.3273	Hs.84183 Hs.89791 Hs.188105 Hs.126280
AA629117 Hs.26361 AA156235 Hs.72128 AA490894 Hs.78494 AA481433 Hs.102314 AA884659 Hs.107351	A22308 Hs.118974 A449487 Hs.74750	AA430751 Hs.86131 H59780 Hs.108194 AA085759 Hs.84672 T40950 Hs.8352 H90565 Hs.41423	AA47882 Hs.16411 AA418896 Hs.88312 AA94792 Hs.127801 AA630343 Hs.116768 W47015 Hs.3273	878468 AA670380 Hs.84183 415043 W93113 Hs.125212 773278 AA425320 Hs.6790 431945 AA678170 Hs.125199 1276370 AA694477 Hs.126280
1035765 505341 824530 752899	130845 785907	773724 208027 488276 61502 241769	788556 767877 1415981 854864 324618	878468 415043 773278 431945 1276370
GF202 GF203 GF203 GF203	GF203	GF200 GF201 GF201 GF201 GF201	GF202 GF203 GF204 GF204 GF201	GF201 GF203 GF201 GF204

1.14032147 1.2447972 1.26819855	-1.4083737 -1.6448606 -2.3409592	-1.349632 1.12212611	-1.0490778	-2.5407906	-2.0193972	1 085/19269	000000000000000000000000000000000000000
583.9415 583.9119 583.7867 583.7474 583.7445	583.6439 583.5506 583.5356 583.4512 583.2701	583.1893 583.181	583.0338 582.9835 582.9706	582.9095 582.9034 582.8613	582.8297 582.8249 582.7353	582.6758	306.30
ElF4B CD34 TGFB3	NIPSNAP1 DPP6 KIAA0481	RANGAP1 LHFP	LRPAP1	KLF7	LOC51283	TCTEL1	ZI LI
eukaryotic translation initiation ifactor 4B ESTs CD34 antigen transforming growth factor, transforming growth factor, ESTs ESTs 4-nitrophenylphosphatase	otein .		low density ilipoprotein-related protein-associated protein 1 (alpha-2-macroglobulin receptor-associated protein 1) LRPAP1 ESTs ESTs Kuppel-like factor 7	(ubiquitous) ESTs ESTs	apoptosis regulator ESTs ESTs t-complex-associated-testis-	expressed 1-like 1 ESTs tissue factor pathway inhibitor	N
Hs.93379 Hs.30581 Hs.85289 Hs.2025 Hs.97643	Hs.173878 Hs.115496 Hs.34074 Hs.263479 Hs.6360	Hs.183800 Hs.93765	Hs.75140 Hs.48523 Hs.47166	Hs.21599 Hs.43761 Hs.217259	Hs.168159 Hs.13041 Hs.48444	Hs.266940 Hs.48364	HS./8045
AA454115 HS 6000 H22824 Hs.30581 AA434483 Hs.85289 AA040617 Hs.2025 AA398495 Hs.97643	AA995464 Hs.7781 AA435982 Hs.115496 W96197 Hs.34074 AA053962 Hs.62566 AA677167 Hs.6360	AA026631 Hs.100203 N58145 Hs.93765	AA486313 Hs.75140 W70259 Hs.48523 N63604 Hs.47166	AA488672 Hs.21599 AA099542 Hs.43761 AA002226 Hs.59875	R37093 Hs.4977 R08790 Hs.13041 N59871 Hs.48444	AA994757 Hs.30081 N69945 Hs.48364	AA3994/3 Hs./8045
788273 51581 770858 486208 727009	1610408 730601 361688 364839 454632	366558 247616	842785 344036 289057	843283 489668 427754	25718 127769 284805	1631194	726086
GF204 GF201 GF200 GF200 GF203	GF204 GF202 GF201 GF202 GF203	GF200 GF200	GF200 GF201 GF201	GF202 GF204 GF202	GF201 GF200 GF201	GF204	GF200

	1.75676432		-1.2972475	1.44765502	-1.1540871	1.12105654
582.5371	582.3724 582.2834 582.2448 582.1378	582.0343	581.952 581.9037 581.8968 581.8875	581.646	581.616	581.5538 581.495 581.4382
SEC63L	PRKDC REA ANKHZN		SMARCE1	ā		CLIC4L KLF2
SEC63, endoplasmic reticulum translocon component (S. consvisiae) life and component (S. STI, Weakly, similar to GPI-ANCHORED PROTEIN P137 [H.sapiens]	protein kinase, DNA-activated, catalytic polypeptide catalytic polypeptide ESTs ESTs ANKHZN protein ANKHZN protein FLJ20845 fis., clone	ADKA01901 SWI/SNF related, matrix associated, actin dependent reculator of chromatin.	subfamily e, member 1 ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! H.sapiens ESTs Kruppel-like factor 12	protease innibitor 1 (anti- elastase), alpha-1-antitrypsin Homo sapiens cDNA El 111219 fis clone	PLACE1008122 chloride intracellular channel 4	like ESTs Kruppel-like factor 2 (lung)
Hs.31575 Hs.262095	Hs.155637 Hs.7771 Hs.98182 Hs.6538	Hs.29748	Hs.241451 Hs.261239 Hs.121570 Hs.23510	Hs.75621	Hs.40337	Hs.25035 Hs.174918 Hs.107740
AA629529 Hs.13787 AA707672 Hs.101025	R27615 Hs.9488 AA464669 Hs.7771 AA416988 Hs.98182 N30075 Hs.15347	R78530 Hs.107181	AA599120 Hs.57644 AA485731 Hs.103444 T97171 Hs.121570 R44213 Hs.23510	AA425302 Hs.84461	AA292064 Hs.34737	AA634261 Hs.25035 AA018412 Hs.60864 W74657 Hs.29405
884335	133637 810552 730866 258688	144849	950473 811142 121196 34367	773073	725392	868472 362552 344648
GF204 GF204	GF201 GF200 GF202 GF201	GF201	GF202 GF201 GF204 GF204	GF202	GF203	GF203 GF203 GF201

1.06250531 -1.8212467 1.11622654	-1.0858239	1.20844837		-1.200668 1.44844331 -1.2226473	-2.1663964 -1.110338	-1.08855 1.04400051
581.4116 581.3552 580.9877 580.925 580.7451	580.7352	580.6131	580.515 580.5054 580.483	580.1796 580.0607 580.0276 580.022	579.9706 579.8824	579.6647 579.5915
KIAA0557	CDC2L5	SEMA3B	CDC10		KIAA0232	ATF3 DLL1
Homo sapiens done 24420 mRNA sequence KIAA0557 protein ESTs ESTs ESTS Homo sapiens clone 24523	mRINA sequence cell division gydle 2-like 5 (cholinesterase-related cell division controller) C sema domain, immunoglobulin domain (lgi), serch basic domain, secreted,	ilar to !!!! J Y !!!!) of S.	PROTEIN (H.saplens) ESTS ESTS ESTS Adderately similar to weak similarity of Arabidopsis	_	activating transcription factor 3 ATF3 delta-like 1 (mouse) homolog DLL1
Hs.159408 Hs.101414 Hs.40730 Hs.56406 Hs.22668	Hs.173108 Hs.59498	Hs.82222	Hs.120784 Hs.120784 Hs.184326	Hs.167709 Hs.29690 Hs.109441 Hs.116666	Hs.109701 Hs.79276	Hs.460 Hs.250500
129538 Hs.26541 722054 Hs.101414 AA504601 Hs.40730 AA425647 Hs.56406 AA460967 Hs.22668	AA488875 Hs.6433 AA917769 Hs.1637	AA455145 Hs.82222	AA718941 Hs.120784 AA73993 Hs.7593	N48970 Hs. 93964 AA167269 Hs. 29690 N93403 Hs. 109441 AA669139 Hs. 116666	T64927 Hs.109701 AA406589 Hs.79276	Hs.460 Hs.22503
H29538 R22054 AA504501 AA425647 AA460967	AA48887 AA91776	AA45514	AI017159 AA71894 AA63399	N48970 AA167269 N93403 AA669139	T64927 AA40658	H21041 R41685
52562 130781 825357 773395 796130	824870	809892	1627568 1292469 858292	279633 595604 307189 854587	66767 753321	51448 30502
GF201 GF200 GF204 GF202 GF202	GF203	GF200	GF204 GF204 GF201	GF202 GF202 GF202 GF204	GF202 GF200	GF200 GF200

ESTs, Weakly similar to

	-1.2156367	-2.318385		-1.7088731	-2.4231507	-1.840577		1.17318901						-1.0376649	1.0126825	1.83923444		-1.0378468				1.25857641					-1.4379267			-1.2588616	-1.1713411		1.07341855	
	579.5721	579.5198	579.4554	579.4221	579.3713	579.2753		578.9896			578.9487			578.8778	578.8599	578.824	578.5944	578.5317	578.4196	578.2684		578.2501	577.5217	577.5157			577.483	577.46	577.3654	577.246	577.1985		577.1749	
			BRCA2	PPARBP	FALZ	KIAA0473		NRBP			EIF2S2				SKIL			DTYMK	LOC51316			HADH2	SH3BP2	SUPV3L1						ZNF165	FOXC1		CDC23	
predicted using Genefinder	C.elegans]	ESTs	preast cancer 2, early onset	PPAR binding protein F	_	KIAA0473 gene product	nuclear receptor binding		eukaryotic translation initiation	factor 2, subunit 2 (beta, 38kD		ESTs, Weakly similar to DNA	TOPOISOMERASE I	[M.musculus]	SKI-like	ESTs	ESTs	deoxythymidylate kinase	hypothetical protein	ESTs	hydroxyacyl-Coenzyme A	dehydrogenase, type II	SH3-domain binding protein 2 8		ESTs, Weakly similar to	alternatively spliced product	using exon 13A [H.sapiens]	EST	ESTs	zinc finger protein 165		sion cycle 23,	yeast, homolog)	
	Hs.86347	Hs.21810	Hs.34012	Hs.15589	Hs.99872	Hs.44896		Hs.272736			Hs.12163			Hs.59507	Hs.38783	Hs.69280	Hs.186810	Hs.79006	Hs.107139	Hs.179724		Hs.171280	Hs.167679	Hs.106469			Hs.90868	Hs.116182	Hs.194392	Hs.55481	Hs,195471		Hs.153546	
	Hs.125171	Hs.21810	Hs.34012	AA453404 Hs.15589	Hs.124691	4A455940 Hs,44896		Hs.101200			Hs.107937			4A173907 Hs.59507	AA84447 Hs.38783	4A488631 Hs.69280	AA699652 Hs.113098	4A464367 Hs.79006	4A431201 Hs.15653	4A626382 Hs.116167		4A458661 Hs.74645	Hs.16227	AA046407 Hs.106469			Hs.90868	AA626871 Hs.116182	4A630217 Hs.131631	Hs.55481	4A495846 Hs.75122		Hs.106416	
	T65948	R45636	H48122	AA453404	R92601	AA455940		R45977			R93622			AA173907	AA844447	AA488631	AA699652	AA464367	AA431201	AA626382		AA458661	R48132	AA046407			R37620	AA626871	AA630217	W31899	AA495846		R20737	
	81662	35725	193736	788196	196257	813275		35789			198093			595090	1390860	843091	436455	810156	782170	745123		813419	153694	488157			25132	745222	855133	328207	768370		26462	
	GF202	GF203	GF201	GF202	GF203	GF203		GF203			GF201			GF202	GF203	GF202	GF204	GF200	GF201	GF204		GF200	GF201	GF201			GF202	GF204	GF204	GF202	GF200		GF203	

-1.6822281	1.6111798 1.25971746	-1.2004986	-1.2680411 -1.3349194 1.28338564	-1.6906954	-1.2067801 -1.3197825 -1.311214
575.2814 575.2637 575.2083 575.033 574.9374	574.778 574.778 574.7294	574.6951 574.6277 574.6022	574.4756 574.4135 574.3983 574.2606 574.1194 573.6767	573.5247	573.3939 573.3069 573.1415 573.1304
PTD007	HNRPDL	۰- SLC11A2	SRPK1 KIAA0838 LMO7	NTRK1 PPP2R5E	a. 2 PTK2
PTD007 protein ESTS ESTS ESTS Phosphatidylinositol glycan,	ES1s heterogeneous nuclear ribonucleoprotein D-like ESTs	solute carrier family 11 (proton- coupled divalent metal ion transporters), member 2 ESTs	Homo sapiens HDCMD45P meRNA, partial cds EST EST SFRS protein kinase 1 KIAA0839 protein LIM domain only 7 ESTS, Weakly similar to Notch? III Aspiens]	neurorophic yrosine kinase, receptor, type 1 protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	ESTs, Highly similar to lambda- crystallin [H.sapiens] PTK2 protein tyrosine kinase 2 PTK2 ESTs
Hs.112110 Hs.92583 Hs.9218 Hs.98520 Hs.177	Hs.28368 Hs.170311 Hs.17919	Hs.57435 Hs.41136 Hs.171956	Hs.103180 Hs.138693 Hs.50369 Hs.259189 Hs.2978 Hs.2978	Hs.85844 Hs.173328	Hs.108896 Hs.740 Hs.62930 Hs.97592
AA864875 Hs.112110 H18927 Hs.92583 AA700971 Hs.9218 AA477409 Hs.98520 AA460986 Hs.177	AA775620 HS.28368 AA598578 HS.466 T96909 HS.17919	AA133656 Hs.57435 AA865916 Hs.41136 AA777799 Hs.12636	AA001745 Hs.103180 NA6998 Hs.46847 N37368 Hs.50369 AA630604 Hs.75761 R89349 Hs.114925 H22826 Hs.5978 AA670417 Hs.116483	AA447537 Hs.99111 H53787 Hs.79326	H99932 Hs.108896 AA404894 Hs.740 AA046322 Hs.62930 AA417031 Hs.97592
_	378475 7 897823 7 121412 7	586990 / 1470119 / 448960 /		782608 /	_ ,,,
GF204 GF201 GF204 GF203 GF200	GF202 GF200 GF200	GF202 GF204 GF204	GF203 GF202 GF202 GF201 GF204 GF204	GF202 GF200	GF204 GF200 GF202 GF202

-1.3375762	-1.053976	-1.053976 1.30203012	-1.8929782		1.5366145	-1.4565487	1.10731425	1.26357302	-2.5264185 -1.8546261	-2.438716
570.4404	570.3723	570.3723 570.2209	570,1294	569.9525	569.5115 569.4343	569.4147	569.4131 569.4077	569.3751	569.2689 569.2251	569.2017 569.1123 568.9919
	CAMK1	CAMK1 LOC51201	SCA7		ALPP	EIF2AK3			PSG9	AIM2
Homo sapiens cDNA FLJ20534 fis, clone KAT10950 calcium/calmodulin-dependent	protein kinase I calcium/calmodulin-dependent	protein kinase l rec	spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration) ESTs, Weakly similar to Lpe5p	[S.cerevisiae] alkaline phosphatase,	placental (Regan isozyme) ESTs	eukaryotic translation initiation factor 2 alpha kinase 3	Homo sapiens cDNA FLJ20624 fis, clone KAT04557 ESTs	ESTs, Weakly similar to diphosphoinositol polyphosphate phosphate phosphotydrolase [H.sapiens]	glycoprotein 9 ESTs	ESTs ESTs absent in melanoma 2
Hs.44344	Hs.184402	Hs.184402 Hs.5943	Hs.108447	Hs.68571	Hs.204038 Hs.15060	Hs.102506	Hs.52256 Hs.17893	Hs.22901	Hs.272620 Hs.25255	Hs.221711 Hs.108288 Hs.105115
AA418905 Hs.44344	H29415 Hs.118414	H29415 Hs.96398 R09585 Hs.20364	46	AA464236 Hs.68571	AA487465 Hs.8231 T90072 Hs.15060	AA436178 Hs.102506	R92227 Hs.75430 AA454719 Hs.17893	AA401433 Hs.22901	R65993 Hs.28475 R37975 Hs.25255	T97590 Hs.91153 H67661 Hs.108288 AA458912 Hs.105115
768060	52629	52629 127682	730408	810120	841615 110578	754387	195903 809739	743187	140107 137663	121611 211181 814410
GF203	GF200	GF200 GF200	GF202	GF204	GF201 GF200	GF203	GF200 GF201	GF202	GF203 GF200	GF200 GF204 GF203

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568.8864 568.7065	568.6306	568.5893 568.5612 568.5178	568.5151 568.515 568.3244 568.2805 568.1489 568.0662	568.0455 567.837 567.871 567.671 567.488 567.488 567.488
SATB1	RAB4	KIAA0008 LOC54505	KIAA0033 ITM2C KIAA0674 PAP	RAB9P40
special AT-rich sequence binding protein 1 (binds to nuclear matrix/scaffold- associating DNA's) ESTs FAB4, member FAS	oncogene family Homo sapiens cDNA FLJ11081 fis, clone PLACE1005187, weakly	similar to APAG PROTEIN KIAA0008 gene product hypothetical protein ESTs, Weakly similar to hypothetical protein	[H.sapiens] Intrados3 protein Intragral membrane protein 2C EST3 KIAA0674 protein poly(A) polymerase EST5. Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]	Homo sapiens cDNA FLJ20419 fis, clone KAT02435 ESTs ESTs Rab9 effector p40 ESTs ESTs
Hs.74592 Hs.125433	Hs.119007	Hs.16577 Hs.77695 Hs.95665	Hs.44789 Hs.174905 Hs.11577 Hs.109992 Hs.49007 Hs.13075	Hs.11184 Hs.124946 Hs.186683 Hs.19012 Hs.47037 Hs.112898 Hs.73251 Hs.73251
AA022561 Hs.74592 AA883114 Hs.125433	H93459 Hs.4969	AA404248 Hs.16577 W93717 Hs.100818 AA521482 Hs.95665	N36113 Hs.44789 AA450037 Hs.22271 AA432058 Hs.11577 AA432058 Hs.14799 N46321 Hs.46591 AA464543 Hs.13075	W73607 Hs.112253 AA82129 Hs.124946 AA21229 Hs.98343 H84815 Hs.19012 N50158 Hs.47037 AA620755 Hs.112898 AA406353 Hs.73251 AA757852 Hs.12154
364510 1466942	230205	758318 357373 826245	272963 788444 471196 784116 712330 279164	344555 1456060 731075 249606 282865 1049281 753193
GF201 GF204	GF200	GF202 GF201 GF203	GF202 GF200 GF200 GF203 GF203 GF201 GF201	GF201 GF204 GF202 GF201 GF202 GF203 GF203 GF203

1.91507385	-1.2675242 -1.4290431	-2.0332502	7900+00	-1.3012204 1.17705565 1.20414534	-1.2424246
567.445 567.3229 567.1465	566.9136 566.9136 566.8184	566.8139	566.5547	566.0317 565.9167	565.8671 565.6184 565.6063
PCYT2	CR2 CRSP3		ED	LYN BAIAP2	ТНВА
phosphate cylidyltransferase 2, athanolamine ESTs ESTs complement component (3d/Epstein Bar wirus)	p1 in, o very	synthetase homolog 1 [H.sapiens] ESTs, Weakly similar to !!!! ALU SUBFAMILY J MARNING ENTRY !!!! [H.sapiens]	optide repeat amaguchi sarcoma ed oncogene	homolog BAI1-associated protein 2 ESTs thyroid hormone receptor, alpha (avian erythroblastic	cDNA clone tial cds
Hs.226377 Hs.222882 Hs.117835	Hs.73792 Hs.7141 Hs.29679	Hs.109274 Hs.119949	Hs.118174	Hs.80887 Hs.7936 Hs.168887	Hs.724 Hs.97635 Hs.155912
R22274 Hs.31998 AA005355 Hs.17844 H65773 Hs.117835	AA521382 Hs.73792 N62192 Hs.7141 AA876357 Hs.29679	N50655 Hs.109274 AA706050 Hs.119949	AA007509 Hs.95030	36 Hs.80887 32 Hs.101249 36 Hs.102829	T66180 RG.16 AA398384 Hs.97635 R48507 Hs.25574
130884 R22274 429196 AA005355 211005 H65773	826984 AA52136 290110 N62192 1493085 AA87635	280784 N50655 379814 AA706050		193913 R83836 178412 H46962 296797 N74086	22074 T66180 726934 AA398384 153520 R48507
GF200 130 GF201 429 GF202 211	GF203 826 GF203 290 GF204 146	GF203 280 GF204 375		GF200 193 GF203 173 GF200 296	GF200 229 GF203 724 GF204 15

	2.16466066	1.00333502	1.01691212 -1.3062975 -1.3211246	1.18830948 -1.124151 -1.841623
565.5206 565.4961 565.4903	565.4266 565.3062 565.1811 565.0943	565.0684 564.9944 564.8882 564.8571	564.7243 564.7183 564.6399	564.5814 564.4854 564.4512
		VDAC	CSRP2 DKFZP58611023	DPAGT1 DKFZP434M098 USP21
Homo sapiens mRNA for KIAA1150 protein, partial cds ESTs ESTs, Weakly similar to	ATPase II [H.sapiens] ESTs ESTs ESTs ESTs ESTS ESTS ETTS ETTS	NT2RP2006052 ESTs ESTs voltage-dependent anion	cysteine and glycine-rich protein 2 (Lift domain only, smooth muscle) DKFZP58611023 protein ESI1s dolichy-phosphate (UDP-N-acety/glucosamine) N-	acety/glucosamnephosphorra nsferase 1 (GlcNAc-1-P transferase) DKFZP434M098 protein ubiquitin specific protease 21
Hs.4779 Hs.119046 Hs.13809	Hs.119857 Hs.203709 Hs.105151	Hs.99545 Hs.15669 Hs.184043 Hs.149155	Hs.10526 Hs.111515 Hs.61312	Hs.26433 Hs.93738 Hs.8015
AA884898 Hs.122790 R39006 Hs.119046 AA148683 Hs.13317	R86333 Hs.14988 AA704962 Hs.119857 W88954 Hs.59127 AA481049 Hs.105151	AA461492 Hs.99545 AA131694 Hs.15669 N39426 Hs.45007	AA026031 Hs.61312	Hs.26433 Hs.93738 Hs.8015
AA884898 R39006 AA148683	R86333 AA704962 W88954 AA481049	AA461492 AA131694 N39426	T59334 AA625786 AA026031	R55619 N30131 H42874
1468222 25099 503033	194524 462620 417413 814670	795820 503843 276871	75254 744905 365667	154749 268115 183062
GF204 GF204 GF201	GF201 GF204 GF202 GF204	GF202 GF201 GF201	GF200 GF203 GF202	GF200 GF202 GF203

1.11790438	-1 066357	-1.7317244	-1.6417985	-1.5845472	1.39694712 -1.6957922 -1.061498	1.51213374	1.12154927	
564.3043 564.303	564.2979	564.1896	564.0757	563.8104	563.7707 563.665 563.4757	563.2144	563.1263	563.1078
KS X d		DKFZP586I1023	HS3ST3A1	TMSB4X	POLR2B		MYGL1	TRAP150
Human DNA sequence from clone RPS-1 10367 /on chromosome 20p1 2.2-13. Contains up to five unknown morel genes, the gene for a novel protein kinase domains procinaling protein similar to phosphoprotein CSFW an the SOX22 gene for SPY (sexes determining region Y).	synaptonemal complex protein	ES18 DKFZP586I1023 protein	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1 FSTs	thymosin, beta 4, X chromosome	polymerase (RNA) II (DNA directed) polypeptide B (140kD) ESTs	ESI Homo sapiens mRNA; cDNA DKFZp434B0616 (from clone DKFZp434B0616); partial cds	v-myc avian myelocytomatosis viral oncogene homolog 1, lung carcinoma derived thyroid hormone receptor-	associated protein, 150 kDa subunit
Hs.28608	Hs.171889	Hs.111515	Hs.48384 Hs 9850	Hs.75968	Hs.148027 Hs.169755	HS.14151 Hs.40193	Hs.92137	Hs.108319
Hs.95173	Hs.106339	AA458814 HS.48820 H13278 Hs.31198	N59438 Hs.48384	AA135813 Hs.128772	Hs.112211 Hs.50569	Hs.14151	RG.11	AA010192 Hs.108319
H79129	R44048	AA458814 H13278	N59438	AA13581;	N74956 N74958	177785 R01451	R83758	AA01019
234999	33076	838408 148352	284542	565733	295551 299498	108763	187616	430179
GF201	GF201	GF202 GF203	GF202	GF202	GF202 GF202	GF200 GF200	GF200	GF201

Ally Doonel No. 2 17 2	-1.6119177	1.15860915		-1.210288	1.01215318			-1.1881065				1.28112176		-2.6303641			*10,000	-1.39042/1	1.10248330	1000	18C987.1-	-1.4193839	-1.4543963			-1.6094125	1.01965/97	-1.61844/2	-1.8889089	1.10422126	
All V	563.031	562.9599		562.9066	562.7224		562.6388	562.5772	562.5303			562.4915		562.4708	: :	562.4349	1007	562.4265	562.3392	562.1865	562.1344	561.8583	561.7889	561.6293	561.5385	561.4423	561.4352	561.4127	561.3338	561.2617	
		EIF4B		UBE2H			ID4									PPP5C		DKFZP434P0721									MSN		CGI-57	CYP2B	
APPENDIX A	ESTs	eukaryotic translation initiation factor 4B	ubiquitin-conjugating enzyme E2H (homologous to yeast	UBC8)	mRNA sequence	inhibitor of DNA binding 4, dominant negative helix-loop-	helix protein	ESTs	ESTs	ESTs, Highly similar to growth factor-responsive protein.	vascular smooth muscle	[R.norvegicus]	ESTs, Moderately similar to	SYNTAXIN 1B [H.sapiens]	protein phosphatase 5,	catalytic subunit	SIMILAR TO MOUSE AMILY DIMINA	protein	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	ESTs	moesin	EST	hypothetical protein	IIB (phenobarbital-inducible)	1
	Hs.191148	Hs.93379		Hs.28505	Hs.82508		Hs.34853	Hs.118142	Hs.269165			Hs.18878		Hs.31581		Hs.75180		Hs.82501	Hs.101762	Hs.44833	Hs.111798	Hs.226171	Hs.99504	Hs.269784	Hs.47522	Hs.11522	Hs.170328	Hs.46835	Hs.4973	Hs.1360	
	Hs.112203	Hs.7947		AA411876 Hs.106329	AA521422 Hs.82508		Hs.22991	Hs.118142	Hs.14664			Hs.18878		Hs.31581		Hs.75180		AA504116 Hs.82501	Hs.101762	Hs.44833	4 Hs.111798	Hs.21294	AA459862 Hs.99504	2 Hs.131047	Hs.47522	Hs.11522	Hs.919	Hs.46835	Hs.4973	Hs.1360	
	R09166	AA398141 Hs.7947		AA411876	AA521422		R43511	N63894	H09325			R00332		H41572		N54551		AA504116	H21070	N36923	AA701864	R40780	AA45986		N52615	R43114	R22977	N48197	N22978	T68351	
cetal.	127586	726596		730622	826166		32567	293759	46108			122982		175759		244951		825197	51462	273517	434778	28106	795797	1048789	283932	31893	131362	282019	267427	83231	
Westbrook et al	GF202	GF203		GF202	GF200	3	GF204	GF203	GF201			GE200	3	GF203		GF201		GF203	GF202	GF201	GF203	GF202	GF202	GF204	GF201	GF202	GF200	GESUS	GF203	GESON	3

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561.1725 561.1074	561.0594 560.9927	560.9374	560.879	560.6675 560.6597	560.6353 560.6245		560.4895	560.232 560.0621	559.9822 559.866 559.8082	559.7308 559.5544 559.4562	559.4481
SET	MST1R	DSIPI	POLR2F		MXI1 YDD19				90 HK1	FLJ20798 ELA3B	te SLC26A2
SET translocation (myeloid leukemia-associated) ESTs macrophage stimulating 1	tyrosine kinase) ESTs	immunoreactor polymerase (RNA) II (DNA	directed) polypeptide F ESTs, Weakly similar to	KIAA0062 [H.sapiens] ESTs	MAX-interacting protein 1 YDD19 protein	ESTs, Weakly similar to GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE	[H.sapiens] Homo sapiens mRNA for	KIAA1376 protein, partial cds ESTs	Homo sapiens cDNA FLJ20655 fis, clone KAT01590 hexokinase 1 ESTs	Homo sapiens mRNA; cDNA DKFZp434F1928 (from clone DKFZp434F1928) hypothetical protein elastase 3B	solute carrier family 26 (sulfate transporter), member 2
Hs.145279 Hs.222404	Hs.2942 Hs.44977	Hs.75450	Hs.46405	Hs.41068 Hs.12535	Hs.118630 Hs.25615		Hs.9475	Hs.24684 Hs.269148	Hs.239720 Hs.118625 Hs.56974	Hs.47159 Hs.111518 Hs.183864	Hs.29981
N52911 RG.19 AA705124 Hs.119557	AA173453 Hs.2942 N39237 Hs.44977	AA775091 Hs.75450	AA418689 Hs.46405	AA287828 Hs.41068 R38381 Hs.12535	AA705886 Hs.118630 B36006 Hs.64065		AA875959 Hs.9475	AA015658 Hs.29871 W02639 Hs.50494	R77125 Hs.11668 AA485272 Hs.118625 H05826 Hs.56974	AA045804 Hs.47159 AA156022 Hs.111518 W40123 Hs.74463	N73101 Hs.29981
244652 462692	612616 276969	868575	767817	700967	435219	3	1492249	360403 296199	144042 840158 44361	488624 590120 328802	291985
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559.2662 558.9238	558.8643 558.8028 558.7785 558.7598	558.7081	558.6837	558.6327 558.6169 558.6026	558.5128	558.3712	558.3457 558.2792	558.2354	558.1695 558.078	557.9548 557.8646	557.8183 557.8174
	ANK3	RBMS1		KIAA0603	RPL37		EMAPL			PKM2 CSNK1G2 c	SPTBN1
ESTs ESTs ankyrin 3, node of Ranvier	(ankyrin G) ESTs ESTs ESTs	RNA binding motif, single stranded interacting protein 1 Homo sapiens cDNA	HEMBA1001702 ESTs, Weakly similar to	B0025.2 [C.elegans] ESTs KIAA0603 nene product	ribosomal protein L37 Homo sapiens cDNA FL.111114 fis. clone	PLACE1005951 echinoderm microtubule-	associated protein-like ESTs ESTs, Weakly similar to	[C.elegans] ESTs, Weakly similar to tumorous imaginal discs	[H.sapiens]	pyruvate kinase, muscle casein kinase 1, gamma 2 spectrin, beta, non-enythrocytic	1 ESTs
Hs.82894 Hs.237306	Hs.75893 Hs.121668 Hs.239666 Hs.14366	Hs.241567	Hs.28661	Hs.17118 Hs.87165 Hs.173803	Hs.179779	Hs.21148	Hs.12451 Hs.121513	Hs.145088	Hs.18471 Hs.17519	Hs.198281 Hs.181390	Hs.107164 Hs.171496
W46439 Hs.82894 R94495 Hs.35167	AA677185 Hs.75893 AA773325 Hs.121668 N73031 Hs.12544	N31587 Hs.55458	AA456646 Hs.28661	AA233565 Hs.17118 AA233565 Hs.87165	4A410437 Hs.31975	AA699494 Hs.21148	AA447196 Hs.12451 H13205 Hs.121513	AA021209 Hs.122983	AA670394 Hs.18471		AA018591 Hs.107164 R60040 Hs.21883
323989 W4 197648 R9	454672 AA 845692 AA 247818 N7	•	811976 AA		767641 AA	432479 AA	784360 AA 148022 H	364133 AJ	878770 Av	# 1	362483 A. 42811 R
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-1.4354692	1.00036216	2.09102989	10000	-1.2025005 -1.4715321		-1.8711569			-2.028274		1.10935021	1.36774061		-2.5209696	-1.3878806						-1.6227752	1.34418835		1.17853285	-1.7/80159	
557.7869	557.5574	557.4808	557.4366	557.4351	557.3737	557.3243	557.2426	557.162	557.0147	556.891	556.8425	556.7408		556.6613	556.5474		556.4222			556.3622	556.2855	556.0967		555.9011	555.8392	555.8059
C17ORF1B	SFRS11	SLC2A2	SULT2B1			KIAA0750			HOXA2		IP30				THBS2		D19S1177E						:	JFD1L	LOC51322	BST2
chromosome 17 open reading frame 1B Csplicing factor, arginine/serine-		er 2 nily 2B,	er 1	ESTs ESTs	EST	750 gene product	ESTs		box A2	ESTs	Tat-interacting protein (30kD) TIP30	ESTs	ESTs, Weakly similar to	HPBRII-7 protein [H.sapiens]		DNA segment on chromosome 19 (unique) 1177	I expressed sequence	ESTs, Weakly similar to	EUSINOPHIL LYSOPHOSPHOLIPASE	[H.sapiens]	ESTs	ESTs	ubiquitin fusion degradation 1-		hypothetical protein bone marrow stromal cell	
Hs.100217	Hs.184571	Hs.167584	Hs.94581	Hs.48823 Hs 98610	Hs.116854	Hs.198793	Hs.118166	Hs.108785	Hs.58116	Hs.165216	Hs.90753	Hs.183299		Hs.107125	Hs.108623		Hs.30928			Hs.24236	Hs.60243	Hs.22057		Hs,181369	Hs.70333	Hs.118110
Hs.100217	Hs.80510	Hs.37775	Hs.94581	V63564 Hs.48823	AA634552 Hs.116854	Hs.5444	4A678014 Hs.118166	Hs.91502	Hs.58116	AA047291 Hs.61448	AA148230 Hs.90753	4A291137 Hs.40346		4A262351 Hs.107125	Hs.108623		AA443094 Hs.30928			Hs.24236	AA007626 Hs.60243	Hs.22057		Hs.10298	Hs.111037	AA485371 Hs.118110
N51614	H56944	R00833	R73584	N63564	AA634552	AA451844 Hs.5444	AA678014	R34224	W72556	AA047291	AA148230	AA291137		AA262351	H38240		AA443094			N30757	AA007626	W01534		T57841	R16545	AA485371
281605	204755	123579	141495	278236	743961	786265	431785	136024	345330	488579	589751	700503		666292	191664		809466			257978	429447	294483		80708	129606	811024
GF203	GF200	GF200	GF201	GF202	GF204	GF203	GF204	GF201	GF202	GF201	GF200	GF203		GF203	GF200		GF201			GF201	GF202	GF200		GF200	GF202	GF201

Atty Docket No. 21726		-1.5833586	-1.1880405	-1.1258139	-1.1605063	1.13459655		-1.5675104			-1.0293096	1.59125983	1.24953256
Atty	555.7484 555.6262	555.522	555.3821	555.3146 555.3004 555.2062	555.1329	555.0599 555.0018		554.9247 554.8213	554.7659	554,6453	554.4833 554.3664 554.3083	554.2829	554.2411 554.1223 554.1151
	MYO10 SMA3	DCTN-50	CREME9		AOC3				RAD51L1		LOC51322	FUS	ITM2A
APPENDIX A	myosin X SMA3	dynamitin (dynactin complex 50 kD subunit)	cytokine receptor-like molecule 9	Hoffio sapieris influxi, curva DKFZp564D016 (from clone DKFZp564D016) ESTs	amine oxidase, copper containing 3 (vascular adhesion protein 1)	ESTs ESTs	Homo sapiens mRNA; cDNA DKFZp434L2221 (from clone	DKFZp434L2221) ESTs	RAD51 (S. cerevisiae)-like 1 Homo sapiens mRNA; cDNA DKFZp761N07121 (from clone	DKFZp761N07121) ESTs, Weakly similar to intrinsic factor-B12 receptor	precursor [H.sapiens] hypothetical protein ESTs	fusion, derived from t(12;16) malignant liposarcoma	Homo sapiens cDNA FLJ20417 fis, clone KAT02301 ESTs integral membrane protein 2A ITM2A
	Hs.61638 п Hs.251397 S	d Hs.84153 5	Hs.7120 m	Hs.14846 D Hs.48348 E Hs.46988 E	-	Hs.17567 E Hs.188780 E	Ξ.	Hs.107205 D Hs.117461 E		Hs.17767 D E	Hs.194104 p Hs.70333 h Hs.179852 E	fi Hs.99969	Hs.10710 F Hs.28733 E Hs.17109 II
	AA700471 Hs.61638 AA028921 Hs.119643	AA757401 Hs.15592	AA608582 Hs.99668	R28280 Hs.106160 AA130117 Hs.48348 AA137196 Hs.46988	AA036974 Hs.79304	N45224 Hs.17567 AA682623 Hs.117274		Hs.107205 Hs.117461	Hs.100669	AA464142 Hs.17767	Hs.17858 Hs.110355 Hs.117705	AA486284 Hs.108354	AA598505 Hs.10710 H24359 Hs.28733 N53447 Hs.107688
	AA70047 AA02892	AA75740	AA60858	R28280 AA13011 AA13719	AA03697	N45224 AA68262		R74478 R33614	N70362	AA46414	T96625 R34584 H40871	AA48628	AA59850 H24359 N53447
k et al.	460646 470261	395400	950707	134712 503926 502772	484535	283124 450859		143450	295412	810326	121285 136534 176371	842839	898147 52294 245277
Westbrook et al	GF204 GF201	GF203	GF202	GF200 GF201 GF201	GF200	GF201 GF203		GF201	GF201	GF201	GF201 GF202 GF203	GF202	GF202 GF201 GF201

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554.0608 554.0289	553.9843	553.9843 553.6992 553.575	553.5645	553.5635 553.558 553.546	553.4961 553.4182 553.354	553.338 552.9312	552.9227	552.9058 552.8373
		KIAA0567					EIF4B	
Homo sapiens mRNA for KIAA1323 protein, partial cds ESTs	ESTs, Highly similar to CALCIUM-DEPENDENT GROUP X PHOSPHOLIPASE A2 PRECURSOR [H.sapiens]	ESTs, Highly similar to CALCIUM-DEPENDENT GROUP X PHOSPHOLIPASE AZ PRECURSOR [H.sapiens] KRAOS67 protein	ESTS ESTS, Weakly similar to SPLICING FACTOR, ARGININE/SERINE-RICH 7	H.saplens] ESTs ESTs, Weakly similar to	neuron-restrictive sitericer actor, form 2 [H.sapiens] ESTs =ST	EST ESTs Honoris translation initiation	actor 4B Homo sapiens mRNA; cDNA	OKFZp761P1423) ESTs
Ho.34892 KIA Hs.194079 ES	ES CA GR Hs.193681 A2		HS.48648 ES HS.48648 ES SP SP	Hs.43847 [H. 125206 ES Hs.126063 ES	Neuro Hs.70589 facto Hs.186918 ESTs Hs.295614 EST		Hs.93379 fac	Hs.15420 DM Hs.79953 ES
AA488851 Hs.34892 AA410289 Hs.87169	293 Hs.110613	35	N62840 HS.49183	AA157011 Hs.43847 AA417558 Hs.25206 AA423823 Hs.126063	T85009 Hs.70589 AA904796 Hs.130754	+ m	AA063398 Hs.5188	R12679 Hs.108401 W93638 Hs.79953
824821 AA44 754452 AA4	119914 T94293		285415 N66 289616 N62	590390 AA1 752643 AA4 755459 AA4	112158 T85i 1504099 AA9		513200 AA0	129320 R12 357236 W90
GF204 GF202	GF200	GF200 GF202	GF202 GF201	GF203 GF203 GF203	GF200 GF204	GF202 GF202 GF202	GF202	GF201 GF202

1.27437715	1.6391145	1.06745775 -1.7114599 -1.8625511 -1.5877226 -1.1765334 1.48989858 -2.7221129 1.00693357	-1.1778145
552.7119	552.636 552.5951 552.461 552.3038	552.0298 552.0156 551.9002 551.807 551.883 551.6805 551.6805 551.6805 551.4877 551.4877	551.2847 551.2751 551.1633 551.1633
MFAP2	SFRS9 RANBP2L1 ADH5	CKMT2 RNASE6 NOBP2 KIAA0848	BMP1 PMVK SHC1
ESTs, Highly similar to multifunctional calcium/calmoutlin-dependent protein kinase II delta2 isoform [H.sapiens] microfibriliar-associated protein ?	rich 9 RAN binding protein 2-like 1 alcohol dehydrogenase 5 (class III), chi polypeptide ESTs creatine kinase, mitochondrial	2 (sarcomeric) ESTS ESTS ESTS ribonuclease, RNase A family, Medicase, RNase A family, Medicase, RNase A family, ESTS ESTS ESTS KIAA0848 protein KIAA0848 protein ESTS, Weakly similar to CGI-	ESTs ESTs bone morphogenetic protein 1 BMP1 phosphomevalonate kinase PMVK SHC (Sirc homology 2 domain- containing) transforming SHC1
Hs.111460 Hs.83551	Hs.77608 Hs.179825 Hs.78989 Hs.42612	Hs.20691 Hs.94309 Hs.71719 Hs.23262 Hs.103885 Hs.108861 Hs.240770 Hs.240770 Hs.26411	Hs.30954 Hs.1274 Hs.30954 Hs.81972
AA283023 Hs.111460 N67487 Hs.83551	H24312 Hs.106715 AA446486 Hs.104583 AA453859 Hs.78989 H98888 Hs.42612	AA460480 Hs.80691 N74888 Hs.94309 AA12875 Hs.77119 AA701545 Hs.2282 AA701545 Hs.2282 AA709873 Hs.103685 N25344 Hs.21861 H19423 Hs.53247 H19423 Hs.101745 H88620 Hs.26411 H11642 Hs.22116	H65410 Hs.39036 AA479900 Hs.55299 R56774 Hs.1274 H09914 Hs.30954 R52961 Hs.101129
AA283023 N67487	H24312 AA446486 AA453859 H98988	AA460486 N74889 AA142876 AA701545 AA099877 N25344 R13925 H19423 H1642	H65410 AA479900 R56774 H09914 R52961
713271 291880	51946 781075 813711 261443	795965 299603 505235 435858 510794 265668 26711 51503 261494 47963	238461 772891 41208 46897 40303
GF203 GF201	GF204 GF201 GF200 GF201	GF202 GF202 GF202 GF201 GF203 GF203 GF203 GF203 GF203	GF202 GF202 GF201 GF200

-1.2650893	-1.1474998		1.40562236						-2.3262642	-1./4513/1	-1.4031463	-1.3340383		1.38165//2	-2.4156842	
550.9535 550.895	550.6026 550.5881 550.4799	FEO 4705	550.4531 550.4416		550.4313 550.4291		550.2198	550.1982	550.1434	550.1428	550.1142	550.0031	549.9704	549.8682	549.832	549.7413
KIAA0831	TRAM		KIAA0323		CCR1		ATM		i	FLJ20015	DPYSL2	CAMLG	MADH6		CLDN7	DIO2
Homo sapiens mRNA for KIAA1426 protein, partial cds KIAA0831 protein	translocating chain-associating membrane protein ESTs ESTs	dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS284, DXS286, D	DXS269, DXS270, DXS272 KIAA0323 protein ESTS	chemokine (C-C motif)	receptor 1 ESTs	ataxia telangiectasia mutated (includes complementation	groups A, C and D) ESTs, Weakly similar to	R31180_1 [H.sapiens] ESTs, Weakly similar to ORF	YOL124c [S.cerevisiae]	hypothetical protein	dihydropyrimidinase-like 2	calcium modulating ligand MAD (mothers against decapentaplegic, Drosophila)	homolog 6	ESTs	claudin 7 delodinase, iodothyronine,	type II
Hs.15441 Hs.103000	Hs.4147 Hs.118117 Hs.187486	<u>.</u>	Hs.7911	HS.23912	Hs.516 Hs.125457		Hs.194382	Hs.183332	Hs.3983	Hs.80618	Hs.173381	Hs.13572	Hs.153863	Hs.42388	Hs.278562	Hs.154424
AA190313 Hs.15441 R71120 Hs.103000	H15707 Hs.117642 H69538 Hs.118117 AA777546 Hs.122622		AA461118 Hs.79012 H90765 Hs.7911	AA256482 HS.23912	AA036881 Hs.516 AA883400 Hs.125457		AA016254 Hs.51187	AA009830 Hs.83756	AA452171 Hs.3983	AA424570 Hs.106736	AA487213 Hs.23461	AA521411 Hs.13572	AA007518 Hs.106305	H97514 Hs.42388	AA487488 Hs.84359	AA864322 Hs.65868
627428 142927	49518 212456 448422		240505	987089	472008		360778	430068	787893	767171	841302	826089	429356	251212	841645	1470657
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549.7325 549.6757 549.5803	549.5629 549.462 549.4471 549.3341 549.0747 549.0398	548.9947 548.9718	548.9656 548.8058 548.7848 548.3914 548.3156	548.0313 547.537 547.469 547.4166	547.4105
UBE2G1	DPYSL2	YDD19 TST	PLOD ADD2 DKFZP58611023 KIAA0330	MU-ARP2 PSCD4	H2AFX
ESTs ESTs Updintin-conjugating enzyme E2G 1 (homologous to C.	dilhydropyrimidinase-like 2 ESTs ESTs ESTs ESTs ESTs	YDD19 protein hiosulfate sulfurtransferase fritodanese) orcoollagen-lysine, 2- oxoglutarate 5-dioxygenase ilysine hydroxylase, Ehlers-	Danlos syndrome type VI) ESTS adducin 2 (beta) NK-ZP58811023 protein DK-ZP58811023 protein Homo sapiens mRNA, cDNA	Intr_Lipta_ADI Jornplex 4, mu 1 subunit Jornplex 4, mu 1 subunit Jornplex 6, mu 1 subunit Jornplex 7, mu 1 subunit Jornplex 7, mu 1 subunit Jornplex 7, mu 1 subunit Jornplex 7, mu 1 subunit Homo sapiens mRNA; cDNA Homo sapiens mRNA; cDNA Homo sapiens mRNA; cDNA Homo sapiens mRNA; cDNA EXTEGEBB076 (from done DNFZp564B076)	H2A histone family, member X H2AFX
Hs.98350 E Hs.106294 E E Hs.78563 e	- 0	, 1010		Hs.21103 6 Hs.21103 6 Hs.21103 6 Hs.21103 6	Hs.147097
AA421479 Hs.98350 R61845 Hs.106294 AA113881 Hs.78563	AA47654 Hs.75397 R07606 Hs.7728 AA005401 Hs.10453 N70740 Hs.38936 R44732 Hs.20880 AA776451 Hs.122669	AA418033 Hs.45204 AA446748 Hs.19362	9 2 8 9 7 9	H02006 Hs.78865 H42006 Hs.78865 R43966 Hs.7189 AA457718 Hs.21103 AA653527 Hs.116910	H95424 Hs.2711
731080 , 42659 531957 , 7	841620 125709 428560 298065 34033 436354		771323 345233 51842 782841 753446 33616	46383 48136 33293 810727 853265	256664
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454192	AA677084	AA677084 Hs.129692	Hs.129692	ESTs ESTs, Weakly similar to cDNA EST EMBL:D72567 comes		547.1216	
299723	N75055	Hs.14632	Hs.14632	from this gene [C.elegans] ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!		546.8732	-1.4792012
703546 1504628 462856	AA278850 AA897696 AA705319 AA002207	AA278850 Hs.28891 AA897696 Hs.118271 AA705319 Hs.119889 AA00207 Hs.17385	Hs.28891 Hs.26471 Hs.119889 Hs.17385	[H.sapiens] Wnt inhibitory factor-1 ESTs ESTs	WIF-1	546.801 546.7125 546.5757 546.5169	
38537 239711	R51015 H79650	Hs.101103 Hs.93372	Hs.169969 Hs.275198	ESTs ESTs kinesin-like 5 (mitotic kinesin-		546.4916 546.4656	-1.8913197
724960 786511	AA291494 AA452107	AA291494 Hs.119616 AA452107 Hs.99263	Hs.99263 Hs.99263	like protein 1) ESTs myeloidfymphoid or mixed- lineage leukemia (trithorax (Drosophila) homolog);	KNSL5	546.3896 546.3896	-1.0987056
137626	R39594	Hs.109559	Hs.249194	translocated to, 6 ESTs, Weakly similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!!	MLLT6	546.3557	-2.5329497
284050	N53395	Hs.47637	Hs.47637	[H.sapiens] Segregation of mitotic chromosomes 1 (SMC1, yeast		546.3035	1.10654213
897997 276848 205239 342712	AA598887 N39408 H60824 W68542	AA59887 Hs.77666 N39408 Hs.45001 H60824 Hs.89615 W68542 Hs.107918	Hs.211602 Hs.215555 Hs.211593 Hs.62515	human homolog of; ESTs protein kinase C, theta KIAA0494 gene product ESTs. Hichly similar to p243	DXS423E PRKCQ KIAA0494	546.0435 545.897 545.8619 545.8231	-1.6770064
726588 120773 811023	AA398138 T95342 AA485380	AA398138 Hs.89278 T95342 Hs.17569 AA485380 Hs.32261	Hs.89278 Hs.17569 Hs.55823	[Haspins] Simon of page 18 [Haspins] ESTs SMC (mouse) homolog, X chromosome	SMCX	545.535 545.4927 545.4769	-1.3625008

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545.428 545.418 545.3521 545.276 545.2517 544.9148	544.908 544.8951 544.8428 544.6514 544.6517 544.657	544.3575 544.3163 544.5163 544.4042 544.3822 544.3575	544.2939 544.2571 544.1801 544.1678 544.0234 543.8217 543.762 543.7516	543.6596 543.6138 543.5638 543.5256 543.3954
GYG2 ADCY2 LAP70	LOC54460 c SPTBN1	KIAA0433	HSA9761	LAMR1 API2
ESTs glycogenin 2 adenylate cyclase 2 (brain) apyrase, lysosomal ESTs	hypothetical protein EST ESTs spectrin, beta, non-erythrocytic 1 ESTs	KIAA0433 protein KIAA0433 protein ESTs ESTs ESTS EST ESTS EST	transferase ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	FLJ10468 lis, clone NT2AP2000007 ESTs laminin receptor 1 (67kD, ribosomal protein SA) ESTs apoplosis inhibitor 2
Hs.44583 Hs.58589 Hs.2352 Hs.201377 Hs.30098 Hs.125430	Hs.97324 Hs.31446 Hs.107164 Hs.6655	Hs.98013 Hs.26179 Hs.30323 Hs.142572 Hs.164811 Hs.20654	Hs. 125819 Hs. 268905 Hs. 263188 Hs. 31447 Hs. 269805 Hs. 167409 Hs. 237731	Hs.48855 Hs.106554 Hs.181357 Hs.26880 Hs.127799
N34415 Hs.44583 H04789 Hs.58589 N45141 Hs.2352 A4452730 Hs.40100 R42536 Hs.30098	AA6003050 TS: 123430 AA443497 H:81281 AA398907 H:87324 H16793 Hs.31446 H98241 Hs.114324 H6111 Hs.108251	AA405884 Hs. 98013 AA704448 Hs. 26179 AI005323 Hs. 30323 AA406212 Hs. 42572 AA406220 Hs. 97702 R10682 Hs. 20654 N33264 Hs. 44463	Hs.125819 Hs.59215 Hs.102244 Hs.31447 Hs.131942 Hs.20896 Hs.26012 Hs.59319	Hs.48855 Hs.106554 Hs.4955 Hs.113977 Hs.91288
N34415 H04789 N45141 AA452730 R42536	AA443497 AA443497 AA398307 H16793 H98241 H63111	AA405984 AA704448 AI005323 AA046112 AA406220 R10682 N33264	R31197 H49873 H79861 H16795 R10099 R41376 R53928 W90358	N63744 R40434 N34316 R98482 H48706
277340 43733 282977 788486 29967	771173 726826 50562 261246	743071 450710 1626201 376643 742890 128905 273501	134363 274097 239951 50565 128861 29237 39813 418198	292936 28298 277173 201151 201890
GF202 GF202 GF203 GF200 GF203	GF204 GF203 GF203 GF201 GF204 GF204	GF202 GF203 GF204 GF201 GF202 GF200	GF203 GF203 GF202 GF201 GF203 GF202 GF202	GF203 GF203 GF203 GF204 GF200

		1.61016678	1.1137762		-1 0100591	1.53963144			1.79435112	1.165/9209	-1.3165636		-2.3289738	1.10904858		-1.3435331	-1.3760734 -1.5776835	
	543.3284	543.259	543.1769	91.00	542.9534	542.8635	542.8569		542.6369	542.5919	542.4716		542.4623	542.2937	542.2711	542.2091	542.1735 542.1058	
		TRAF2			PRKAR2A		OMD	_	i d	SECTORI	SMAP					FLJ20273		
APPENDIX A	ESTs TNF receptor-associated	factor 2 Homo sapiens cDNA FLJ20216 fis, clone	COLF3242	protein kinase, cAMP- dependent, regulatory, type II,	alpha	ESTs	osteomodulin	Homo sapiens cDNA FLJ1164 fis, clone PLACE1007226, weakly similar to PROBABLE CXYGEN-INDEPENDENT COPROPORPHYRINOGEN III	OXIDASE (EC 1)	SEC10 (S. cerevisiae)-like 1 thyroid hormone receptor	coactivating protein ESTs. Weakly similar to dal2.	len:343, CAI: 0.17, ALC_YEAST P25335 ALLANTOICASE	[S.cerevisiae]	ESTs	ESTs	hypothetical protein	ESTs EST	
	Hs.14555	Hs.200526	Hs.20082	HS.ZU3Z4	Hs.8454	HS.269272 Hs.21906	Hs.94070		Hs.8033	Hs.29494	Hs.5464		Hs.97899	Hs.48990	Hs.268774	Hs.95549	Hs.193574 Hs.41391	
	AA707148 Hs.14555	3 Hs.2206	75	7/ HS.16545	AA664240 Hs.51759	AA13/096 HS.11093/ AA608546 HS.21906	11 Hs.94070		0	37 Hs.29494	10 Hs.91440		AA469952 Hs.97899		40 HS.33864	05 Hs.24248	AA757588 Hs.107504 H91257 Hs.41391	
	452091 AA707	191 T55353		284101 N53427		566255 AA13, 950603 AA608				144905 R78597	34364 R44210		730366 AA469		234444 H95346 47400 H10413	_	395609 AA7575 241350 H91257	
	GF204 452	GF200 77391		GF201 284		GF202 566 GF202 950		•		GF200 14 ²	GF202 343		GF202 730		GF201 23		GF203 396 GF200 24	

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541.6053	2007-1-1-20	041.4000	541.3873	541.2161	541.2072 541.1964	541.1495	541.1294 540.9175	540.8622
CDK7	SOME							DGAT
cycin-dependent kinase / (homolog of Xenopus MO15 cdk-activating kinase) sex comb on midleg	ESTs, Weakly similar to predicted using Genefinder	[C.elegans] ESTs, Weakly similar to predicted using Genefinder	[C.elegans] BCL2/adenovirus E1B 19kD-	interacting protein 3-like ESTS, Weakfy similar to Chair A, Coagulation Factor Xa- Trypsin Chimera Inhibited Wittl D-Phe-Pro-Arg- Chloromethylketone	[H.sapiens] ESTs	ESTs Homo sapiens clone 24774	unknown mRNA, partial cds ESTs diacylglycerol O-	acyltransferase (mouse) homolog
Hs.184298	HS.1/1558	Hs.106534	Hs.7807	Hs.132955	Hs.98609 Hs.44930	Hs.174006	Hs.44235 Hs.125720	Hs.225935
		7 Hs.7282	12 Hs.7807	35 Hs.3990	57 Hs.98609 Hs.44930		Hs.108718 Hs.125720	AA453512 Hs.14553
R22625	N/1462	AA49600	AA45604	AA02518	AA42869	H66675	H94063 H37809	AA4535
130242	294913	759144	812169	365098	781441	211387	242840 191530	795401
GF201	GF204	GF204	GF202	GF200	GF202	GF203	GF201 GF203	GF201
	130242 R22625 Hs.83088 Hs.184288 cdk-activating kinase) CDK7 130242 R22625 Hs.83088 Hs.184288 cdk-activating kinase) CDK7	Cyclin-depthoria niase 1 130242 R22625 Hs.83088 Hs.184286 cdk-activating kinase) CDK7 130242 R22625 Hs.83088 Hs.184286 cdk-activating kinase) CDK7 130242 R22625 Hs.70256 Hs.171558 (Drosophila)-like 2 1294913 N71462 Hs.70256 Hs.171558 (Drosophila)-like 2 1294913 N71462 Hs.70256 Hs.771558 predicted using Genefinder	Confind-alpenduck nulsas 7 (profind-alpenduck nulsas 8 (profind-alpenduck nulsas 8 (profind-alpenduck nulsas 9 (pr	Control of the Control of Annopus MO15	Control of the cont	190242 R22625 Hs.83088 Hs.184298 Cdk-activating kinase) CDK7	190242 R22625 Hs.83088 Hs.184298	190242 R22625 Hs.83088 Hs.184298

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	540.8088	540.4824 540.4783	540.3367 540.3133 540.2912	540.2092	540.1572	540.1495	539.8942 539.8726 539.8156 539.7856	539.7414 539.6998
				1 IL13RA1	- AUH	RABGGTA	5	
ESTs, Weakly similar to CATHEPSIN B PRECURSOR	H.sapiens] ESTs, Weakly similar to serine/threonine kinase	[H.sapiens] ESTs	Homo sapiens cDNA FLL20504 fis, clone KAT09455, highly similar to SYV_FUGRU VALYL-TFINA SYNTHETASE ESTS	interleukin 13 receptor, alpha 1 IL13RA1	AU RNA-binding protein/enoyl- Coenzyme A hydratase Rab	geranylgeranyltransferase, alpha subunit Homo sapiens mRNA for KIAA1357 protein partial cds	Homo sapiens cDNA FLJ10849 fis, clone TO SEPTIN 2 HOMOLOG ESTS ESTS	Homo sapiens cDNA FLJ10483 fis, clone NT2RP2000157 ESTs
шО	Hs.35433 [F	Hs.21420 [F	HS.6294 S Hs.79856 E Hs.187622 E	Hs.250911 ir	A Hs.81886	Hs.78920 a		Hs.6877 P
	AA778900 Hs.35433	H15288 Hs.21420 H09616 Hs.12764	82	AA478570 Hs.21516	AA448711 Hs.81886	AA776294 Hs.78920	Ø	H12254 Hs.6877 AA699632 Hs.113093
	453322 A	49810 H 46183 H	0.80	753153 A	786213 A	453689 A	,	48167 H 436431 A
	GF204	GF201 GF201	GF203 GF201 GF201	GF203	GF200	GF203	GF203 GF203 GF204 GF204	GF202 GF204

Atty Docket No. 21726/9		-2.06131 -2.4604483	1.03895189	1.2905223	-1.6092984	-1.2158274		-1.4169527 1.20771099	-1.0629445 -1.0280286	-2.7337709 -1.3105049 1.27840772
7#4	ŶijŲ.	539.6759 539.572	539.5259 539.4433 539.2125	539.1868 539.0545 538.8796	538.7929	538.6974	538.5532	538.5173 538.501	538.363 538.3214	538.235 538.215 538.1997 538.1736
Company			DKFZP566D193	PAFAH1B3 XAP4		EIF4B	DDX21	COX15	HBG2	KIAA0443
COMBYYSB DYDDD1	APPENDIX A	ESTs ESTs	DKFZp434C2019 (from clone DKFZp434C2019); partial cds DKFZp566D193 protein ESTs	platelet-activating factor acetylhydrolase, isoform lb, gamma subunit (29kD) HBV associated factor ESTs	Human DNA sequence from clone RP1-111B22 on chromosome 6q 16-21 Contains a novel pseudogene, a pseudogene similar to ribosomal protein L3, ESTs, STS, GSSs and CpG Islands ESTs.	eukaryotic translation initiation factor 4B	DEAD/H (Asp-Glu-Ala- Asp/His) box polypeptide 21 COX15 (yeast) homolog,	assembly protein ESTs	hemoglobin, gamma G ESTs	KIAA0443 gene product ESTs ESTs ESTs
		Hs.59142 Hs.65771	Hs.8888 Hs.106909 Hs.149611	Hs.6793 Hs.247280 Hs.269228	Hs.163724	Hs.93379 Hs.28538	Hs.169531	Hs.226581 Hs.37560	Hs.272812 Hs 50547	Hs.113082 Hs.45050 Hs.245292 Hs.24120
		AA678203 Hs.59142 AA489639 Hs.65771	W57698 Hs.8888 AA431408 Hs.106909 H61608 Hs.70405	AA464346 Hs.6793 AA447671 Hs.127315 T54780 Hs.9792	2	N33430	80	AA677070 Hs.113841 N80451 Hs.37560	9	တု ဟု
	k et al.	430864 823694	340974 782385 206094	810124 813585 73807	1031532	50648	810367	454159	449037	436741 276397 361897 133333
	Westbrook et al.	GF203 GF202	GF201 GF201 GF200	GF200 GF202 GF201	GF202	GF204	GF201	GF203	GF203	GF201 GF202 GF203 GF200

-2.0508939 -2.2388764	-1.121179 -2.3705982	-2.0220602 1.51615136 1.57676617	-1.6803972	-1.0815191
538.0458 537.9805 537.9686	537.9668 537.9542 537.9199	537.7859 537.7237 537.5676 537.5181 537.4541	537.2866 537.1583 536.9257	536.88 536.852 536.805
KIAA0657	MLH1 VWF	NR1H4	WBP1	CYBB
	mutt. (E. coli) homolog 1 (colon cancer, nonpolyposis type 2) ESTs von Willebrand factor ESTS, Highly similar to Trio	EST EST nuclear receptor subfamily 1, group H, member 4 ESTs ESTs	WW domain binding protein 1 WBP1 ESTs, Highrly similar to G protein-coupled receptor knase 6, splice variant B H.sapiens] eyfortome P245, beta	portypetron (vicenses) granulomatous disease) translin-associated factor X Homo sapiens cDNA FLJ11016 fis, clone PLACE1003334
Hs.6654 Hs.122049 Hs.97540	Hs.57301 Hs.190503 Hs.110802	Hs.108514 Hs.47630 Hs.171683 Hs.28884 Hs.113153 Hs.32458 Hs.193191	Hs.20988 Hs.169478	Hs.88974 Hs.96247 Hs.210859
AA456035 Hs.115555 AA778646 Hs.122049 AA401482 Hs.97540	R10662 Hs.57301 AA889399 Hs.126079 AA487787 Hs.110802	N26724 Hs.108514 N53369 Hs.47630 H91456 Hs.77606 H68409 Hs.28884 AA700433 Hs.113153 H29198 Hs.32458 A4676633 Hs.122530	AA040699 Hs.6555	H72119 Hs.39368 AA477514 Hs.96247 H59837 Hs.37230
812170 1048995 742616	128493 1468078 840486	266300 283981 241160 137853 460589 49728 454973	1575008 53319 486102	213660 740027 205152
GF203 GF204 GF204 GF202	GF201 GF204 GF200	GF203 GF202 GF200 GF200 GF204 GF204	GF204 GF202 GF204	GF200 GF200 GF201

-1.0873704	-1,4890821 -1,603226 -1,7813881 1,23184383	1.32896582	1.27469882
536.5876 536.5508 536.5342 536.4451	536.3855 536.2979 536.2979 536.2379 536.039 536.0739 536.0739 536.539	535.764 535.7603	535.7171 535.426 535.3618
	SYCP3 PACE FOXC1 YWHAZ		PAK2 S100A3 YARS
Homo sapiens mRNA; cDNA DKF2p7611.1223 (from clone DKF2p7611.1223) KIAA0160 protein ESTs wyosin phosphatase, target subunit 2 synaptonemal complex protein	paired basic amino acid cleaving anzyme (furth, membrane associated receptor protein) ESTS ESTS EST EST FORTH EST FORTH EST EST FORTH SHAPPHOPHOPHORDONO OXYGGHARS activation protein, zata polypeptide ESTS, Wadkly similar to IIII [H. sapiens] MARNING ENTRY IIII [H. sapiens] EST WARNING ENTRY IIII [H. sapiens] EST H. Sapiens] EST Homo sapiens cDNA	FLJ20777 fis, clone COL05728 ESTs	ptr (Contrarty) contracts kinase 2 S100 calcium-binding protein A3 tyrosyl-iRNA synthetase
Hs.6084 Hs.197803 Hs.26609 Hs.130760	Hs.171889 Hs.59242 Hs.19471 Hs.19471 Hs.114096 Hs.75103 Hs.75103	Hs.6844 Hs.250722	Hs.30692 Hs.2961 Hs.239307
H16821 Hs.6084 Al023724 Hs.101939 R58959 Hs.26609 AA774808 Hs.130760	AA856874 Hs.59242 R61187 Hs.29242 R61187 Hs.293766 W947179 Hs.86849 AA701999 Hs.114086 AA701999 Hs.114086 AA976477 Hs.75103 AA002091 Hs.92733 H79979 Hs.108472	N53214 Hs.6844 AA099138 Hs.82633	R32088 Hs.24497 AA055242 Hs.2961 AA486761 Hs.109631
GF203 50578 GF204 1654974 GF204 41333 GF203 399142	GF201 67440 GF203 1374571 GF200 358885 GF204 438128 GF204 1591788 GF201 428124 GF201 428124	GF200 246808 GF201 489495	GF200 134439 GF201 377441 GF202 841070

-2.3752086	-1.2122339	-2.2484585 -1.2977343		-1.861827	-1.3438408	-2.0912998	1.27227683	-1.5879782
535.3467 535.2252 535.1381	535.0993 535.0993 534.9682 534.9652	534.9611 534.911	534.7788 534.7788 534.7769	534.709	534.5737	534.4669 534.4067 534.1741	533.9833 533.9133	533.7308
	YDD19 DKFZP564J102 HEM1	KIAA0515	MMP15 NCOA3			MAPRE1	ETV5	
Homo sapiens mRNA for KIAA1243 protein, partial cds ESTs ESTs ESTs, Weakly similar to neuron-restrictive silencer	factor, form 2 (H.sapiens) YDD19 protein DKFZP564.102 protein hematopoletic protein 1	CS15, Wearly Silling to MAGE-B4 [H.sapiens] KIAA0515 protein matrix metalloproteinase 15	(membrane-inserted) nuclear receptor coactivator 3 Homo sapiens cDNA FLJ10815 fis, clone NT2RP4000989, weakly similar to UNC-47 PROTEIN	ESTs, Highly similar to NESTIN [H.sapiens] ESTs, Weakly similar to proline-rich protein MP4	[M.musculus] microtubule-associated protein, RP/EB family,	member 1 ESTs ESTs ets variant gene 5 (ets-related	eas variant gene of (co. rotace) molecule) ESTs Homo sapiens mRNA; cDNA	DKFZp434J0828)
Hs.151076 Hs.42570 Hs.189914	Hs.70589 Hs.25615 Hs.101735 Hs.132834	Hs.94011 Hs.108945	Hs.80343 Hs.225977 Hs 10499	Hs.127356	Hs.29896	Hs.234279 Hs.27768 Hs.98133	Hs.43697 Hs.97693	Hs.7759
AA151572 Hs.13240 H98757 Hs.42570 AA701664 Hs.124745	AA490985 Hs.102894 AA009596 Hs.6458 H17463 Hs.101735 AA668726 Hs.804	AA416894 Hs.94011 AA481143 Hs.108945	AA443300 Hs.80343 H52110 Hs.103886 AA905628 Hs.10499	N21633 Hs.127356	AA489707 Hs.16141	AA001749 Hs.77374 AA699908 Hs.27768 AA452885 Hs.98133	AA463830 Hs.43697 AA626927 Hs.97693	AA489224 Hs.7759
503214 261592 433594	824588 365536 50266 854284	730025 815161	784589 197520	266135	824377	428223 435291 788596	796542 1048760	825053
GF201 GF202 GF204	GF203 GF201 GF201 GF201	GF202 GF203	GF201 GF201	GF203	GF203	GF201 GF203 GF204	GF200	GF203

-1.1377794	1.65107982		-1.5262154		-1.4543431	-1.288625			-1.1500775	-1.1175282	-1.8107027	1.287829		1	-1.242641/		1.29568809	CU/0024.1-	1.43448684
533.5011 533.4778	533.408	533.2607	533.2084	533.1714	533.153	532.9982		532.8928	532.6761	532.6003	532.5578	532.4746	532.472	532.3952	532.3/1	532.2739	532.23//	532.1898	532.1835
DKFZP547E2110				CYP				UBE2E2	C2F					TPR		KIAA0808			STX7
Homo sapiens cDNA FLJ20501 fis, clone KAT09263 DKFZP547E2110 protein Homo sapiens mRNA; cDNA DKFZp434K0172 ffrom clone	DKFZp434K0172) ESTs Homo sapiens mRNA; cDNA	DKFZp434M092) Homo sapiens cDNA FLJ20254 fis, clone	COLF6926	Clk-associating RS-cyclophilin Homo sapiens mRNA for	KIAA1333 protein, partial cds	ESTs	ubiquitin-conjugating enzyme E2E 2 (homologous to yeast	UBC4/5)	putative protein	ESTs	ESTs Homo sapiens mRNA for	KIAA1155 protein, partial cds	ESTs translocated promoter region	(to activated MET oncogene)	ESTs	KIAA0808 gene product	ESTs	ESTs	syntaxin 7
Hs.9676 Hs.108110	Hs.121073 Hs.131755	Hs.260622	Hs.15356	Hs.77965	Hs.79828	Hs 248367		Hs.108323	Hs.12045	Hs.191478	Hs.11637	Hs.102657	Hs.74911	Hs.169750	Hs.180696	Hs.184297	Hs.72222	Hs.93842	Hs.8906
AA629986 Hs.9676 R33570 Hs.24651	AA453607 Hs.13991 AA496543 Hs.131755	AA625850 Hs.116091	AA488079 Hs.15356	T99037 Hs.94882	R27552 Hs.24169	AA621025 HS.112934 AA496110 Hs 112249		AA453584 Hs.85203	AA701981 Hs.12045	AA181723 Hs.85487	R60193 Hs.11637	H94554 Hs.41978	T40640 Hs.74911	AA454176 Hs.50630	AA609332 Hs.111937	AA404337 Hs.91338	¥	H52247 Hs.93842	T71551 Hs.29363
884498 135999	795229 755895	745434	840698	122734	134482	1056212		795197	436106	612782	42827	243154	60738	795323	743412	758298	592777	235909	110281
GF203 GF200	GF201 GF203	GF204	GF202	GF201	GF200	GF202	3	GF201	GF203	GF202	GF202	GF200	GF201	GF201	GF202	GF201	GF202	GF203	GF200

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-1.0723571 -1.9065853		-1.303193	-1.3521267	-1.1129579	1.19944735	1.70181397		1.62257368	-1.1525509	-1.7617688			-1.055953	-2.2239759					-1.2893461		-2.5027301		-1.8062937 1.9514456
531.917 531.9022	531.8994	531.829	531.8161	531.7673	531.6921	531.6603		531.6043	531.5313	531.4194	531.3803		531.3571	531.2906	531.1332	530.8777			530.7918	530.7896	530.7418		530.7037 530.7009
		NRBP				TSC2				DKFZP586G1517			NCBP1										PAFAH1B1
ESTs ESTs Homo sapiens chromosome	19, cosmid R26660 nuclear receptor binding	protein Homo sapiens cDNA El 111157 fis clone	PLACE1006961	ESTs	ESTS	tuberous sclerosis 2	Human mRNA for ornithine decarboxylase antizyme, ORF	1 and ORF 2	ESTs	DKFZP586G1517 protein	ESTs	nuclear cap binding protein 1,	80kD	EST	ESTs	ESTs	Homo sapiens cDNA FLJ10702 fis, clone	NT2RP3000759, weakly	SIMILIAT TO AUP- RIBOSYLATION FACTOR	ESTs	ESTs platelet-activating factor	acetylhydrolase, isoform lb,	alpha subunit (45kD) ESTs
Hs.184522 Hs.16491	Hs.90010	Hs.272736	Hs.21806	Hs.146150	Hs.52170 Hs.37637	Hs.90303		Hs.125078	Hs.91687	Hs.44155	Hs.49162		Hs.89563	Hs.94162	Hs.38448	Hs.269004			Hs.104222	Hs.136182	Hs.58093		Hs.77318 Hs.268920
AA496993 Hs.45106 R60731 Hs.16491	AA448181 Hs.90010	W59987 Hs.109917	AA479976 Hs.21806	Ω	N30655 Hs.41010 N78198 Hs.37637			T97803 Hs.27266	H65300 Hs.114187	AA424504 Hs.44155	N68977 Hs.49162		AA757918 Hs.31166	N64597 Hs.94162	H66043 Hs.38448	W93147 Hs.40425			R51818 Hs.42698	m	W70264 Hs.58093		AA424564 Hs.8051 N49439 Hs.53179
897536 42225	782792	338599	754026	452134	258242	190491		121546	208225	20292	289196		396147	289903	210636	415111			39677	377433	344834		767180 243428
GF202 GF202	GF201	GF202	GF202	GF203	GF201	GF200		GF200	GF203	GF202	GF201		GF203	GF202	GF201	GF201			GF202	GF201	GF202		GF203 GF200

1.00154882	1.03375588	-1.2316351	-1.2758121 -1.4565835			-1.8993643 -1.2594017 -1.6881664	-1.8157355 -1.2825673 1.03174728 -2.4862537	
530.6104	530.6072	530.6069	530.4573 530.3386	530.3111	530.1483 530.1191	530.0947 530.0074 529.9371	529.8735 529.8071 529.7851 529.7584 529.6338	529.6259 529.6246 529.4318
on UBTF	9 GPR49 VE		В НҮРВ			IGSF3 PCL1	FKBP8 3 GAP43	ide FGA g FZD7 PMS2L2
upstream binding transcription iactor, RNA polymerase I	G protein-coupled receptor 49 GPR49 ESTs, Weakly similar to MITOCHONDRIAL CARNITINE CARNITINE CARNITINE PROTEIN	[H.sapiens]	Huntingtin interacting protein B HYPB ESTs Fish vimilar to CGL	135 protein [H.sapiens] ESTs, Weakly similar to !!!! ALU SUBFAMILY SBI	[H.sapiens] ESTs memporphylin synodamily	member 3 prenylcysteine lyase ESTS	(38K) (38K) growth associated protein 43 ESTs ESTs	fibrinogen, A alpha polypeptide FGA frizzled (Drosophila) homolog 7 postmeiotic segregation increased 2-like 2
Hs.89781	Hs.246996	Hs.129539	Hs.6947 Hs.112612	Hs.84344	Hs.133526 Hs.190583	Hs.81234 Hs.278627 Hs.15936	Hs.173464 Hs.79000 Hs.170042 Hs.90489 Hs.107708	Hs.90765 Hs.173859 Hs.277777
N92443 Hs.89781	AA460530 Hs.98384	H05645 Hs.21262	AA165325 Hs.6947 AA608902 Hs.112612	AA454862 Hs.84344	N21103 Hs.7495 AA633809 Hs.131778	AA425437 Hs.81234 H91256 Hs.99918 AA682583 Hs.15936	W25035 Hs.15815 H05445 Hs.79000 W31919 Hs.55491 R70760 Hs.90489 H04200 Hs.107708	AA011414 Hs.80943 N69049 Hs.93795 AA437275 Hs.118780
308281	796624	43662	594164 , 1048645 ,	809995	265350 I 858147	773335 / 241348 450801 /	308588 44563 328287 142540 151967	429555 , 298122 758206 ,
GF200	GF202	GF202	GF202 GF202	GF201	GF201 GF204	GF202 GF200 GF203	GF200 GF200 GF202 GF204 GF203	GF201 GF201 GF201

						· Comp	The second of the
WestDrook et al.				APPENDIX A			
504536	AA150043 F	4s.103203	Hs.184325	CGI-76 protein ESTs, Moderately similar to 10-	LOC51632	529.374	
767082	AA424511 F	4s.98407	Hs.98407	formyltefranydrofolate dehydrogenase [H.sapiens] carboxylesterase 1		529.2435	-1.119861
82215	T68878	4s.111133	Hs.76688	(monocyte/macrophage serine esterase 1)	CES1	529.2249	1.17421273
450983	AA704421 F	4s.998/2	Hs.998/2	neta Azneimer antigen NADH dehydrogenase (ubiquinone) Fe-S protein 4	FALZ	323.1402	706141907
977159	AA055101 F	4e 10758	Hs 10758	(18kD) (NADH-coenzyme C	NDUFS4	529.0201	1.13351605
				Homo sapiens mRNA; cDNA DKFZp434B1517 (from clone			
796240	AA460666 F	Hs.33476	Hs.33476	DKFZp434B1517); partial cds		528.71	-2.1780486
195723	R89067 H	Hs.75407	Hs.77741	kininogen	KNG	528.6766	
392350	AA707889 F	Hs.120054	Hs.120054	ESTs		528.6719	1.17273221
726815	AA398302 F	Hs.127437	Hs.127437	ESTs		528.6621	-1.6733206
855134	AA630208 F	Hs.119896	Hs.169346	ESTs		528.6012	
341901	W61374 F	Hs.11317	Hs.11317	ESTs		528.5135	
376839	AA047618 h	Hs.109927	Hs.226770	DKFZP566C0424 protein	DKFZP566C0424	528.3399	-1.015266
51532	H20652 F	Hs.75249	Hs.75249	KIAA0069 protein	KIAA0069	528.2545	-1.4265099
811821	AA463484 F	Hs.17904	Hs.17904	ESTs		528.2057	-1.6341899
727137	AA398757 H	Hs.97305	Hs.131336	ESTs		527.9606	-2.4769132
43831	H05772 F	Hs.30567	Hs.30567	ESTs		527.8599	
				interleukin 1 receptor	4	11	10204000
137063	R35903	Hs.112305	Hs.173880	accessory protein	ILTHAP	527.7468	0.09046763
743211	AA400125 I	Hs.71711	Hs.71711	ESTs		527.6801	-2.5854471
				NADH dehydrogenase			
307933		Hs.19236	Hs.19236	subcomplex, 5 (16kD, SGDH)	NDUFB5	527.6522	
				Homo sapiens mRNA for putative glucosyltransferase,			
595109	AA173926 I	Hs.42832	Hs.155356	partial cds		527.5874	1.73548972
	504536 767082 82215 450883 377152 377152 855134 392360 378839 51532 811821 37833 311901 37833 311903 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137 727137			AA424511 Hs.98407 T68878 Hs.111133 AA460666 Hs.33476 R8967 Hs.75407 AA460666 Hs.33476 AA60666 Hs.33476 AA60666 Hs.33476 AA60666 Hs.33476 AA60666 Hs.33476 AA60666 Hs.33476 AA60666 Hs.7437 AA60768 Hs.10896 W61374 Hs.11317 AA6178 Hs.1037 AA6384 Hs.17904 AA6384 Hs.17904 AA98757 Hs.8705 H05772 Hs.30667 R35603 Hs.112305 AA400125 Hs.71711	AA424511 Hs.98407 Hs.184325 AA424511 Hs.98407 Hs.98407 T68878 Hs.111133 Hs.76688 AA704421 Hs.99872 Hs.39872 AA60666 Hs.33476 Hs.33476 AA70789 Hs.13047 Hs.7741 AA70789 Hs.13077 Hs.7741 AA60202 Hs.11399 Hs.17343 AA46344 Hs.11397 Hs.1317 AA44344 Hs.17904 Hs.7849 AA46344 Hs.17904 Hs.7904 AA68757 Hs.9705 Hs.1336 Ho5772 Hs.90677 Hs.3067 R35803 Hs.112305 Hs.17389 AA400125 Hs.7771 Hs.77711 N93053 Hs.19236 Hs.19236	AAPENDIX A AAPENDIX A AAPENDIX A AAPENDIX A AAPENDIX A AA424511 Hs.98407	APPENDIX A AAPENDIX A AA150043 Hs.103203 Hs.184325 GGI-76 protein AA24511 Hs.38407 Hs.39407 Hs.39407 dehyydrogenase [H.sapiens] T68878 Hs.111133 Hs.7688 dehydrogenase [H.sapiens] AA704421 Hs.39872 Hs.39872 Hs.39872 Hs.39872 Hs.39873 Hs.10738 Hs.29873 Hs.33476 Hs.33476 Hs.29873 Hs.33476 Hs.29873 Hs.29873 Hs.33476 Hs.29873 Hs.29873 Hs.29873 Hs.13943 Hs.10898 Hs.16934 Hs.29873 Hs.29873 Hs.1394 Hs.2988 Hs.18948 Hs.18948 Hs.18948 Hs.18948 Hs.2988 Hs.2988 Hs.2989 H

1,0000	-1.180131/	1.21609117	1.21609117					0.00000	-2.492339		-1.1406968	1.07255571	-1.3790646					-1.6441886	1.39871038	-2.1592094		1	-1.9578152	-1.1068898	-2.8613744	1.9691473	-1.3126399	1.31510028		-1.3231221	-1.7303895
100	527.5496	527.4489	527.4489	527.4489			697 9750	50.10.120	527.2475	527.213	527.0467	526.9936	526.8986				526.8562	526.7886	526.7423	526.6131			526.559	526.5231	526.3254	526.3003	526.2274	526.1298	526.0023	525.9242	525.8347
	NRZFZ	NR2F1	NR2F1				OTONIA	SINLL			MLSN1	HSP105B		÷						PLTP				SNX2	TYK2		KIAA0890	KIAA0797			
nuclear receptor subfamily 2,	group F, member 2 nuclear receptor subfamily 2,	group F, member 1	group F, member 1	ESTs	protein tyrosine phosphatase,	non-receptor type 13 (APO-	I/ODSO (1 as)-associated	phosphatase)	ESTs	ESTs	melastatin 1	heat shock 105kD	EST	ESTs, Highly similar to dolichyl-	phosphate beta-	glucosyltransferase	[H.sapiens]	ESTs	ESTs	phospholipid transfer protein	Homo sapiens mRNA full	length insert cDNA clone	EUROIMAGE 51358	sorting nexin 2	tyrosine kinase 2	ESTs	KIAA0890 protein	SUMO-1-specific protease	ESTs	ESTs	ESTs
	Hs.1255	Hs.144630	Hs.144630	Hs.97171				HS.211595	Hs.49181	Hs.220817	Hs.43265	Hs.36927	Hs.55240				Hs.227933	Hs.250722	Hs.9515	Hs.154854			Hs.13223	Hs.11183	Hs.75516	Hs.58632	Hs,6141	Hs.27197	Hs.125087	Hs.24649	Hs.152207
	AA418544 Hs.27473	AA452909 Hs.36082	AA452909 Hs.92398	AA904738 Hs.97171				0	N66346 Hs.49181	W90689 Hs.17573	N33322 Hs.42867	Q	W02043 Hs.55240				AA425769 Hs.106226	H98981 Hs.118523		4			N56960 Hs.13223	AA169814 Hs.11183	AA482128 Hs.75516	W81649 Hs 58632		~	H11453 Hs.21468		-
	767313	789049	789049	1504201				866702	285364	418276	270601	815781	327325				773240	261444	68052	741831			277512	610113	756452	347345	229937	739237	47459	50988	813393
	GF203	GF200	GF200	GF204				GF201	GF202	GF201	GF203	GF200	GF202				GF201	GF203	GF202	GF202			GF203	GF202	GESOO	GE202	GESOS	GE203	GF201	GF202	GF203

DOBOTTOS TOTOL

APPENDIX A

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	1.15389923	-1.3494657			1.40221727	-2.5355311	1.0230954	-2.0823873	-1.4127882		1.09181142	-1.8178585								-2.3040938		000	-1.8355096			1.13789328	-1.2875241	1.09388974		-2.1218811
	525.7518	525.7308	525.6682	525.6315	525.6135	525.4909	525.4885	525.3517	525.2178		525.1471	524.9818			524.7721			524.7595	524.5564	524.5561	524 4755	0001-100	524.226	524.2133	524.0964	524.0514	524.0494	524.0077		523.8008
	G6PT1			DKFZP586I1023	snox	KIAA0009		KIAA0440											KIAA0099			!	P24B	SPAK	KIAA0746	1 NEO1		2 ATF2		
glucose-6-phosphatase, transport (glucose-6-	chosphate) protein 1	ESTs	ESTs	DKFZP586I1023 protein	sulfite oxidase	KIAA0009 gene product	ESTs	KIAA0440 protein	ESTs	Homo sapiens clone 23765	mRNA sequence	ESTs	ESTs, Weakly similar to	organic anion transporter 1	[H.sapiens]	Homo sapiens cDNA	FLJ20337 fis, clone	HEP12138	KIAA0099 gene product	ESTs	E013	ESIS	integral type I protein	Ste-20 related kinase	KIAA0746 protein	neogenjn (chicken) homolog 1 NEO1	ESTs	activating transcription factor 2 ATF2 ESTs, Weakly similar to IIII	ALU SUBPAMILY J WARNING ENTRY !!!!	[H.sapiens]
	Hs.26655	Hs.226858	Hs.23213	Hs.111515	Hs.16340	Hs.170198	Hs.269311	Hs.172180	Hs.59609		Hs.5548	~			Hs.19102			Hs.26898	He 153834	Lo 194109	US. 124103	HS.26/158	Hs.179516	Hs.199263	Hs.49500	Hs.90408	Hs.7882	Hs.198166		Hs.56236
	AA490159 Hs.26655	26 Hs.23075	36 Hs.23213		4A443181 Hs.16340	78 Hs.113733		AA417567 Hs.11911	4,A486427 Hs.59609		88 Hs.5548				AA033972 Hs.19102			A4456029 Hs 26898	48 He 119678			55 Hs.50588	4A633805 Hs.7092	71 Hs.100187	4A456569 Hs.71492	AA447658 Hs 90408	AA479967 Hs.7882	64 Hs.80285		372 Hs.56236
	839980 AA490	_	52949 H29336	_		Ξ	_	_			234036 H68988				429904 AA03			R12159 AA45		•	> r	67765 149655	858152 AA63	249603 H84871	-	784959 AA44		50765 H17364		340994 W57872
	GF202	GF203	GF201	GF201	GF200	GF203	GF203	GF202	GF202		GF200	GF202			GF201	3		CESOM		GFZ01	GF202	. GF201	GF203	GF201	GF201	CESO	GF203	GF200		GF202

-1.317575	1.5985413	-2.4651057 -1.4671285	1.0653001 -2.0860788	1.22530362	-1.5670679	-1.5655983 -1.1791528 -1.6407473	1.10367293 1.12881515	1.13514056	-1.6209137
523.7371 523.6969 523.6619	523.3145 523.2765	523.2725 523.1198	522.8723 522.8269	522.6339 522.4754	522.4199	522.2998 522.2286 522.1357	521.9495 521.7168	521.6921 521.6785 521.663	521.6289
	ZID CLNS1A		F0X01A		MAPK4	EMR1	ZNF124 KIAA1021	티	
Human clone 191B7 placenta expressed mRNA from chromosome X ESTs ESTs zinc finger protein with	interaction domain chloride channel, nucleotide- sensitive. 1A	ESTs ESTs forkhead box O1A	(rhabdomyosarcoma) ESTs ESTs, Weakly similar to JM27	[H.sapiens] ESTs mitogen-activated protein	kinase 4 egf-like module containing, mucin-like, hormone receptor-	like sequence 1 ESTs ESTs zinc finger protein 124 (HZF-	16) KIAA1021 protein transcriptional intermediary	factor 1 ESTs ESTs FSTs Home sapiens cDNA FL.11146 fis. clone	PLACE1006673
Hs.82171 Hs.14373 Hs.187569	Hs.3053	Hs.20506 Hs.20506	Hs.170133 Hs.59324	Hs.98380 Hs.46517	Hs.269222	Hs.2375 Hs.91582 Hs.64896	Hs.180248 Hs.29189	Hs.183858 Hs.4283 Hs.46677	Hs.3385
H15095 Hs.82171 R64306 Hs.14373 AA011551 Hs.20398	Hs.3053 Hs.84974	AA446344 Hs.99068 N58392 Hs.20506	AA194765 Hs.175 AA701948 Hs.59324	AA423978 Hs.98380 W65459 Hs.46517	AA401035 Hs.75649	Hs.2375 Hs.75974 Hs.64896	AA873762 Hs.73103 H80707 Hs.29189	AA016973 Hs.128763 R53478 Hs.4283 N47113 Hs.46677	Hs.3385
H15095 R64306 AA011551	AA397823 Hs.3053 T52435 Hs 8497	AA446344 N58392	AA194765 Hs.175 AA701948 Hs.593	AA423978 W65459	AA401035	T66981 T40899 R06479	AA873762 H80707	AA016973 R53478 N47113	N64429
49249 139579 429626	725501	781283 248073	628955 435919	758271 342376	741429	66507 61387 126321	1475746 241482	360787 40154 280375	294304
GF203 GF204 GF201	GF201	GF202 GF203	GF200 GF203	GF202 GF201	GF200	GF200 GF202 GF200	GF203 GF200	GF203 GF204 GF201	GF200

-1.5291509	-1.0952255	1.24400236	-1.5671254			-2.0235155	-1 1881428	1.31225642	1.0434609	-1.2474954
521.6088 521.354	521.3121	521.1751	521.1469	521.1444 521.1431 521.1263	521.0192	520.987	520.9196	520.7477	520.6224 520.6118	520.4567
RCV1	PP35		PSMD3	CEBPD TBR1	NFATC1	FJX1	ATDRI	ITGAX		
Homo sapiens cDNA FLJ20101 fis, clone COL04655 Precoverin		gene) ESTs proteasome (prosome,	_		rr factor of activated T- sytoplasmic 1	al cds	se, H+ transporting, mal (vacuolar proton	antigen oha	ESTs, Highly similar to CGI-07 protein [H.sapiens] ESTs	Homo sapiens clone 24877 mRNA sequence
Hom FLJS Hs.263925 COL Hs.80539 reco	Hs.97627 and Horr	Hs.26320 gene) Hs.125230 ESTs protea	Hs.9736 ATP	Hs.76722 proteir Hs.210862 T-box, Hs. 238730 FSTs			Hs.183646 ESTs		8	Hs.3964 mRI
AA459394 Hs.115163 AA074224 Hs.80539	Hs.33999	Hs.26320 Hs.125230	Hs.9736	AA043506 Hs.76722 H10054 Hs.22138 H59118 Hc.0578	AA679278 Hs.96149	H72368 Hs.39384 AA436405 Hs.38002	H17063 Hs.27952	Hs.51077	Hs.108905 Hs.34656	Hs.3964
AA459394 AA074224	H48105	H60572 N27125	AA485052 Hs.9736	AA043506 H10054 TE3118	AA679278	H72368 AA436405	H17063	N64384	N20328 N64504	T61888
810947 383188	193397	207850 269751	815861	487820	432072	213850	50240	950086 290234	264597 290359	78736
GF203 GF201	GF203	GF200 GF203	GF203	GF201 GF201	GF201	GF201 GF203	GF201	GF202	GF203 GF201	GF202

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-1.2225057		2.4754775	1.2588872				1.2933812	-2.0176028							1.07009279		-1.1602271		-1.2951527			1.03542496				-2.0642694		-1.4864124	
-1.22		-2.47	1.258				-1.29	-2.01							1.070		-1.16		-1.29			1.03				-2.06		-1.48	
520.4243		520.1859	520.1489		520.1248		520.0837	520.078	520.0331	520.009	519.9939	519.9681			519.9629		519.9302	519.8875	519.8313			519.6451		519,4449		519.3448	519.3309	519.2747	519.2642
TYROBP			PLGL		POLD1		ENG			DNM1							LIG4		LOC51668			SSR1				C80RF1			DKFZP586I1023
TYRO protein tyrosine kinase binding protein ESTs	ESTs, Weakly similar to similar to other protein	phosphatases 1, 2A and 2B [C.elegans]	plasminogen-like	polymerase (DNA directed), delta 1, catalytic subunit	(125kD)	endoglin (Osler-Rendu-Weber	syndrome 1)	ESTs	ESTs	dynamin 1	ESTs	ESTs	Homo sapiens cDNA	FLJ20156 fis, clone	COL08823	ligase IV, DNA, ATP-	dependent	ESTs	HSPCO34 protein	signal sequence receptor,	alpha (translocon-associated	protein alpha)	ESTs, Highly similar to CGI-35	protein [H.sapiens]	chromosome 8 open reading	frame 1	ESTs	ESTs	DKFZP586I1023 protein
Hs.9963		Hs.69485	Hs.262869		Hs.99890		Hs.76753	Hs.47315	Hs.187985	Hs.166161	Hs.134441	Hs.21558			Hs.12692		Hs.166091	Hs.134478	Hs.46967			Hs.250773		Hs.44369		Hs.40539	Hs.267365	Hs.271945	Hs.111515
Hs.9963	1000	AA286819 Hs.69485	Hs.100533		AA429661 Hs.99890		AA446108 Hs.75962	Hs.47315	4A719016 Hs.131457	4A496334 Hs.126	Hs.68969	Hs.21558			Hs.59547		Hs.26109	Hs.100404	4A479933 Hs.46967			AA099394 Hs.76152		Hs.44369		4A027049 Hs.110332	AA151295 Hs.80564	Hs.23600	Hs.23884
H12338	0623	AA28681	T67549		AA42966		AA44610	W84859	AA71901	AA49633	W84667	H48165			W94555		R54358	T49816	AA47993			AA09939		N62169		AA02704	AA15129	R23952	H16560
148469	0 0	701261	66982		780947		774409	415771	1292523	755228	415715	178999			357996		39274	68637	772925			510679		287676		469383	505005	131446	49145
GF201	202	GE203	GF200		GF201		GF200	GF203	GF204	GF201	GF201	GF201			GF202		GF200	GF201	GF202			GF200		GF201		GF202	GF201	GF200	GF204

		-2,4110489		-1.2192993		-1 2000604			1.0984247		-2.2364193		-1.0660676				-1.3087877		-1.3743603	-1.0825761		-1.8159647	-1.6966536			1.05463635		-1.1468562	21//8//-1-
519.2327	519.2088 519.1362	519.0749		519.0521		518 087			518.9781		518.97		518.961				518.8307		518.7656	518.6124	518.6112	518.5858	518.4495	518.0708		518.0697		518.0427	517.9915
lu.	K 1	KIAA1105		IA2		aic	<u>a</u>				SSH		-						\$4	ш						52			
BACE	ROCK1	KIAA		PTP4A2		NEVDID					PRKCSH		SIPA1				CAD			SOLE						TIMP2			
beta-site APP-cleaving enzyme Rho-associated, colled-coil	containing protein kinase 1 ESTs	KIAA1105 protein	protein tyrosine phosphatase	type IVA, member 2	nuclear factor of kappa light	polypeptide gene emianoei in	ESTs. Weakly similar to	similar to beta tubulin	[H.sapiens]	protein kinase C substrate 80K	ı	signal-induced proliferation-	associated gene 1	carbamoyl-phosphate	synthetase 2, aspartate	transcarbamylase, and	dihydroorotase	splicing factor, arginine/serine-	rich 4	squalene epoxidase	ESTs	ESTs	ESTs	ESTS	tissue inhibitor of	metalloproteinase 2	Homo saniens cDNA	FLJ20624 fis, clone KAT04557	ESTs
Hs.49349	Hs.17820 Hs.186568	Hs.23440	19:01	Hs.82911		1010	HS.9/31		Hs.34851		Hs.1432		Hs.7019				Hs.154868		Hs.76122	Hs.71465	Hs.62448	Hs.226907	Hs. 5327	Hs.270263		Hs.6441		Hs.52256	Hs.176669
AA136283 Hs.106646	T57805 Hs.109450 AA705819 Hs.120840	AA045176 Hs.48022	19.91340	AA504327 Hs.82911			AA806371 HS.9731		Hs.34851		AA496810 Hs.1432		AA160906 Hs.7019				Hs.66260		4A496787 Hs.76122	Hs.71465	Hs.62448	Hs,50482	Hs 5327	Hs.106442		AA486280 Hs.1795		AA443698 Hs.104918	Hs.87694
AA13628	T57805 AA705819	AA04517	+/+7 0	AA50432			AA80637		N48792		AA49681		AA16090				R84263		AA49678	R01118	N63057	W02624	N70520	R53235		AA48628		AA44369	N26829
490377	80649	487753	120243	825442			1350468		279460		897669		593114				274638		897646	124781	284714	296141	299059	40435		842846		784016	257111
GF201	GF201 GF204	GF201	00215	GF200			GF203		GF203		GF200		GF202				GF200		GF200	GF200	GF201	GF200	CESOS	GF204		GF200		GF202	GF203

	0000	-1.4/48106	-1.8865665	1.20758858					-1.3576594	-1.8469343						-1.7519372	-1.0568348	1.33028053						1.15/60431			-1.1281032	1.28996478	
517.8981		517.8921	517.8545	517.7469	517.741	517.6403			517.5212	517.0763	517.0625			516.9174	516.8812	516.8672	516.8094	516.7933					516.6482	516.4155	516.348	516.3269	516.3266	516.3035	516.1346
		BHF1	ARPC1B		LOC51318											KIAA0924									RPL27A				
ESTs, Highly similar to G protein-coupled receptor kinase 6, splice variant B H saniens!	butyrate response factor 1	(EGF-response factor 1) actin related protein 2/3	complex, subunit 1B (41 kD)	ESTs	hypothetical protein	ESTs	Homo sapiens cDNA	FLJ20085 fis, clone	COL03604	ESTs	ESTs	Homo sapiens mRNA; cDNA	DKFZp434H1235 (from clone	DKFZp434H1235); partial cds	ESTs	KIAA0924 protein	ESTs	ESTs	Homo sapiens guanine	nucleotide exchange factor	smgGDS (RAP1GDS1)	mRNA, alternatively spliced,	complete cds	ESTs	ribosomal protein L27a	ESTs	ESTs	ESTs	ESTs
He 169478	13.103470	Hs.85155	Hs.11538	Hs.96112	Hs.93814	Hs.10762			Hs.118964	Hs.97593	Hs.77208			Hs.238927	Hs.98908	Hs.190386	Hs.15098	Hs.169440					Hs.7940	Hs.142373	Hs.76064	Hs.184591	Hs.46656	Hs.123645	Hs.95044
n 107830	BS: 107.938	AA424743 Hs.85155	4A188155 Hs.11538	AA171715 Hs.96112	7 Hs.25878	1 Hs.10762			4A458840 Hs.75353	AA398245 Hs.97593	AA044732 Hs.77208			24 Hs.55314	AA994467 Hs.98908	AA706892 Hs.119975	8 Hs.15098	9 Hs.121596					6 Hs.7940	AA421055 Hs.97364	AA446013 Hs.81755	AA131760 Hs.14594	3 Hs.46656		AA011210 Hs.95044
107146	E 2	AA424	AA188		W87917	T61351			AA458	-	-			W16424				H14569							-	-	N47013	R68207	
250005	220022	768299	626502	610362	417208	78064			814357	726659	487912			322443	1628599	451646	140171	48320					283436	731395	781007	503889	280159	138405	359823
0	GFZU	GF200	GF200	GF202	GF201	GF201			GF200	GF203	GF201			GF201	GF204	GF203	GF200	GF203					GF201	GF202	GF201	GF201	GF202	GF203	GF201

-1,3199285 -1,4569723 -1,2063237	1.17373978 -1.0666483 -1.142304	1.1399637		-1.633803	-1.7066776
516.074 515.9447 515.8475	515.8307 515.7689 515.6296 515.6011	515.5202 515.4679 515.4616 515.4495	515.3776 515.3553 515.1642 515.0266	514.7095	514.6605 514.6077
MYL2	RPS18 KIAA0185	РІК4СВ ТМРО	NEK1 SYT1	P63 KIAA0440	
ESTs, Weakly similar to KIAA0704 protein [H.sapiens] ESTs myosin, light polypeptide 2, regulatory, cardiac, slow Hono sapiens mRNA, ciDNA DIRZPASBR213 ffrom clone	DKFZp586K2123) ESTs ribosomal protein S18 KIAA0185 protein		DKTZp586C1817, (mon done DKTZp586C1817) NIMA (rover in mitosis gene a)-related kimase 1 synaptotagmin 1 ESTs, Highly similar to CGI-82 protein [H. sapiens]	transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment (54AAA0440 protein ESTs, Weakly similar to similar to acyl-CoA	dehydrogenases and epoxide hydrolases [C.elegans] ESTs
Hs.21288 Hs.30591 Hs.75535	Hs.17639 Hs.101014 Hs.275865 Hs.239499	Hs.154846 Hs.170225 Hs.269434 Hs.11355	Hs.42458 Hs.48332 Hs.154679 Hs.90677	Hs.74368 Hs.172180	Hs.247177 Hs.112704
AA452824 Hs.21288 AA459949 Hs.30591 N78927 Hs.75535	R06429 Hs.17639 AA194941 Hs.101014 H96900 Hs.42247 AA666405 Hs.45028	AA448094 Hs.78443 H21943 Hs.119407 R99849 Hs.108046 T63980 Hs.11355	AA039595 Hs.19207 N71695 Hs.50072 AA683073 Hs.5042 T61899 Hs.90677	AA598787 Hs.74368 R37938 Hs.129670	H17854 Hs.21284 AA609414 Hs.112704
3 788558 3 796395 3 300051	126338 665082 251709 859627	782692 160233 201090 79761	376343 290607 971399 79032	898073 1 24033	1 50170 2 743517
GF203 GF203 GF202	GF200 GF203 GF203 GF201	GF200 GF203 GF201 GF201	GF201 GF201 GF201 GF201	GF200 GF204	GF201 GF202

-1.1165257 -1.1364086	-1.2275158	-1.0359145 1.52561383	1.06443522	-1.1406989		1.06840664					-1.0247419	1.23336378		-1.8653675			
514.3948 514.392	514.1868 514.1542	514.1286 514.0777	514.0766	513.7945		513.7548	513.7143	513.6974	513.5466		513.5344	513.5165	513.5046	513.1384	512.9284	512.9008	512.8885
LOC51251	NdH		KIAA0648	SNRPB				TLR5	CSR1		CYP19	DRG1	aUCA1A	SSH3BP1	Z39IG	ISG15	
Homo sapiens mRNA for KIAA1155 protein, partial cds hypothetical protein Lansmembrane	2	Homo sapiens cDNA FLJ20667 fis, clone KAIA596 EST	KIAA0648 protein K small nuclear	tein polypeptides	Homo sapiens mRNA; cDNA DKFZp434M0420 (from clone	DKFZp434M0420)		or 5	_	cytochrome P450, subfamily XIX (aromatization of	7			spectrin SH3 domain binding protein 1	lg superfamily protein		ESTs, Weakly similar to KIAA0609 protein [H.sapiens]
Hs.102657 KI Hs.55189 hy	Hs.823 pr Hs.187846 ES	HS.18955 FL HS.101687 ES		rib Hs.83753 B	ĬÒ	Hs.273369 DF		3	Hs.128856 C.	ই ≍	Hs.79946 ar	de Hs.115242 G	gu Hs.92858 (re	sp Hs.24752 pr	Hs.8904 lg	Hs.833 15	E: Hs.86543 K
H77707 Hs.93363 AA187938 Hs.104021	H62162 Hs.823 AA702686 Hs.119641	N91198 Hs.53095 H10060 Hs.101687	92	AA599116 Hs.83753		AA873427 Hs.100526	342823 Hs.22229		R10675 Hs.18285		H13181 Hs.113779	AA488466 Hs.115242	AA431439 Hs.110261	R16667 Hs.24752		AA406020 Hs.833	AA278321 Hs.86543
233419 H 626016 A	208413 H 448067 A	292416 N 46630 H	· ·	950482 A			32339 F	_	128515 F		148954 F	842980 ₽	782462 A	129644 F	-	742132 A	703810 /
GF200 GF202	GF200 GF204	GF200	GF203	GF200		GF204	GF201	GF201	GF201		GF203	GF200	GF201	GF200	GF201	GF201	GF204

1.22126082	1.3661441 -1.4336448 -2.3580797 1.18442153	-1.5761585 -1.4760382 -1.3994193 -1.3495879	1.04408708	-1.8944408
512.8774 512.7226 512.6703	512.4981 512.2376 512.1078 512.1036	512.0435 511.9911 511.9274 511.377	511.7785 511.774 511.7017 511.6798	511.6435
SLC22A3	ABCB2	MGAT3 LGALS8		
solule carrier family 22 (extraneuronal monoamine transporter), member 3 EST ESTs Farbinding cassette, sub- family B (MDR/TAP), member	Lett's Christian of the Carlot	mannosyl(beta-1,4-)- glycoprotein beta-1,4-N- acetylglucosaminyltransferase MGAT3 EESTs soluble, 8 (galectin 8) ESTs ESTS	FLJ20847 fis, clone ADKA01746 ESTs, Moderately similar to heat shock protein 27 [H.sapiens] ESTs ESTs ECTS	ESTs, riginy sirinar to nouviv- interacting protein [M.musculus] ESTs
Hs.81086 Hs.117694 Hs.40289	Hs.158164 Hs.46722 Hs.48759 Hs.272115	Hs.112 Hs.250786 Hs.4082 Hs.109007	Hs.13479 Hs.121979 Hs.183834 Hs.90220	Hs.81063 Hs.259541
151617 Hs.81110 H30055 Hs.117694 AA406294 Hs.40289	AA487637 Hs.78587 AA401496 Hs.124068 N63312 Hs.48759 H84048 Hs.87	H46487 Hs.112 N21007 Hs.23840 R92197 Hs.34564 AA634424 Hs.109007	H16997 Hs.13479 AA777737 Hs.121979 H69022 Hs.38787 R40102 Hs.90220	R98434 Hs.81063 AA609304 Hs.112685
T51617 H30055 AA406294	AA487637 AA401496 N63312 H84048	H46487 N21007 R92197 AA634424	H16997 AA777737 H69022 R40102	R98434 AA609304
72441 190291 754543	279018 249856	178468 265885 195852 743851	50238 449487 211301 30078	206992 1031568
GF201 GF203 GF203	GF200 GF202 GF202 GF200	GF200 GF203 GF200 GF203	GF201 GF204 GF203 GF203	GF200 GF202

-1.4869431	-1.3481593 -1.273816	-1.6043529	-2.0271013	-2.0797532	1.61534549	-1.0820533	-1.1570015	1.26878234	-1.0362359 -1.8230301 -1.4080869 1.47515255
511.4869	511.2329 511.2317 511.1777	511.0976 510.9294 510.9197	510.8232 510.5307 510.5269	510.4901	510.3151	510.2886	510.2838	510.2818 510.1553	510.1211 509.9964 509.9413 509.899 509.8832 509.8586
KIAA0073	SCYA15	KLK13 NCOA3	ITIH1 XBP1			HNRPA0	HHARI		PCI M9
Homo sapiens cDNA FLJ20519 fis, clone KAT10365 KIAA0073 protein small inducible cytokine subfamily A (Ovs-Cyts).	member 15 ESTs	ESTS kallikrein 13 nuclear receptor coactivator 3 ESTs	inter-alpha (globulin) inhibitor, H1 polypeptide ESTs X-box binding protein 1	ESTS, Weakly similar to ZFX gene [H.sapiens] Homo sapiens mRNA; cDNA	DKFZp434G0827) heterogeneous nuclear	ribonucleoprotein A0 ariadne, Drosophila, homolog	of Homo sapiens mRNA for	KIAA1162 protein, partial cds ESTs protein C inhibitor (plasminogen activator	inhibitor III) ESTs muscle specific gene ESTs ESTs
Hs.79457 Hs.1191	Hs.272493 Hs.61271	ns.17694 Hs.165296 Hs.225977 Hs.97603	Hs.2777 Hs.11765 Hs.149923	Hs.7542	Hs.49599	Hs.77492	Hs.181461	Hs.169358 Hs.274185	Hs. 76353 Hs. 97127 Hs. 770120 Hs. 72549 Hs. 264065 Hs. 92848
AA131253 Hs.110319 AA018569 Hs.1191	R96668 Hs.20144 AA025538 Hs.61271	A4431571 HS.17894 AA401397 HS.97730 AA156793 HS.108100 AA398163 HS.97603	AA677388 Hs.2777 H85201 Hs.125255 W90128 Hs.103237	AA463267 Hs.7542	AA678190 Hs.49599	AA599176 Hs.77492	AA188416 Hs.28583	AA457223 Hs.91715 N27935 Hs.44007	W86431 Hs.18440 A4448257 Hs.97127 A4487441 Hs.107323 R59335 Hs.12549 A4088231 Hs.91732 W69216 Hs.92848
503505	199663 365738	743113 502333 726747	454822 219963 417867	811737	430837	949934	626300	838639	416567 782826 841348 37814 511117 343737
GF202 GF201	GF200 GF202	GF201 GF202 GF203	GF201 GF203 GF203	GF203	GF203	GF200	GF202	GF202 GF201	GF201 GF202 GF202 GF202 GF200

1,40342415	-2.3792639	-1.332017	-1.1652657 1.02096731	-1.5066816	-1.0210283 -1.2255319 -1.7543329	-1.5320108	-1.1790933
509.775 509.6819 509.6457 509.6315 509.5182 509.5547 509.3557	509,246 509.1654 509.0999	509.0395 508.8632 508.8481 508.7927	508.7523 508.745	508.3787 508.3447	508.2653 508.2545 508.227	508.1859 508.1574	508.1043
ZNF177 CSNK1A1 IL15		KIAA0761 YDD19 PLAB	WRB HBE1	ABCB8		MOV34-34KD ACY1	MPHOSPH10
ESTs zinc finger protein 177 casein kinase 1, alpha 1 ESTs interleukin 15	ESTs, Weakly similar to KIAA0927 protein [H.sapiens] ESTs EST	Homo sapiens cDNA FLJ20507 fis, clone KAT09540 KIAA0761 protein YDD19 protein prostate differentiation factor	tryptophan rich basic protein hemoglobin, epsilon 1 ATP-binding cassette, subfamily B (MDR/TAP), member	8 EST Human mRNA for ankvrin	motif, complete cds ESTs ESTs COP9 subunit 6 (MOV34	homolog, 34 KD) aminoacylase 1 M-phase phosphoprotein 10 (U3 small nucleolar	ribonucleoprotein)
Hs.6659 Hs.10862 Hs.172979 Hs.144477 Hs.30164 Hs.168132	Hs.21837 Hs.187863 Hs.229165	Hs.202955 Hs.93121 Hs.25615 Hs.116577	Hs.117848	Hs.118634 Hs.238672	Hs.73073 Hs.191400 Hs.172870	Hs.15591 Hs.79	Hs.201676
128794 Hs.6659 186587 Hs.10862 1806513 Hs.22556 181944 Hs.301628 100587 Hs.30164 189270 Hs.111867 146943 Hs.44545	H29245 Hs.21837 AA708157 Hs.124883 AA449791 Hs.99226	H20442 Hs.31242 AA406603 Hs.50235 AA778356 Hs.12429 N96311 Hs.109000	"	R89046 Hs.118634 AA702674 Hs.114134	AA431245 Hs.73073 AA004944 Hs.121261 AA088177 Hs.49258	AA992441 Hs.15591 AA402915 Hs.79	AA504113 Hs.28240
49654 274529 280688 282267 149735 289606 243980	52716 460793 785983	172892 753675 505958	758329 739611	167041 448056	782315 428296 488246	1602675 741988	825214
GF201 GF200 GF201 GF201 GF203 GF200	GF201 GF204 GF203	GF201 GF203 GF204	GF200 GF203	GF203 GF204	GF200 GF203 GF202	GF204 GF203	GF200

1.59849768 -1.8175809 -1.6105634 -1.4110865	-1.1950512 1.11567386	-1.0819432	1.18884602 -1.4802944 1.480227 -1.0420381	1.57524307	-1.0814772	1.10192023
508.0709 508.0525 507.9217 507.8922 507.8307	507.8028 507.7468	507.7207 507.5591	507.5041 507.4691 507.38 507.3404	507.3331	507.2001	507.1622 507.045
ARGBP2 YDD19	GNAI1 KIAA0965		SLC4A4		GNA12	SCYE1 DKFZP586J0619
ESTs. Weakly similar to cDNA EST EMB.: T01421 comes from this gene [C-olegans] ESTs Arg/Ab!-interacting protein Arg/Ab!-interacting protein ArgPP2 ESTs YDD19 protein	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 GNA11 KIAA0965 protein KIAA0	ESTs, Weakly similar to adenylate kinase 5 [H.sapiens] ESTs Solute carrier family 4, sodium sicondonals ochoods	productorate contraporter, member 4 EST ESTs ESTs Homo sapiens mRNA; cDNA	DKF2p434G0614 DKF2p434G0614 ESTs, Highly similar to Ras like GTPase [H.sapiens]	guarmer de proteine protein (G protein) small inducible cytokine subfamily E, member 1	certocational monocytes activating) DKFZP586J0619 protein
Hs.82933 Hs.112639 Hs.278626 Hs.25324 Hs.25615	Hs.203862 Hs.184523	Hs.26904	Hs.5462 Hs.28613 Hs.114761 Hs.239283	Hs.39337 Hs.27453	Hs.182874	Hs.146401 Hs.112184
AA488060 Hs.82933 AA609067 Hs.112639 AA142922 Hs.71737 AA463483 Hs.25324 H90893 Hs.82781	AA406420 Hs.1468 AA148542 Hs.21603	AA629801 Hs.11463 N24028 Hs.26904	AA452278 Hs.5462 R66994 Hs.28613 AA017468 Hs.114761 R69677 Hs.29011	H71854 Hs.39337 H24206 Hs.27453	H79130 Hs.94765	AA504333 Hs.77050 AA454689 Hs.104668
840657 AA41 1031285 AA61 505225 AA14 811819 AA44 240960 H908	753215 AA40 491545 AA1	884531 AA6 268818 N240	787938 AA44 140334 R668 361291 AA0 141723 R696	214823 H718 51716 H24	235008 H79	825433 AA5 809674 AA4
GF202 GF202 GF202 GF203 GF203	GF200 GF203	GF203 GF204	GF200 GF200 GF203 GF200	GF200	GF200	GF200 GF201

-1.6618995 -2.5498053 -2.130878	-1.1940883 -2.3138366 -1.6973068	1.51753302		-1.0681659	-1.060338 -2.8625074
506.9681 506.9227 506.7164 506.7133 506.6812 506.6812 506.4132 506.3206	506.2593 506.1851 505.9688 505.9108	505.91 505.8595	505.6364 505.6321 505.602 505.4889 505.4436	505.4294 505.4156 505.3557 505.293	505.2905 505.2614
DYT1 KIAA0166 KIAA1036	JAG1 PAI2 LOC51035	SF3A3	PTPN3	HSPA9B ACTN1	KIAA1034
dystonia 1, torsion (autosomal dominant torsin A) KIAAQ166 gene product ESTs KIAA1036 protein ESTS ESTS ESTS	jagged1 (Alagille syndrome) plasminogen activator initibitor, type II (arginine- sepin) ORF ESTs	splicing factor 3a, subunit 3, 60kD ESTs	protein tyrosine phosphatase, mon-receptor type 3 ESTS ESTS ESTS ESTS ESTS ESTS ESTS EST	[H.sapiens] heat shock 70kD protein 9B (mortalin-2) ESTs	KIAA1034 protein ESTs
Hs. 19261 Hs. 115778 Hs. 15333 Hs. 155182 Hs. 82554 Hs. 191402 Hs. 59509 Hs. 48659	Hs.91143 Hs.75716 Hs.77868 Hs.21417	Hs.77897 Hs.58606	Hs.153932 Hs.124187 Hs.269267 Hs.27772 Hs.183745	Hs.24170 Hs.3069 Hs.19313	Hs.33536
N71095 Hs.9653 AA415708 Hs.115778 AA41890 Hs.3213 WW7810 Hs.31751 N63988 Hs.82554 AA504779 Hs.103283 W93943 Hs.56509 W93943 Hs.56509		R17811 Hs.77897 AA188619 Hs.58606	AA682684 Hs.644 AA03411 Hs.35008 R88764 Hs.34202 N67839 Hs.27172 T61246 Hs.101397	N62372 Hs.24170 AA987644 Hs.3069 W88965 Hs.19313	N49196 Hs.5962 R85509 Hs.33536
299517 588840 768068 417084 289496 825845 357449	141815 70692 155896 26759	31866 626326	461804 430003 195034 291712 77882	290560 1604342 417707	280229 275372
GF201 GF201 GF203 GF201 GF203 GF203	GF201 GF200 GF203 GF203	GF200 GF202	GF201 GF201 GF201 GF201 GF201	GF203 GF204 GF201	GF203 GF203 GF203

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-1.0118375	-2.2717078	-2.0757873 -1.8667383	-1.2891493	-1.0173985		-2.0813403 -1.5361524	1.39144802	-1.228646		-1.2647303	-1.2402747
505.11 505.0603	504.6492	504.4856 504.4856	504.4134	504.3193	504.0446	503.9848 503.9236 503.7513	503.5681	503.3917	503.3527	503.0895	503.0715 502.7419 502.7245
TAF2A CGI-96		GCH1			ARI2	TACC2			NPFF	MCM4	HS1-2 HOXA10
TATA box binding protein (TBP)-associated factor, RNA polymerase II, 4, 250kD CGI-96 protein	ESTs, Highly similar to KIAA0822 protein [H.sapiens] GTP cyclohydrolase 1 (dopa-	responsive dystonia) ESTs Homo sapiens cDNA FLJ10416 fis, clone NT2RP1000111, moderately	similar to COP1 REGULATORY PROTEIN	ESTS, Weanly Similar to ug [R.norvegicus] ariadne-2 (D. melanogaster)	inducible RING finger)	containing protein 2 ESTs	ESTS ESTS ESTE Highly elmilar to	unknown [H.sapiens]	peptide precursor	minichromosome maintenance deficient (S. cerevisiae) 4	protein EST homeo box A10
Hs.1179 Hs.239934	Hs.46909	Hs.86724 Hs.6674	Hs.105737	Hs.29128	Hs.241558	Hs.272023 Hs.90638	Hs.35406 Hs.35406	Hs.88845	Hs.104555	Hs.154443	Hs.99364 Hs.61300 Hs.110637
Hs.79503 Hs.69492	Hs.46909	AA443688 Hs. 86724 N64635 Hs. 6674	AA041406 Hs.105737	AA400074 Hs.29128	AA037810 Hs.95212	AA779380 Hs.90415 W03787 Hs.90638	4A448255 Hs.37902 4A432096 Hs.35406	AA046023 Hs.88845	AA460688 Hs.104555	AA485983 Hs.89699	AA454207 Hs.99364 AA025426 Hs.61300 AA953229 Hs.110637
W05157 R45964	N49215	AA443688 N64635	AA04140	AA40007	AA03781	AA77938 W03787	AA44825 AA43209	AA04602	AA46068	AA48598	AA45420 AA02542 AA95322
299093 35575	280261	783849 289977	376515	742569	375857	459941 297063	782822 784154	488715	796689	843049	795498 365893 1592006
GF200 GF203	GF202	GF200 GF203	GF200	GF202	GF201	GF203 GF200	GF201 GF202	GF202	GF201	GF200	GF200 GF202 GF204

1.29998338		-1.1618416	1.20906764	-1.5341362	000	1.19763769	-1.1062369	-1.7835729	-1.1871037 -1.2016341 -1.5780855
502.7	502.5862	502.5302	502.5246 502.4417	502.437 502.434	200	502.1911	502.0973 501.9897	501.8936	501.6106 501.5577 501.4954
PLGL	RUNX3	NPEPPS	LYN			PSMC2	EIF4B KIAA0171		FUCA1
plasminogen-like	3 aminonantidase nuromycin	sensitive v-ves-1 Yamaguchi sarcoma	viral related oncogene homolog ESTs	Human DIAN sequence from clone RP3-351K20 vo. chromosome 6q22-1-22-33. Contains the gene for a novel croyol protein, the gene for a novel enough to oxAeol food hydratasedehydrogenase type protein, a WWHAZ (tyrosine 5-monoxoggenase).	proteasome (prosome, macropain) 26S subunit,	ATPase, 2 EST eukarvotic translation initiation	factor 4B KIAA0171 gene product	EST ESTs ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	[H.sapiens] fucosidase, alpha-L- 1, tissue ESTs
Hs.262869	Hs.170019	Hs.132243	Hs.80887 Hs.238246	Hs. 239218 Hs. 5510		Hs.61153 Hs.63279	Hs.93379 Hs 155623	Hs.189584	Hs.113613 Hs.576 Hs.14570
Hs.93227	Hs.2536	Hs.16987	RG.12 Hs.29334	Hs.28644 Hs.5510		Hs.61153 Hs.63279	Hs.32533 Hs 78945	Hs.78592	H18428 Hs.113613 N95761 Hs.576 AA625991 Hs.14570
H59201	N67778	AA504109	R83837 AA136664	AA173573 T54527		AA251770 AA056383	N92749 H15458	R40480 H63361	H18428 N95761 AA625991
204208	291478	825200	193913 490959	595420 73659		684655 509463	303152	27816 209296	50883 308437 745495
GF200	GF201	GF203	GF200 GF201	GF202 GF201		GF203 GF202	GF203	GF202 GF200	GF202 GF200 GF203
	204208 H59201 Hs.33227 Hs.262869 plasminogen-like PLGL 502.7	204208 H59201 Hs.33227 Hs.262869 plasminogen-like PLGL 502.7 291478 N67778 Hs.2536 Hs.170019 3 502.5862	204208 H59201 Hs.33227 Hs.262869 plasminogen-like PLGL 502.7 291478 N67778 Hs.2536 Hs.170019 3 aminopeptidase puromycin 502.5862 825200 A4504109 Hs.16987 Hs.132243 sensitive NPEPPS 502.5302 vyves-1 'variation's arroma vyves-1 'variation's arroma NPEPPS 502.5302	204208 H58201 Hs. 262869 plasminogen-like PLGL 502.7 291478 N67778 Hs. 2536 Hs. 170019 aminopeptidase puromyclin actorn FULKZ 502.5862 825200 AA504109 Hs. 16987 Hs. 132243 sansitive vyses 1 Yamaguchi sarcoma 502.5302 193913 R6312 Hs. 80887 homolog LYN 502.5246 490959 AA136664 Hs. 29824 Hs. 238246 ESTs 502.4417	291478 H58201 H5.93227 H5.262869 plasminogen-like PLGL CHCL 291478 N67778 H5.2536 H5.170019 3 aminopeptidase puromycin factor 291478 N67778 H5.2536 H5.170019 3 aminopeptidase puromycin RUNX3 S02.5862 aminopeptidase puromycin NPEPPS 502.5862 sonsitive vital related ornocygene VIAI related ornocygene VIAI related ornocygene VIAI related ornocygene VIAI related ornocygene S02.5302 vital related ornocygene CHCL CHCL VIAI related ornocygene S02.5447 H5.0959 A413664 H5.238246 EST's CHCL CHCL VIAI S0687 homolog chcle R575 CHCL VIAI R6845 H5.238246 EST's CHCL CHCL VIAI R6845 H5.238246 EST's CHCL CHCL VIAI R6845 H5.23824 H5.238246 EST's CHCL CHCL VIAI R6945 H5.23824 H5.238246 EST's CHCL R694 CHING firegery protein, it to gene for a novel chcle chcle viai viai viai related ornocygenes S02.437 F5510 H5.5510 EST's CHCL CHCL VIV. S02.437 EST's CHCL VIAI R6945 H5.5510 EST's CHC	291478 H5.2536 H5.170019 H5.2536 H5.170019 GEGEE	189913 H58201 H5.83227 H5.82889 plasminogen-like PLGL PLGL 502.7	PLGL	183913 HS 2527 HS 25266 HS 170019 Unit-related transcription factor PLGL FUNX3 S02.5962

	-2.4056192	-2.3289141 -1.3807451	-1.7669428	1.29999544	-1.3152126	-2.3534338 -2.1041877		-1.5913912	-1.1196776	-1,4464419		-1.524723	-1.0590/06		
	501.4938	501.2791	501.2735	501.2304	501.1554	501.0955 501.0696		501.028	500.6669	500.6274	500.5727	500.5726	500.4321	500.4012 500.3654	500.3301
	OFIM	SH3BGR NY-REN-57	NDUFA10	IGBP1	MMP12				FPGS		YDD19 XBP1	PSMD5		CNR1 DOCK3	DXS1357E
pre-mRNA cleavage factor Im	(68kD) SH3-binding domain glutamic	acid-rich protein F-box protein Fbx9 NADH dehydrogenase	D) 79A)	12	(macrophage elastase) EST, Highly similar to ubiquitin- conjugating enzyme	[M.musculus] ESTs	ESTs, Highly similar to TRANSCRIPTION INITIATION FACTOR TFIID	135 KD SUBUNIT [H.sapiens]	ESTs folylpolyglutamate synthase	ESTs, Weakly similar to gene	Y DD 19 protein X-box binding protein 1	protessorie (prosorie, macropain) 26S subunit, non- ATPase, 5	EST	cannabinoid receptor 1 (brain) CNR1 dedicator of cyto-kinesis 3 DOCK	accessory proteins BAP31/BAP29
	Hs.64542	Hs.11050	Hs.198271	Hs.3631	Hs.1695	Hs.112647 Hs.30662		Hs.187883	Hs.94133 Hs.754	Hs.15984	Hs.25615 Hs.149923	Hs.193725	Hs.121251	Hs.75110 Hs.7022	Hs.181373
	Hs.64542	N52254 Hs.47438 AA454639 Hs.11050	AA088428 Hs.68840	1 Hs.3631	Hs.1695	AA609134 Hs.112647		4A777696 Hs.121959	Hs.94133 Hs.754	Hs.15984	4A418737 Hs.11426 4A394240 Hs.830	AA113407 Hs.78418	AA757806 Hs.121251	Hs.75110 Hs.7022	AA625628 Hs.79119
	R18985	N52254 AA454639	AA088428	AA463498 Hs.3631	R92994	AA609134		AA777696	N63153 R44864	H96654	AA418737 Hs.114; AA394240 Hs.830	AA113407	AA757806	R20626 R53937	AA625628
	33690	284341	511835	796996	196612	1031363		449270	285261 33478	251826	767844 725968	563403	396186	26295 39922	877832
	GF200	GF200 GF202	GF202	GF200	GF200	GF202		GF203	GF202 GF200	GF202	GF203 GF201	GF200	GF203	GF201 GF201	GF201

	AA410708 Hs.115717	.115717	Hs.111515	トリビじんは、さらことの記念は APPENDIX A DKFZP58611023 protein DKFZP5861102	DKFZP58611023	Atty 500.2629	Atty Docket No. 2172l
422171 Hs.10176 4A432275 Hs.90825 H74165 Hs.93347 N75967 Hs.33264 R11047 Hs.77418	e: e: e: c: √	Hs.101766 Hs.90825 Hs.93347 Hs.33264 Hs.77418	Hs.101766 Hs.90825 Hs.102708 Hs.33264 Hs.111219	protein -1 ESTs DKFZP434A043 protein ESTs	TRAP-1 DKFZP434A043	500.2311 500.2182 500.1026 499.9526 499.9121	2,43738142 1,74197818 -2,1159712
28 23	ω, −.	16875 16875	Hs.87726 Hs.116875	KIAA0154 protein; ADP- ribosylation factor binding protein GGA3 KIAA0156 gene product	KIAA0154 KIAA0156	499.8934 499.8806	1.32093207
AA426092 Hs.98454	ο,	8454	Hs.97411	Human DNA sequence from clone 413H6 on chromosome edges, 29-24, a. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs substry (Drosophila) homolog		499.8755	-1.7257131
AA055440 Hs.88044 R53561 Hs.12363 H54384 Hs.36892 AA005292 Hs.33958	80 + 60 €	3044 2363 3892 3958	Hs.88044 Hs.12363 Hs.36892 Hs.269196	i (alitegoriist or or signaling) ESTs ESTs ESTs	SPRY1	499.8207 499.777 499.7043	-2.0169646
H07878 Hs.9 R37224 Hs.		Hs.92458 Hs.108642	Hs.92458 Hs.108642	G protein-coupled receptor 19 GPR19 ESTs complement component 1	GPR19	499.6209 499.5968	1.1572246 1.16606795
W03794 Hs.5233	42	233	Hs.151242	inhibitor (angioedema, hereditary) EST, Weakly similar to	C1NH	499.4691	-1.1184663
AA777927 Hs.121992	`.;	121992	Hs.121992	CATHEFSIN G FRECONSON [H.sapiens] ESTs, Weakly similar to Pro-		499.3985	
N54993 Hs.		Hs.35755	Hs.35755	[M.musculus]		499.3145	1.6193245

-1.1996855	1.28233175	1.11280248 -1.7289626	-1.4410783	1.15446037	1.60093706 -2.6106596 1.56580921			1.14042604	-1.7491349
499.304	499.2951	499.0257 498.9384 498.9383	498.9043 498.8684	498.7165	498.5659 498.5355 498.4611 498.4507	498.3806	498.2433	498.0675	498.0104 497.9176 497.8937
	HMOX1	CCNC DKFZP586I1023	PSMB8	KPNA2 C4.4A	LATS2 YDD19) ZNF23	RODH		PLOD2 FLJ20746
ESTs	heme oxygenase (decycling) 1 HMOX1 ESTs, Weakly similar to jerky gene product homolog	H.sapiens) cyclin C DKFZP58611023 protein proteasome (prosome, macropain) subunit, beta type,	8 (large multifunctional protease 7) ESTs karvonherin alpha 2 (BAG	GPI-anchored metastasis- associated protein homolog	LATS (large tumor suppressor, Drosophila) homolog 2 YDD19 protein ESTs	zinc finger protein 23 (KOX 16) ZNF23 oxidative 3 alpha hydroxysteroid dehydrogenase: retinol	dehydrogenase Homo sapiens BM-001 mRNA	complete cds procollagen-lysine, 2- oxoglutarate 5-dioxygenase	(lysine hydroxylase) 2 ESTs hypothetical protein
Hs.148093	Hs.202833	Hs.58924 Hs.118442 Hs.111515	Hs.180062 Hs.50955	Hs.159557 Hs.11950	Hs.19074 Hs.25615 Hs.24139 Hs.131870	Hs.22182	Hs.11958	Hs.4859	Hs.41270 Hs.27160 Hs.92374
Hs.57550	Hs.75967	W86853 Hs.58924 AA453231 Hs.30770 AA453170 Hs.23552	AA181300 Hs.1550 N81093 Hs.50955	AA676460 Hs.2397 AA479609 Hs.11950	N64139 Hs.19074 AA406266 Hs.31943 W93847 Hs.24139 H55854 Hs.37203	AA047413 Hs.22182	AA034945 Hs.11958	AA465166 Hs.4859	AA136707 HS.28484 AA424905 HS.27160 H93328 HS.92374
N92955	T71757	W86853 AA453231 AA453170	AA181300 N81093	AA676460 AA479609	N64139 AA40626l W93847 H55854	AA04741:	AA03494	AA46516	AA13670 AA42490 H93328
307741	85259	416361 789318 788087	624360 300512	882510 739578	285736 754594 357396 203434	488107	471641	815047	490995 768217 242037
GF202	GF200	GF201 GF200 GF203	GF202 GF201	GF202 GF203	GF202 GF203 GF201 GF200	GF201	GF201	GF203	GF201 GF203 GF200

-1.353791	-1.5964786 -1.3434393 -1.0333509	-1.7352386 -1.6765381	1.07427068 -1.1538564 1.21922554 -1.5690891	1.22930726 1.22930726 -1.010061	1.18359086	-1.8859895
496.1926 495.9843	495.9478 495.8062 495.6895 495.687	495.6364 495.6083 495.54 495.511	495.3769 495.3769 495.3753	495.1236 495.1236 495.1032	494.9579 494.9113 494.9076 494.8929	494.8414 494.8283
KGNQ1		АЯНGЕF2		NR2F1 NR2F1	AZU1 LOC51324 DKFZP566C134 LOC51248	S100A11 RANBP7
potassium voltage-gated channel. KQT-like subtarnily, member 1 EST Phono sapiens cDNA FLJ20024 fis, clone	ADSE01831 ESTs ESTs ESTs Andrea quentine quelectine	Michael gramme inchessione exchange factor (GEF) 2 ESTs ESTs ESTs ESTs, Weakly similar to IIII MARANINT SO MARANING ENTRY IIII	[H.sapiens] ESTs ESTs ESTs, Highly similar to	geniiiii [Licapheno] nuclear receptor subfamily 2, group F, member 1 group F, member 1 ESTs	azurocidin 1 (cationic antimicrobial protein 37) hypothetical protein DKFZP566C134 protein hypothetical protein	A11 (calgizzarin) RAN binding protein 7
Hs.156115 Hs.203717	Hs.267923 Hs.127128 Hs.125209 Hs.26568	Hs.155120 Hs.269026 Hs.104920 Hs.92202	Hs.51615 Hs.48554 Hs.20289	Hs.144630 Hs.144630 Hs.84507	Hs.72885 Hs.71475 Hs.20237 Hs.11042	Hs.256290 Hs.5151
W93500 Hs.41736 AA127063 Hs.71063	AA49597 Hs.65490 R22003 Hs.127574 AA884755 Hs.125209 R56906 Hs.26568	AA464578 Hs.20948 H95669 Hs.117971 AA431992 Hs.104920 R68581 Hs.92202	T70413 Hs.51615 N62498 Hs.48554 N94198 Hs.20289	AA447 002 NS.39900 AA452909 HS.36082 AA452909 HS.92398 NS9789 HS.84507	AA702802 Hs.72885 AA165403 Hs.71475 AA448164 Hs.99153 AA464192 Hs.11042	N29374 Hs.118740 T61866 Hs.5151
357344 502201	768481 130703 1467293 41321	810567 243024 782231 137890		813586 789049 789049 248599		260181 78695
GF200 GF202	GF203 GF202 GF204 GF202	GF201 GF202 GF202 GF201	GF200 GF202 GF200	GF200 GF200 GF200 GF200	GF201 GF202 GF202 GF201	GF203 GF201

-1.0812453 1.03827201 -1.1906052 -1.2269612	-1.0828522	-1.0081202	-1.8867717	-1.2281908	-1.965683		-1.2865334 1.10557271	-1.9061838	-1.1288956
493.4539 493.2612 493.168 493.1122	492.9287 492.9287	492.9037	492.6622	492.6485	492.5157	492.503	492.3331 492.3149	492.2943 492.206 492.2022 492.1557	492.1444
SPOCK KIAA0670 MLF2				MASP2	SLC21A11	NSMAF	SMARCA3		ZNF265
sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) KIAA0670 protein/acinus EST myeloid leukemia factor 2 ESTs, Weakly similar to The KIAA0191 gene is expressed	ubiquitously. [H.sapiens] ESTs Homo sapiens cDNA FLJ10731 fls. clone	NT2RP3001325 Homo sapiens mRNA for	KIAA1191 protein, partial cds mannan-binding lectin serine	protease 2 solute carrier family 21 (organic anion transporter),	member 11 neutral sphingomyelinase (N- SMase) activation associated	factor SWI/SNF related, matrix associated, actin dependent regulator of chromatin,	subfamily a, member 3 ESTs Homo sapiens cDNA FLJ20156 fis, clone	COL08823 ESTs ESTs ESTs	zinc-finger protein 265
Hs.93029 Hs.227133 Hs.112847 Hs.79026	Hs.157909 Hs.125039	Hs.30738	Hs.8594	Hs.119983	Hs.14805	Hs.78687	Hs.3068 Hs.22917	Hs.12692 Hs.36247 Hs.108785 Hs.184532	Hs.194718
H97788 Hs.113967 H75861 Hs.103456 AA61747 Hs.112847 AA480835 Hs.79026	Hs.106004 Hs.16594	AA490611 Hs.99838	AA293701 Hs.8594	AA706982 Hs.119983	AA707527 Hs.14805	Hs.78687	AA459632 Hs.3068 R44717 Hs.22917	419123 Hs.12692 N74360 Hs.36247 R32951 Hs.62203 AA007615 Hs.107945	Hs.7332
R97788 H75861 AA6217 ² AA4808	R10043 W84716	AA4906	AA2937(AA70698	AA70752	N62766	AA45963 R44717	H19123 N74360 R32951 AA0076	N66014
200144 230562 1030848 810743	128632 415692	824126	725618	431381	1292058	289570	810974 33817	51237 296149 135219 429434	293884
GF202 GF200 GF202 GF200	GF200 GF201	GF203	GF203	GF203	GF203	GF201	GF200 GF202	GF204 GF200 GF200 GF201	GF203

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-1,7452608	-1.2901408 -1.3492288 -1.1519301		-2.0391271 -1.1367301 1.19347836 -2.3326693		1.18724034
492.1184 491.9453 491.9255	491.6878 491.6467 491.5797	491.1828	491.1067 491.1001 491.0822 490.9125 490.7453	490.7275 490.7031	490.6913
RBMS2		MLL2	CANX FLJ20752	CSNKIE	CAMKK2
Homo sapiens clone 24741 mRNA sequence EST RNA binding motif, single stranded interacting protein 2 Homo sapiens clone 24781	mRNA sequence ESTs Homo sapiens cDNA FLJ11350 fis, clone Y79AA1001647	myelotavympholo or mixeo- lineage leukemia 2 ESTS, Highly similar to lin-10 protein homolog IR.noovedicus		Human, DNA sequence from clone 109F14 or chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 6b2 Ribosomal Protein RPL10A gene, and the PPARD for Peroxisome Proliferator casein kinase 1, epsilion	calcium/calmodulin-dependent protein kinase kinase 2, beta
Hs.25770 Hs.25818 Hs.20938	Hs.29024 Hs.233694 Hs.233694	Hs.153638 Hs.55923	Hs.3981 Hs.3981 Hs.39140 Hs.101364 Hs.222340	Hs.203846 Hs.79658	Hs.108708
AA431981 Hs.25770 R51758. Hs.25818 AA456629 Hs.20938	Hs.108112 Hs.29024 Hs.129141	415703 Hs.57016 AA148532 Hs.55923	4A148532 Ts.:5952 4A010619 Hs.16446 4A418555 Hs.:3914 AA165348 Hs.:39140 AA190629 Hs.101364 R09747 Hs.113197	AA150053 Hs.72152 AA669272 Hs.79658	AA491295 Hs.27355
AA431981 R51758 . AA456629	N74911 R92034 N26486	H15703	AA 148532 AA010619 AA418569 AA190629 R09747	AA15005.	AA49129
782222 38931 809585	295473 195313 266218	49311	491527 430336 767347 593239 627118	504543 854138	824643
GF201 GF203 GF201	GF203 GF203 GF203	GF201	GF201 GF203 GF202 GF202 GF202 GF202	GF201 GF201	GF203

	-1.221226	-1.1201789			1.02445039	-1.2749504	1.0017936	1.15482601 -1.156271	-1.188261	-1.1548576	1.02848109	-1.7990915 -1.7964274
•	490.6691 490.6382	490.5992 490.3569	490.2778	490.2576	490.1905 490.1823	490.154	490.0323	489.9619 489.9244	489.8902	489.8337	489.4469	489.4377 489.2479
		TRAM	FPGT	SLC25A11	CEBPG		KIAA0153	FYN A		TP53BPL		
APPENDIX A	ESTs ESTs	translocating chain-associating membrane protein EST	fucose-1-phosphate guanylyltransferase solute carrier family 25 (mitochondrial carrier;	oxoglutarate carrier), member 11 CCAAT/enhancer binding	protein (C/EBP), gamma EST	FLJ11227 fis, clone PLACE1008309 ESTs	KIAA0153 protein FYN oncogene related to	SRC, FGR, YES protein "A"	ESTs, Weakly similar to ORF YGR021w [S.cerevisiae]	protein	ESTs, Weakly similar to coded for by C. elegans cDNA CEESW58F [C.elegans] Hono sanians mBNA for	cytochrome b5, partial cds ESTs
	Hs.43145 Hs.237520	Hs.4147 Hs.195499	Hs.150926	Hs.184877	Hs.2227 Hs.98448	Hs.45080 Hs.72465	Hs.82563	Hs.169370 Hs.86122	Hs.174134	Hs.179982	Hs.28436	Hs.31086 Hs.104093
	S Hs.43145 Hs.48814	AA452556 Hs.4147 AA679067 Hs.117155	Hs.12299	AA670357 Hs.3816	AA676804 Hs.2227 AA426068 Hs.98448	N49852 Hs.45080 A4164630 Hs.72465	Hs.82563	H91826 Hs.75390 AA479981 Hs.86122	AA434454 Hs.103750	AA628154 Hs.87537	Hs.28436	H73591 Hs.129901 AA194143 Hs.104093
	W61236 N63529	AA4525 AA6790	R38619	AA6703	AA6768 AA4260	N49852 AA16463	R44546	H91826 AA47998	AA4344	AA6281	R63782	H73591 AA1941
	342232 278168	788493 383619	22883	878413	455121 757240	282498	34106	221172 754031	770319	1055753	139331	214443 665620
	GF201 GF202	GF200 GF203	GF201	GF201	GF201 GF202	GF201 GF202	GF200	GF200 GF200	GF203	GF203	GF200	GF202 GF203

-1.2400906 1.14254426 -1.6073256	-1.169/008	1.14110887	1.16905454	-2.3652362	-1.1298572	-1.2830111	-1.4967755 1.19240937		1.6891966	-1.8251833	-1.5507612
489.1935 489.1361 489.1159 489.0563 489.0507 489.0149	488.9748 488.9112	488.8313	488.7679 488.7108	488.5994	488.5735	488.5251	488.4738 488.4138		488.3915	488.3735	488.2956
TGFA DKFZP564A043	AWA.	MAPK8IP1					VAMP4		GBE1	SPRR1B	PSMB7
transforming growth factor, alpha DKFZP564A043 protein ESTs ESTs ESTs ESTs vitamin A responsive;	cytoskeleton related ESTs, Weakly similar to coded for by C. elegans cDNA	CLEGWOOI (Coeregrans) mitogen-activated protein kinase 8 interacting protein 1 Homo sapiens mRNA; CDNA DKFZ0761 B101 (from cione	DKFZp761B101) ESTs	ESTS	ESTs	ESTs vesicle-associated membrane	protein 4 ESTs	glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme, Andersen disease, glycogen storage disease type	IV) small proline-rich protein 1B	(cornifin) proteasome (prosome,	7
Hs. 170009 Hs. 169329 Hs. 50925 Hs. 94292 Hs. 21116 Hs. 260860	Hs.92384	ns.234249 Hs.234249	Hs.235390 Hs.50745	Hs.47402	HS.47566 Hs.191721	Hs.119143	Hs.102664 Hs.114198		Hs.1691	Hs.1076	Hs.118065
23 23	R78725 Hs.92384		AA757678 Hs.121240 N78661 Hs 50745		N45083 HS.47566 AA486273 Hs.100472	AA398074 Hs.119143	AA448191 Hs.99160 H66629 Hs.114198		R09069 Hs.1691	AA447835 Hs.1076	AA002063 Hs.118065
1553998 730361 1493137 297178 26460	144977	31918	395573	282481	243700 840837	726527	782791 229601		127509	813614	428043
GF204 GF202 GF204 GF200 GF201	GF200	GF202	GF204	GF202	GF200 GF202	GF203	GF202 GF202		GF200	GF200	GF203

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-1.1448922 1.38577711	1.02843097	1.02843097	1.08150812	-1.1671415 1.17525243		-1.8659172	1.08260609	1.10418839 -1.8773638 -1.1776066	-1.1627101	-2.0023431 1.10187105	-1.2368597
488.177 488.1465	488.0034	488.0034	487.9617	487.9305 487.722	487.7177	487.6281 487.6148	487.5903	487.4369 487.2174 487.1597 487.0392	486.899	486.7656 486.6884	486.5428 486.3927
	SKI	SKI				KIAA0014	DCT	SSP29		BAG2	
ESTs EST	v-ski avian sarcoma viral oncogene homolog v-ski avian sarcoma viral	oncogene homolog ESTs. Weakly similar to tro	[R.norvegicus] ESTs, Weakly similar to hynothetical protein 2	[H.sapiens] ESTs	Homo sapiens glucocorticoid receptor AF-1 coactivator-1 mRNA, partial cds Homo sapiens mRNA; cDNA	DKFZp586J0720 (from clone DKFZp586J0720) KIAA0014 gene product	dopachrome tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) ESTs, Weakly similar to	/prediction ESTs acidic protein rich in leucines ESTs	ESTs, Weakly similar to putative [C.elegans] BCL2-associated athanogene	2 ESTs ESTs Highly similar to hook1	protein [H.sapiens] ESTs
Hs.42646 Hs.41919	Hs.2969	Hs.2969	Hs.8982	Hs.5291 Hs.19631	Hs.7367	Hs.169694 Hs.155650	Hs.240217	Hs.17230 Hs.112910 Hs.84264 Hs.190368	Hs.6820	Hs.55220 Hs.201591	Hs.167642 Hs.125029
3 Hs.42646 8 Hs.41919	71 RG.45	71 Hs.2969	AA026709 Hs.77735	AA430677 Hs.5291 R08297 Hs.19631	AA431887 Hs.7367	T97843 Hs.18152 AA292382 Hs.89869	AA478553 Hs.472	AA057742 Hs.17230 AA620817 Hs.112910 AA489201 Hs.84264 AA702795 Hs.118031	7 Hs.6820	AA418744 Hs.55220 N45282 Hs.17413	AA159497 Hs.65609 N68594 Hs.38228
H99213 H93608	W69471	W69471	AA026	AA4306 R08297	AA431		AA478		N95657	AA418744 N45282	
261841 242779	343646	343646	366580	770430 127243	773639	121898 725927	753104	510575 1055533 825013 448017	293977	768008 283196	592403 294136
GF202 GF200	GF200	GF200	GF200	GF203 GF200	GF201	GF200 GF201	GF200	GF202 GF202 GF200 GF200	GF200	GF203 GF203	GF202 GF201

Atty Docket No. 21 /26/9	-1.24976	-1.2670229	-1.6634741		1.00055934	-1.0892206		-1.0657447				-1.8603487			-1.2604586	-1.2244631			-2.6571173	-1.0511687	-1.0812877	-1.1908941				1.46384093	1.14587629		-1.9174995		-1.1986189	1.20148719	1.11247801	
Atty	486.294	486.162	486.0091	485.9434	485.7517	485.715	485.658	485.321			485.3165	485.3065			485.2951	485.2741	485.0976		485.0883	485.0809	485.0665	484.9267			484.853	484.846	484.4514	484.4249	484.3983		484.3643	484.3148	484.3143	
	FLJ10404	IMOGN38		NSAP1	CCNB2			DKFZP586I1023			TCF12				PSMA5					ZNF238						KIAA0317					PES1		FUBP3	
APPENDIX A	hypothetical protein	Imogen 38	ESTs	NS1-associated protein 1	cyclin B2	ESTs	ESTs	DKFZP58611023 protein	transcription factor 12 (HTF4,	helix-loop-helix transcription	factors 4)	ESTs	proteasome (prosome,	macropain) subunit, alpha	type, 5	ESTs	ESTs	ESTs, Weakly similar to CGI-	82 protein [H.sapiens]	zinc finger protein 238	ESTs	EST	ESTs, Weakly similar to PTB-	ASSOCIATED SPLICING	FACTOR [H.sapiens]	KIAA0317 gene product	ESTs	ESTs	ESTs	pescadillo (zebrafish) homolog	1, containing BRCT domain	EST far unstream element (FUSE)	binding protein 3	
	Hs.111279	Hs.154655	Hs.269619	Hs.155489	Hs.194698	Hs.64193	Hs.106397	Hs.111515			Hs.21704	Hs.26173			Hs.76913	Hs.110771	Hs.9012		Hs.178617	Hs.69997	Hs.31189	Hs.114033			Hs.28794	Hs.20126	Hs.6879	Hs.22590	Hs.58885		Hs.13501	Hs.48621	Hs.153636	
	Hs.111279	Hs.13335	AA701026 Hs.121068	4A142968 Hs.31730	AA774665 Hs.20483	4A704222 Hs.64193	4A460707 Hs.106397	AA401305 Hs.23257			Hs.102382				4A598815 Hs.76913	AA188789 Hs.110771	AA460171 Hs.34817		4A48884 Hs.76089	Hs.69997	AA425723 Hs.31189	AA701008 Hs.114033			AA044814 Hs.107257	AA496541 Hs.20126	4	Hs.91731	3 Hs.58885			Hs.48621	7 Hs.31867	
	W84558	R51362	AA7010	AA1429	AA7746	AA7042	AA4607	AA4013			H98856	R41943			AA5988	AA1887	AA4601		AA4888	R79722	AA4257	AA7010			AA0448	AA4965	AA1813	R43972	W86728		R13806	N62745	W07367	
ketal.	356707	39313	397575	504661	856289	450515	796730	743136			261836	31225			897952	626208	795901		824873	146081	773375	397268			488584	755891	624390	33523	416754		26578	289513	300482	
Westbrook et al.	GF200	GF202	GF203	GF201	GF203	GF203	GF204	GF202			GF201	GF203			GF200	GF202	GF201		GF203	GF200	GF202	GF203			GF201	GF200	GF202	GF201	GF202		GF200	GF202	GF200	

-2.0406267 -1.1603657	1.17560209	-1.5012555 -1.2274347 -1.7997521 1.03538043 -1.8310507	-1.0706859	-1.9708282
484.2756 484.265 484.265 484.2134 484.11644	484.0902 483.8999 483.8991 483.8942	483.8001 483.4122 483.231 483.1814	483.1357 482.9687 482.7246 482.7062	482.5255
IFITM1 SIAH1	GTF2H2 YDD19 CCT8	SIGMA1B		
Homo sapiens cDNA FL_20699 fis, clone KAIA2372 ESTS ESTS interferon induced interferon induced Tansmembrane protein 1 (9- 27) seven in absentia (Drosophila) homolog 1	general transcription factor III+, polypeptide 2 (44kD subunit) ESTs YDD19 protein chaperonin containing TCP1, subunit 8 (freats) admin-related protein admin-related protein	complex 1, sigma 2 subunit ESTs ESTs ESTs ESTs ESTs ESTs wheakly similar to coded for by C. elegans cDNA yk157/8.5 [C.elegans]	ESTs, Weakly similar to similar to Yeast hypothetical protein YEY6 like [C.elegans] ESTs ESTs ESTs, Moderately similar to PMSs homolog mismatch repair protein [H.sapiens]	Homo sapiens mKNA for KIAA1376 protein, partial cds
Hs.15125 Hs.191618 Hs.56044 Hs.146360 Hs.184081	Hs.191356 Hs.33106 Hs.25615 Hs.15071	Hs. 40368 Hs. 247277 Hs. 192895 Hs. 177398 Hs. 9265	Hs.15760 Hs.31433 Hs.260903 Hs.63163	Hs.24684
AA459420 Hs.15125 AA435984 Hs.98854 W49670 Hs.56044 AA419251 Hs.118548 T71889 Hs.100721	W72437 Hs.88919 W74802 Hs.33106 R59470 Hs.106695 AA630016 Hs.84021	AA453805 Hs.40368 AA054643 Hs.40876 AA483200 Hs.9984 H72914 Hs.39407 W86823 Hs.9265	AA401345 Hs.15760 AA488282 Hs.31433 R16566 Hs.22036 AA055179 Hs.63163	R33609 Hs.24684
810981 730730 324897 755599 85320	345525 345081 37821 884690	813756 381036 796885 214136 416436	742565 897296 129629 377217	135900
GF201 GF202 GF202 GF201 GF201	GF201 GF201 GF203 GF201	GF202 GF203 GF202 GF200 GF200	GF201 GF202 GF203 GF201	GF203

unknown orf, len 451, CAI: ESTs, Weakly similar to 0,14, some similarity to B38637 ras inhibitor

1.23699334 -1.4106573 -1,9196785 1.97584871 -2.0863606

481.0476

TRIO PP1 OA1 ESTs, Highly similar to CGI-07 ocular albinism 1 (Nettleshipodk inhibitor p21 binding O-type cyclin-interacting riple functional domain Homo sapiens cDNA PTPRF interacting) FLJ10276 fis, clone protein [H.sapiens] HEMBB1001182 S.cerevisiae] protein 1 STS **ESTs** ESTS Falls) TS 4s.104685 4s.181022 Hs.171957 Hs.59236 Hs.12947 Hs.49204 Hs.36794 4s.74124 4s.60171 W81124 Hs.108340 AA398261 Hs.104685 AA437140 Hs.59236 Hs.12947 Hs.49204 AA452873 Hs.36794 AA007299 Hs.82218 AA489210 Hs.23752 AA865729 Hs.74124 AA005039 Hs.60171 Hs.6937 V69677 T66813 **V66472** 469234 726697 788580 285636 825031 428901 757383 429234 415437 43654 36315 GF202 GF202 GF202 GF201 GF202 GF202 GF203 GF201 GF203 GF203

1.17728783

480.8163

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481.0406 481.0207 480.8565 1.65345684 -1.3538046

-1.2388041

1.48623847

-1.8411371

479.7677 479,6364 479,5981

-1.0444364 -1.5718372 -1,6867455

479,8009 480.7415 180.6895 180.4612 180.3297 480.1173 180.5508 180.5494 HYAL1 T0K-1 nembrane protein)-associated hyaluronoglucosaminidase 1 VAMP (vesicle-associated protein B and C protein Hs.171835 Hs.182625 4s.75619

CUGBP2 **GLRA3** glycine receptor, alpha 3 CUG triplet repeat, RNAbinding protein 2 ESTS ESTs STS STS STS 4s.122139 4s.112689 4s.211610 4s.167742 4s.102480 4s.99807 Hs.7094

AA780080 Hs.122139 4A609323 Hs.112689

1033710 824913 1031583

810391

GF200

796640

3F202 3F203 3F203 3F201

AA489023 Hs.99807 4A461464 Hs.5005

4A464791 Hs.75619

2.44543334 -1.2270229 -1.3384691 -1.6829273 479.4784 479.3838 479.3278 179.2812

STS

4s.104415

Hs.111833 Hs.102480 AA262235 Hs.104415

T84491

111426

Hs.7094

H29032

52802

GF202 GF204 GF203 GF200 GF203

AA283885 Hs.89247

H78433

234537

700668 28322

R11532

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Westbrook et al.

-2.685264	1.04402074 -1.0360239	1.06726999	-1.3256601		1.00499817 1.09906782		-2.0652247 1.10093763		-1.4373612	-1.3622441 -1.9770198 -1.0666466 -1.7086097 -1.3858419
479.2093	479.1564 478.8051	478.6049 478.3329	478.2993	478.1705	478.1629 477.9511 477.9364		477.6702 477.6348	477.6252	477.5023	477.4924 477.4923 477.4677 477.3804 477.3018
	NDUFS6	CSPG6	SRP19	H1F0	AKAP11				DVL3	INPPL1
ESTs, Moderately similar to Su(var)3-9 homolog [H.sapiens] NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13k)) (NADH-coenzwne 0	reductase) ESTs	chondroitin sulfate proteoglycan 6 (bamacan) ESTs	signal recognition particle 19kD	H1 histone family, member 0 A kinase (PRKA) anchor	protein 11 ESTs EST	Homo sapiens cDNA FLJ11018 fis, clone PLACE1003602, highly similar to Homo sapiens mRNA	expressed in placenta expressed in placenta ESTs ESTs, Moderately similar to proliferation potential-related	protein [M.musculus] dishevelled 3 (homologous to	Drosophila dsh) inositol polyphosphate	phosphatase-like 1 ESTs EST ESTs
Hs.252835	Hs.49767 Hs.233650	Hs.24485 Hs.185946	Hs.2943	Hs.226117	Hs.232076 Hs.191118 Hs.47247		Hs.56851 Hs.17589	Hs.91065	Hs.174044	Hs.75339 Hs.268936 Hs.73601 Hs.62905 Hs.26714
AA417344 Hs.98220	AA176453 Hs.49767 R88680 Hs.130852	6	AA411407 Hs.2943		T61647 Hs.7914 T80834 Hs.13959 N51388 Hs.47247		AA424545 Hs.56851 W88952 Hs.17589	W73001 Hs.91065	AA700736 Hs.83558	AA279072 Hs.75339 H58453 Hs.117803 AA179392 Hs.73601 AA460708 Hs.62905 AA495918 Hs.26714
731168	611467	328567 448267	754998	343744	78144 109279 283237		767136 417409	344949	435341	703964 206370 612613 796732 768448
GF202	GF202 GF203	GF202 GF204	GF200	GF201	GF201 GF200	}	GF202 GF202	GF204	GF203	GF200 GF203 GF202 GF202 GF203

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-1.0283944	-1.2493146 1.34976475 -1.6608422 1.06804979	-1.3916887	-1.7016519 -1.2376852 -1.2270164	-1.3306876	-1.4463807	1.2173727 -1.2732445 1.190323
477.2873	477.1536 477.123 476.6301 476.5856 476.4818 476.46	476.3699 476.3212 476.2632	476.263 476.2328 476.1514	476.0777 475.8567 475.8235	475.8231	475.7455 475.7196 475.662
AGXT	CGR19 SRM OSBP KIA0182 PIM1	IL13RA2 KIAA0952 ALDH5	DKFZP586I1023 KIAA0562	CREBL2 RALGDS TNFSF13		DKFZP564E1962
alanine-glyoxylate aminotransferase (oxalosis I; hyperoxaluria I; glycoltaciduria; serine- pyruvate aminotransferase) cell growth regulatory with ring	finger domain sypermidine synthase oxysterol binding protein KIA40182 protein ESTs pim-1 oncogene	interleukin 13 receptor, alpha 2 IL13RA2 KIAA0952 protein KIAA095 aldehyde dehydrogenase 5 ALDH5 ESTs Waakh eimilar to	Core, weavy similar to Knockout [D.melanogaster] DKFZP58611023 protein KIA40562 gene product cAMP responsive element	binding protein-like 2 ral guanine nucleotide dissociation stimulator tumor necrosis factor (ligand) superfamily, member 13	Homo sapiens clone 24987 mRNA sequence ESTs, Moderately similar to p53 regulated PA26-T2 nuclear protein [H.sapiens]	ESTs ESTs, Weakly similar to ORF2 [M.musculus] DKFZP564E1962 protein
Hs.144567	Hs.59106 Hs.76244 Hs.24734 Hs.75909 Hs.87518 Hs.81170 Hs.193783	Hs.25954 Hs.7935 Hs.169517	Hs.37636 Hs.111515 Hs.200595	Hs.13313 Hs.106185 Hs.54673	Hs.239340 Hs.8026	Hs.174310 Hs.167634 Hs.24766
Hs.81554	AA676705 Hs.59106 AA689545 Hs.76244 AA012888 Hs.24734 405563 Hs.75909 AA418721 Hs.87518 AA099404 Hs.69307 AA431968 Hs.97322	R52796 Hs.25954 AA454990 Hs.7935 R93551 Hs.35149	AA452877 Hs.37636 R44346 Hs.106548 AA678196 Hs.118401	N53406 Hs.109313 H19201 Hs.106185 AA041396 Hs.106215	H65078 Hs.81495 AA454079 Hs.106805	H19804 Hs.46797 H84915 Hs.40747 AA173189 Hs.24766
N57872	AA676705 AA669545 AA012838 H05563 AA418721 AA099404 AA431968	R52796 AA45499 R93551	AA45287 R44346 AA67819	N53406 H19201 AA04139	H65078 AA45407	H19804 H84915 AA173189
247117	455025 856796 360245 43977 767795 489663	41648 811918 197657	788575 34294 430848	284076 50887 376475	210599	172817 249517 595695
GF200	GF201 GF201 GF200 GF200 GF203 GF202	GF201 GF203 GF203	GF203 GF202 GF203	GF203 GF203 GF201	GF201 GF203	GF203 GF203 GF202

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1.74944755	-1.7384345 -1.28058 1.35288901	-1.255758	-1.4868222 1.43768367	-1.4472348 1.16367205 -1.3871532		-1.1439592	1.28373715
475.6356	475.5623 475.5247 475.5085 475.396	475.2544	475.0924 475.049 475.0196	474.9052 474.8415 474.7599	474.7447 474.6738 474.5508	474.5032 474.4793 474.2116	474.1275 474.1202 474.065
	ADAM12 KIAA0260	SAP30	ELAVL1 DKFZP4340125	S.) KIAA0566	KATNB1	13CDNA73
ESTs a disintegrin and metalloproteinase domain 12	(metrin alpha) EST EST KIAA0260 protein	ESTs, Highly similar to CAMPATH-1 ANTIGEN PRECURSOR [H.sapiens] sin3-associated polypeptide, 30kD	ELAV (embryonic lethal, abnormal vision, Drosophila)- like 1 (Hu antigen R) DKFZP4340125 protein ESTs	Homo sapiens cDNA FLJ20502 fis, clone KAT09323 ESTs ESTs	ATPase type IV, phospholipid transporting (P-type) (putative) KIAA0566 ESTs ESTs tests and AMDAA.	containing) subunit B 1 EST EST	ESTS putative gene product ESTs
Hs.9250	Hs.8850 Hs.86241 Hs.157922 Hs.82635	Hs.108338 Hs.20985	Hs.12379 Hs.102669 Hs.21868	Hs.23956 Hs.269577 Hs.269535	Hs.44697 Hs.106137 Hs.118321	Hs.275675 Hs.262966 Hs.112695	Hs.194152 Hs.181304 Hs.268838
T50974 Hs.9250	AA099554 Hs.8850 AA206311 Hs.86241 H80847 Hs.102252 W16916 Hs.82635	T87077 Hs.108338 AA126982 Hs.90852	W72322 Hs.12379 H79705 Hs.102669 R55658 Hs.21868	AA459255 Hs.23956 AA704548 Hs.121041 AA700687 Hs.124100	N35112 Hs.44697 AA115761 Hs.106137 W81290 Hs.58543	96 5	N80384 HS.82698 W58342 Hs.12817 R88915 Hs.34216
76585	489755 647679 230316 301380	115292	345208 240208 40277	814455 451150 434966	271737 490718 347520	810697 46131 743415	292559 341654 195387
GF202	GF203 GF203 GF201 GF200	GF200 GF201	GF200 GF200 GF201	GF203 GF203 GF203	GF201 GF201 GF201	GF201 GF202 GF202	GF200 GF201 GF200

1.30340262	-1,1684298 -2.0146626	-1.0047309 -2.5033682 -1.39838 -1.0742635	1.17030234 -1.3252101 -1.3236858
473.9329	473.884 473.6181 473.6161 473.558	473.1642 473.1455 472.996 472.897 472.8433 472.8136 472.7661	472.7582 472.7129 472.6754 472.616 472.4971
	несн	GDI1 LOC51663 ST3GALVI	SURB7 HSD17B4 DKFZP727C091
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	heterochromatin-like protein 1 HECH ESTs EST EST DKF2434A2410 (from clone DKF2494A2410 (from clone DKF24943A2410); partial cost ESTs, Weady similar to ZINC FINGER PROTEIN 135 [H.sapiens]	ESTs, Weakly similar to KIAA0822 protein [H-saplens] ESTs ESTS GDP dissociation inhibitor 1 M-phase phosphoprotein homolog ESTs alpha2,3-sialyfiransferase	SRB7 (suppressor of RNA polymerase B, yeast) homolog SURB7 ESTs ESTs hydroxyseroid (17-beta) dehydrogense 4 DKFZP7C091 protein DKFZP
Hs.94149	Hs.278554 Hs.192943 Hs.90459 Hs.25897 Hs.23019	Hs.108677 Hs.15140 Hs.19525 Hs.74576 Hs.173518 Hs.5301 Hs.34578	Hs.250855 Hs.25557 Hs.192223 Hs.75441 Hs.43141
Hs.94149	Hs.103153 Hs.62818 Hs.90459 Hs.106424 Hs.23019	H91281 Hs.108677 N72705 Hs.15140 A4466228 Hs.19525 A4488661 Hs.74576 F50389 Hs.110221 T58434 Hs.5301 N32285 Hs.34578	AA130736 Hs.6967 AA059477 Hs.25557 AA707094 Hs.68835 AA488029 Hs.75441 H15570 Hs.28835 AA010328 Hs.39379
N94143	W69106 N20820 T40760 R52161 H17016	H91281 N72705 AA465228 AA488681 T50389 T58434 N32295	AA130736 AA058477 AA707099 AA488029 H15570 AA010328
293564	343490 265114 61112 154323 50571	241392 295713 814224 843110 72666 75650 272706	567265 489373 451616 840606 49505 430192
GF200	GF201 GF201 GF202 GF200	GF200 GF203 GF203 GF200 GF201 GF201	GF200 GF201 GF203 GF200 GF204 GF201

		-1.5174875	-1.4985473		-1.5486404	-1.0231407	-1.5406952								-1.265743		-1.265/43				1.30815365			1.04821269	-1.1508635	1.14789725	-2.1018124		1 9230077	1,56555.1-		-2.0426/18
		472.1628	472.1169	472.0553	472.0448	471.9504	471.9263						471.8126		471.7942		471.7942		,	471.7825	471.6616			471.6324	471.6279	471.3114	471.0257		470 0000	47.0.3333		470.9264
٠		CSF1R	DKFZP566A0946		HSS	KIAA0551					L				PTGER4		PTGER4								PIM1							99
colony stimulating factor 1	feline sarcoma viral (v-fms)	oncogene homolog	DKFZP566A0946 protein	ESTs	sperm surface protein	KIAA0551 protein	ESTs	ESTs, Weakly similar to	similar to C.elegans	hypothetical protein	CET01H8.1, CEC05C12.3, CEF	54D1.5. similar to trp and trp-	like proteins [H.sapiens]	prostaglandin E receptor 4	(subtype EP4)	prostaglandin E receptor 4	(subtype EP4)	ESTs, Weakly similar to	hypothetical protein	[H.sapiens]	ESTs	ESTs, Highly similar to	proteine kinase JNK2 alpha1	[H.sapiens]	pim-1 oncogene	EST	ESTs	Homo sapiens mRNA; cDNA	DNFZp36611420 (IIOIII CIOIIE	UKFZp58611420); parilal cds	Homo sapiens cDNA	FLJ20523 fis, clone KAT10456
		Hs.174142	Hs.78006	Hs.100748	Hs.129872	Hs.170204	Hs.109528						Hs.13322		Hs.199248		Hs.199248			Hs.269211	Hs.33856			Hs.246857	Hs.81170	Hs.113960	Hs.182382			Hs.112423		Hs.193326
		RG.13	Hs.91756	AA005108 Hs.100748	Hs.129872	Hs.25771	4A176867 Hs.109528						AA644080 Hs.13322		AA019996 Hs.109641		3 Hs.980			Hs.33688	Hs.33856			Hs.115528	AA873152 Hs.58512	Hs.113960	AA625563 Hs.15526			Hs.112423		AA434090 Hs.93841
		R92609	R45114	AA005108	N66167	N25621	AA17686						AA644080		AA01999(AA019996 Hs.980			N22486	H52739			R20616	AA87315	R95893	AA62556			R09815		AA43409
		196282	34901	429165	278556	267816	609155						845352		363569		363569			254229	179878			26185	1472698	199285	745273			128208		837908
		GF200	GF203	GF201	GF203	GF203	GF202						GF204		GF200		GF200			GF201	GF203			GF203	GF203	GF203	GF203			GF200		GF202

Atty Docket No. 21726	Domer No. 2 17 24	-1.6543387	-1.2406389	-1.5313519	-1.5313519		1.11898356	1.15927881			1.1100421		!	-1.8375017	-1.2569131		-1.852429			1.31491459	-1.3653595	-1.5214657	-1.5914971			-1.0809731	1.6356919		-1.2637557		-1.1148411	-2.1896192	-1.1296352		-1.1401205	
Δthν	Św.	470.8978	470.8245	470.7282	470.7282		470.5976	470.5908	470.5229	470.4312	470.3971			470.396	470.3656	470.346	470.3004			470.1485	470.1294	469.8208	469.803	469.7249		469.6902	469.5611		469.5372		469.5065	469.4242	469.422		469.255	
hand word these shoes dard langs family hand		FLJ20273		FKBP5	FKBP5		PP15	DKFZP564M182	KIAA0579	ZNF220				NDUFA10		SH3D1B				SLC2A3						AVPR1A			IDH3G		USP13	CDZZ	UBL3		PROSC	
Hand there there fould that the	APPENDIX A	hypothetical protein	ESTs	FK506-binding protein 5	FK506-binding protein 5	nuclear transport factor 2	(placental protein 15)	DKFZP564M182 protein	KIAA0579 protein	zinc finger protein 220	ESTs	NADH dehydrogenase	(ubiquinone) 1 alpha	subcomplex, 10 (42kD)	ESTs	SH3 domain protein 1B	ESTs	solute carrier family 2	(facilitated glucose	transporter), member 3	ESTs	ESTs	ESTs	ESTs	arginine vasopressin receptor	14	ESTs	isocitrate dehydrogenase 3	(NAD+) gamma	ubiquitin specific protease 13	(isopeptidase T-3)	CD22 antigen	ubiquitin-like 3	proline synthetase co- transcribed (bacterial	homolog)	
		Hs.95549	Hs.191343	Hs.7557	Hs.7557		Hs.151734	Hs.20760	Hs.81505	Hs.82210	Hs.269210			Hs.198271	Hs.109381	Hs.46571	Hs.269388			Hs.7594	Hs.191967	Hs.72815	Hs.191925	Hs.37890		Hs.2131	Hs.55896		Hs.75253		Hs.85482	Hs.171763	Hs.173091		Hs.210749	
		Hs.23305	_	_	_		Hs.82337	5	Hs.43669	0	Hs.28478			Hs.40893	Hs.109381	Hs.46571	AA490483 Hs.109067			AA406551 Hs.7594	4A706824 Hs.120952	4A169606 Hs.72815	AA778756 Hs.115322	Hs.37890		AA448190 Hs.2131	AA152351 Hs.55896		AA459380 Hs.75253		4A211448 Hs.85482	V53534 Hs.51170	4A151852 Hs.22990		AA486104 Hs.100624	
		W37780	N33229	W86653	W86653		N75595	AA4642	N35383	AA1016	R64066			N72263	R07196	N45979	AA4904			AA4065	AA7068	AA1696	AA7787	W80741		AA4481	AA1523		AA4593		AA2114	N53534	AA1518		AA4861	
	retal.	322192	270537	416833	416833		299388	810140	272073	490482	140000			291341	126847	277627	823881			753467	451816	594266	452512	415619		782789	504810		810942		613126	284220	566339		840808	
	Westbrook et al.	GF203	GF203	GF200	GF200		GF200	GF202	GF201	GF201	GF200			GF203	GF203	GF201	GF203			GF200	GF203	GF202	GF203	GF201		GF200	GF202		GF200		GF200	GF203	GF202		GF202	

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	-1.6814025 -1.2118413	1.03091901		-1.2535819	-1.3656214	-1.0023546	-2.1533207 -1.1844377 -1.8171393 -2.7550046	-1.1742463
469.2242	469.0743 468.9631	468.9498 468.8196		468.665 468.6347	468.5753 468.5533	468.5358	468.516 468.312 468.2139 468.2021	468.0619 467.942
SPTA1	SLC22A4 LOC51778	EIF4B				TYR	PRKAR2A GS2NA RXRB	
spectrin, alpha, erythrocytic 1 (elliptocytosis 2) solute carrier family 22	(organic cation transporter), member 4 muscle-specific protein	eukaryonic transiation initiation factor 4B ESTs	Human DNA sequence from clone RP4-588C11 on chromosome 20th 1.21-11.23. Confains the CST7 gene for confains the CST7 gene for solventin F (leukocystatin), the gene for a novel protein similar to worm, plant and thy probeins, and the 3 end of the gene for a novel AMR-bindine arryme	simil ESTs ESTs Moderataly similar to	PFT27 [M.musculus] ESTs	albinism IA) protein kinase, cAMP-	uepeniueni, regulauny, type ni, alpha nuclear autoantigen retinoid X receptor, beta ESTs	ESTs, Weakly similar to acetyl- CoA carboxylase [H.sapiens] EST
Hs.1985	Hs.77239 Hs.42346	Hs.93379 Hs.24218		Hs.7218 Hs.26812	Hs.236510 Hs.137383	Hs.2053	Hs.8454 Hs.183105 Hs.79372 Hs.63311	Hs.202362 Hs.21641
AA001897 Hs.95006	N26836 Hs.77239 AA064973 Hs.91217	AA677504 Hs.7127 N51838 Hs.24218		N67766 Hs.7218 AA464736 Hs.26812	Hs.49729 Hs.103247	Hs.2053	AA634287 Hs.116041 AA418918 Hs.2429 H42247 Hs.79372 AA195318 Hs.63311	Hs.44354 Hs.21641
AA001897	N26836 AA064973	AA677504 N51838		N67766 AA464736	N94270 W93523	N42770	AA634287 AA418918 H42247 AA195318	N34945 R41169
427750	257135 382773	897215 281870		291426 810603	293676 357138	271985	743739 767994 177621 665316	276911 29093
GF201	GF203 GF200	GF203 GF201		GF203 GF201	GF200 GF201	GF200	GF202 GF200 GF200 GF203	GF201 GF203

-1.1810332		-1.0377587			-2.507145	1.08782014	-2.3865428	-1.1499445		-2.515522	-1.7075981		-1.5694951					-1.110405	-2.2487003	1.46974145	-1.8950403	-1.3081587		-1.4587032		
467.7384	467.5625	467.4836	467.4152	467.3872	467.319	467.1754	467.1066	467.0405		466.9973	466.8118		466.7734	466.7201	400 0000	400.000		466.5083	466.2709	466.2136	466.151	466.1366		465.7993	465.7287	465.4785
CHGA	ACYP1	EDN3						HNRPU			INPP₁				7000	וחשמ				KIAA0626	DKFZP566B133	CCND2			PLOD3	272120
chromogranin A (parathyroid secretory protein 1)	acylphosphatase 1, erythrocyte (common) type	endothelin 3	ESTs	ESTs	ESTs	ESTs	ESTs	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	Human Chromosome 16 BAC	clone CIT987SK-A-211C6	inositol polyphosphate-1-	ESTs, Moderately similar to	pig-c protein [H.sapiens]	ESTS BBCA1 associated BING	demois 4	EST Weekly similar to 40S	RIBOSOMAL PROTEIN S15A	[H.sapiens]	ESTs	KIAA0626 gene product	DKFZP566B133 protein	cyclin D2	Homo sapiens mRNA for	KIAA1223 protein, partial cds procollagen-lysine, 2-	oxoglutarate 5-dioxygenase 3	ESTs
Hs.172216	Hs.18573	Hs.1408	Hs.46608	Hs.55287	Hs.3991	Hs.186937	Hs.33314	Hs.103804		Hs.28607	Hs 32309		Hs.47974	Hs.7948	00071	US.34009		Hs.50272	Hs.27004	Hs.178121	Hs.110571	Hs.75586		Hs.28783	Hs.153357	Hs.8957
Hs.119190	Hs.18573	Hs.1408	Hs.46608	4A447985 Hs.55287	AA608646 Hs.3991	4A700815 Hs.131791	Hs.33314	Hs.103804		Hs.28607	Hs 32309		AA732983 Hs.120329	Hs.7948	0007	AA676233 US.34069		Hs.50272	AA449455 Hs.27004	AA398341 Hs.124067	AA504354 Hs.110571	Hs.75586		AA397920 Hs.28783	AA459305 Hs.6652	Hs.8957
T56470	W80489	T67005	N59158	AA447985	AA608646	AA700815	H47048	T97593		N39229	H52141	2	AA732983	H16790	10000	AA0/0233		N73448	AA449455	AA398341	AA504354	H84153		AA397920	AA459305	T49222
72969	415388	66532	287728	782721	950781	436059	178524	121621		276962	180803		399049	50559	40000	430320		291633	785610	726821	825461	249688		726599	810928	67318
GF203	GF201	GF200	GF201	GF201	GF202	GF203	GF203	GF200		GF203	GESOO	5	GF203	GF201	0	0215		GF202	GF203	GF203	GF203	GF200		GF203	GF201	GF201

1.35710462	1.16746218	1.25197371	-1.5478087 -1.1684732 -1.5222912	1.60938291
465.2937 465.1268 465.0313	465.0069 464.9855 464.8755	464.8492 464.7125 464.6739	464.5826 464.516 464.4818 464.4276 464.4206 464.4155	464.3817 464.367
LIFR HSPA1A !!	PLXNC1	CD36 PTP4A2	e FGG XPNPEPL KNG ETAA16	
leukemia inhibitory factor receptor ESTs heat shock 70kD protein 1 ESTs. Moderately similar to IIII ALU SUBFAMILY SX WARNING FYTRY IIII	[H.sapiens] plexin C1 ESTs CD36 antigen (collagen type I	receptor, incomposition receptor) EST protein tyrosine phosphatase type IVA, member 2	fibrinogen, gamma polypeptide FGG X-prolyl aminopeptidase (aminopeptidase P)-like XPNI ESTS Kalinogen KNG ETAA16 protein ETAA	Homo sapiens Mut S homolog 5 gene, parlial cds; and NCZ7, NG30, NG31, NG24, NG25, NG32, NG26, NG38, Caselin kineal libea subunit, BAT2, AlF-1, 1C7, LST-1, lymphotoxin beat, tumor necrosis ledor, and lymphotoxin alpha genes, com EST
Hs.2798 Hs.78521 Hs.8997	Hs.268986 Hs.184697 Hs.41322	Hs.75613 Hs.245990 Hs.82911	Hs.75431 Hs.56542 Hs.269543 Hs.77741 Hs.82664 Hs.58875	Hs.247478 Hs.49135
N67017 Hs.78369 AA150891 Hs.71924 N52970 Hs.107165	T81261 Hs.14842 AA041362 Hs.42654 N24715 Hs.41322	Hs.75613 Hs.74014 Hs.11015	194626 Hs.75431 AA453477 Hs.56542 AA699633 Hs.124146 Hs9834 Hs.77741 AA041476 Hs.82264 W86575 Hs.58875	AA460293 Hs.15802 N66169 Hs.49135
N67017 AA150891 N52970	T81261 AA041362 N24715	N39161 H22563 T55728	T94626 AA453477 AA699633 H69834 AA041476 W86575	AA460293 N66169
295889 505047 283739	109271 376476 269224	243816 51916 73638	119882 795191 436435 213280 376551 416745	795735
GF200 GF201 GF201	GF200 GF201 GF201	GF200 GF200 GF201	GF200 GF201 GF204 GF200 GF201	GF201

1.18509734		1.06806014			-2.0032995	1.11792646	-1.6060296		1.06632622		-2.1398158	-1.2412921		-1.1732291	-1,1100249	-1.2178132	1.15164178				1.04697562	-1.1759652
464.3372 464.3193	464.2739	464.2678	464.0149	464.0102	463.8483	463.815	463.7592		463.6187	463.4656	463.3857	463.2225		463.2112	463.1817	463.157	463.0299	462.9996		462.9491	462.8485	462.6361
BOK1			C190RF3							STAT12	RXRA				KIAA0630					LAMA3	PMSCL1	NIFS
ATP-dependent RNA helicase ROK1 ESTs Hono saplens hair and skin epidermal-type 12- lipoxygenase-related protein (ALOX/22E) mRNA, complete	pseudogene sequence Homo sapiens cDNA FLJ11034 fis, clone	PLACE1004258 chromosome 19 open reading	frame 3	ESTS	ESTS	EST	ESTs	ESTs, Weakly similar to	putative p150 [H.sapiens] STAT induced STAT inhibitor-	2	retinoid X receptor, alpha	ESTs	ESTs, Highly similar to heme-	binding protein [H.sapiens]	KIAA0630 protein	ESTs	ESTs	ESTs	laminin, alpha 3 (nicein (150kD), kalinin (165kD),	BM600 (150kD), epilegrin)	autoantigen 1 (75kD)	cysteine desulfurase
Hs.99423 Hs.20007	Hs.88844	Hs.31718	Hs.6454	Hs.23012	Hs 31524	Hs.91381	Hs.22801		Hs.268026	Hs.110776	Hs.20084	Hs.118152		Hs.108675	Hs.12259	Hs.37380	Hs.222048	Hs.23850		Hs.83450	Hs.91728	Hs.194692
AA460140 Hs.99423 AA701289 Hs.20007	AA419264 Hs.88844	T71382 Hs.13820	AA434159 Hs.103927	96	N/114/ HS.44862 HAG768 Hs 31524		_		AA421352 Hs.125142	AA137031 Hs.110776	AA464615 Hs.20084	AA702561 Hs.118152		AA469923 Hs.108675	N80491 Hs.12709	H56931 Hs.37380	9	N34849 Hs.23850		AA001432 Hs.83450	AA458994 Hs.91728	R16676 Hs.113309
795876 435658	755630	110198	770614	505064	178394	30207	34966		739257	491121	812994	384116		730346	292749	204638	452570	276523		362059	814270	129664
GF201 GF203	GF201	GF200	GF201	GF201	CESO	GE203	GF203		GF203	GF201	GF203	GF203		GF202	GF200	GF200	GF203	GF201		GF201	GF200	GF203

	-1.4228282	-2.1131809	-1.7624165								00000	1.29023933					1.30425811			1.37171086			1.08728844	-1.4830608	
		462.2266		461.9932		461.9495		461.8604	0000	461.7336		461.6815		461.6/79	461.6573			461.5789		461.4412		461.1595	461.1112	460.7869	460.7115
FAP			MUT							UBE2L6		RBBP8	;	RRM1			EIF4B	MYLE		B3GAT1		STAT6		HEY1	
fibroblast activation protein, alpha; seprase ESTs, Weakly similar to	Unknown [H.sapiens] ESTs	EST methylmalonyl Coenzyme A	mutase	ESTs	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone	DKFZp564D016) Homo sapiens cDNA	FLJ10540 fis, clone	NT2RP2001245	ubiquitin-conjugating enzyme	E2L 6	retinoblastoma-binding protein		ribonucleotide reductase M1	polypeptide	ESTs	eukaryotic translation initiation	actor 4B	MYLE protein	beta-1,3-glucuronyltransferase	1 (glucuronosyltransferase P)	of transcription 6, interleukin-4	nduced Homo sanians mRNA for	KIAA1268 protein, partial cds	with YRPW motif 1	ESTs
fib Hs.418 alg ES	Hs.31236 Ur Hs.50344 E8	6	Hs.155212 mi		ĬŌ	Hs.14846 DF	4	Hs.14559 N	_	Hs.169895 E2		Hs.29287 8			Hs.66219 Et		_	Hs.11902 M		Hs.3353 1	o, g	Hs.181015 in	Hs.152925 KI		Hs.128790 E
9 Hs.418	H87246 Hs.31236 AA099709 Hs.50344	AA620807 Hs.112909	AA211855 Hs.86512	Hs.42414		AA482278 Hs.14846		AA131909 Hs.14559		AA292074 Hs.12158		Hs.29287		AA633549 Hs.2934	AA454012 Hs.66219		AA044205 Hs.62663	Hs.11902		AA598504 Hs.3353		Hs.75610	Hs.10841	Hs.124955	Hs.23014
AA405569 Hs.418	H87246 AA099706	AA620807	AA21185	98086H		AA482278		AA131909		AA292074		H23021		AA633548	AA454012		AA044205	T68845		AA59850		T72202	T64956	R60705	R44164
772425	220395 489691	1055530	682984	260965		824665		504308		725395		51737		856489	795274		486279	82173		898145		85541	66815	41903	34449
GF201	GF203 GF201	GF202	GF203	GF201		GF204		GF201		GF201		GF200		GF201	GF201		GF200	GF201		GF202		GF201	GF200	GF203	GF201

					DORDYYOR DYDYD1			
Westbrook et al.	ok et al.				APPENDIXA		Affy	Atty Docket No. 217
GF200 GF201	123730	R01281 AA461501	R01281 Hs.19126 AA461501 Hs.21968	Hs.19126 Hs.182740	src kinase-associated phosphoprotein of 55 kDa ribosomal protein S11 ESTs, Weakly similar to !!!! ALU SUBFAMILY SB2	SKAP55 RPS11	460.5263 460.4865	-1.1764864
GF200 GF200	361097 136856	AA017199 R36207	AA017199 Hs.118797 R36207 Hs.25092	Hs.15617 Hs.25092	WARNING ENTRY !!!! [H.sapiens] ESTs ESTs, Moderately similar to		460.4752 460.419	-1.4812125 -1.8410979
GF202 GF200 GF203 GF201	811867 40721 767328 342720	AA454963 R55750 AA418486 W68396	AA454963 Hs.32196 R55750 Hs.26455 AA418486 Hs.98299 W68396 Hs.79025	Hs.32196 Hs.26455 Hs.231111 Hs.79025	metargidin precursor [H.sapiens] ESTs EST KIAA096 protein	KIAA0096	460.2249 460.0121 459.8333 459.8269	1.06579862 -1.0015679 -1.5459401
GF200 GF200 GF200 GF203	236305 244227 212542 878411	H62115 N52994 H68663 AA670356	NS2994 Hs.42179 NS2994 Hs.42179 H68663 Hs.107207 AA670356 Hs.61268	Hs.156110 Hs.42179 Hs.21851 Hs.61268	mmunogobulin kappa variable 1D-8 KIAA1286 protein Horno sapiens mRNA; cDNA DKFZp586J2118 (from clone DKFZp586J2118)	IGKV1D-8 KIAA1286	459.803 459.7687 459.7379 459.6698	-1.3685046 1.02417763 -2.1030741 -1.5539507
GF200 GF203 GF200 GF200	240637 413089 704697 85609	H90225 AA707806 AA282255 T62040	H90225 Hs.40094 AA707806 Hs.121234 AA282253 Hs.35804 T62040 Hs.5843	Hs.40084 Hs.222052 Hs.35804 Hs.74047	Human DNA sequence from clane 167A19 on chromosome 1922.1-33. Contains three genes for novel proteins, the DIO1 gene for type I coothynorine delicities (EC 3.8.1.4, TXDII, ITDII) and an HNRNP A3 (Heterogenous Nuclear Bionoucleoprotein A3, FBRNP) pseudoge ESTIS hect domain and RLD 3 electron-transfer-flavoprotein, beta polypeptide	HERC3	459.6648 459.3266 459.0639 458.7394	-1.5874213 -2.5140763 1.259775

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-1.8347928	-1.2088986		-1.8479662	1.6393599		-1.3219389	1.02244782	-2.7893615
458.613 458.2713 458.2575 458.2506	458.1391 458.1095	458.0662 458.0582	457.9616 457.9187 457.8888	457.7824 457.7169 457.6759	457.6391	457.4821	457.4066	457.2715 457.1685
Ali		SLC10A1	SDFR1		SIGLEC5 IRAK1	PTPN7		SPIB DKFZP434D222
Homo sapiens mRNA full length insert cDNA clone LEPOIMAGE 743169 ESTs ESTs ESTs hepatitis delta antigenimentalin monian A interaction monian A	Horno sapiens o'DNA FLJ10907 fis, clone OVARC1000060 EST solute carrier family 10	(sodium/bile acid collarisporter family), member 1 ESTs stromal cell derived factor	receptor 1 ESTs ESTs	ESTs EST EST	sialic acid binding lg-like lectin 5 interleukin-1 receptor- associated kinase 1	protein tyrosine phosphatase, non-receptor type 7 Homo sapiens cDNA	FLJ10486 fis, clone NT2RP2000205 Spi-B transcription factor (Spi-	1/PU.1 related) DKFZP434D222 protein
Hs.201525 Hs.113314 Hs.107680	Hs.31696 Hs.21842	Hs.952 Hs.16129	Hs.6354 Hs.83097 Hs.103896	Hs.188635 Hs.65407 Hs.144168	Hs.117005	Hs.35	Hs.173946	Hs.192861 Hs.3862
AA401406 Hs.97736 R4454 Hs.22277 H37909 Hs.107680		T68568 Hs.952 AA001658 Hs.16129	AA130671 Hs.6354 H06517 Hs.83097 AA155748 Hs.103896	R10311 Hs.20586 AA448161 Hs.65407 H53964 Hs.36835	22 25	AA262719 Hs.35	N68686 Hs.49559	AA465158 Hs.99631 T56874 Hs.3862
743169 AA4 34007 R44 190972 H37		83444 T68 428056 AA0	586731 AA1 44278 H06 505376 AA1	128993 R10 782768 AA4 202795 H53			293243 N68	815046 AA4 68259 T56
GF202 GF201 GF203	GF203 GF203	GF201 GF201	GF201 GF203 GF202	GF200 GF201 GF201	GF201	GF203	GF203	GF203 GF201

-1.0856775	1.36183161	-2.2875623	-1.7829205		-1.2269077	1.2705934	-1.7909642					-2.5439348	٠			
456.9501	456.8716 456.8369 456.7644	456.5169	456.4312	400.087.0	456.2846	456.28 456 1341	456.0795	455.9508		455.9312	455.7926	455.7434	7404	455.693		455.6149
	KIAA1128	EIF4B	CYP24	NALAZ		GABRA2				BUB3	DKFZP434B187			CREMES		
ESTs	Homo sapiens mRNA; cDNA DKFZp43401230 (from clone DKFZp43401230); partial cds MAA1128 protein	ES IS eukaryotic translation initiation factor 4B	cytochrome P450, subfamily XXIV (vitamin D 24- hydroxylase)	nescient nelix loop nelix z Homo sapiens ornithine decarboxylase antizyme 2	(OAZ2) mRNA, complete cds gamma-aminobutyric acid	(GABA) A receptor, alpha 2	EST	ESTs	BUB3 (budding uninhibited by benzimidazoles 3, yeast)	homolog N-acetylglucosamine-	phosphate mutase;	ESTs	cytokine receptor-like	molecule 9 ESTs	Homo sapiens cDNA FLJ11008 fis, clone PLACE1003100, moderately	similar to HEP27 PROTEIN
Hs.62711	Hs.7517 Hs.81897	HS.5/24 Hs.93379	Hs.89663	Hs.46296	Hs.74563	Hs.91343	HS.222377 Hs.112620	Hs.34246		Hs.40323	He 937493	Hs.107883	:	Hs.7120 Hs.23575		Hs.6318
AA056377 Hs.62711	AA016225 Hs.93386 AA114106 Hs.81897	AA291159 Hs.5724 W92963 Hs.24003		Hs.46296	Hs.63977	Hs.91343	AA452118 Hs.99264 AA608959 Hs.112620	Hs.34246		Hs.107700	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Hs.107883	:	Hs.44200 Hs.23575		AA429946 Hs.6318
AA056377	AA016225 AA114106	AA291159 W92963	N21576	H29557	T67029	R39763	AA452118 AA608959	N51843		H38804	A A 0.004 077	R49731		N46830 W74636		AA42994
509462	359269 563201	700517	266146	52881	66535	26162	786534 1030729	281865		191904	997007	38554		279150 346643		781295
GF202	GF201 GF200	GF203	GF202	GF201	GF200	GF200	GF203 GF202	GF201		GF201	Č	GF203		GF201	5	GF201

		-2.1845858	-1.9655586		-1.4837018		1.90072371		1.16370509					1.1640823/		-1.4280892			-1.2799973	-1.7963328
455.6051		455.4614	455.3933 455.3665		455.2488		455.2124	455.1851	455.0571		454.9862	454.8/		454.7422	454.7319	454.6882		454.6758	454.619	454.4448
		CALM2	CHST2		IGSF4			CUL5				UKFZP564M18Z		TAF2J	ZNF262	ADAM10			S100B	
ESTs, Highly similar to growth factor-responsive protein, vascular smooth muscle R nonverious	calmodulin 2 (phosphorylase	kinase, delta) carbohydrate (N- acetylglucosamine-6-0)	sulfotransferase 2 ESTs	immunoglobulin superfamily,	member 4 ESTs, Weakly similar to	homolog of Drosophila discs large protein, isoform 2	[H.sapiens]	cullin 5	ESTs	origin recognition complex,	subunit 3 (yeast homolog)-like	DKFZP564M182 protein TATA box binding protein	(TBP)-associated factor, MNA	polymerase II, J, 20kD	zinc finger protein 262 a disintegrin and	metalloprotease domain 10	Homo sapiens mRNA; cDNA DKFZp434D0935 (from clone	DKFZp434D0935) S100 calcium-binding protein,	beta (neural) ESTs: Moderately similar to	LIV-1 protein [H.sapiens]
10078	0/00/0	Hs.182278	Hs.8786 Hs.181315		Hs.70337		Hs.66295	Hs.101299	Hs.37297		Hs.74420	Hs.20760		Hs.82037	Hs.150390	Hs.172028		Hs.7200	Hs.83384	Hs.32699
A A 4 50 100 D. 6 1 5 1 4	150196 HS.61514	AA663941 Hs.7614	AA682637 Hs.8786 AA448251 Hs.21196		AA708201 Hs.120752		784156 Hs.90383	Ŋ	456331 Hs.37297			W85854 Hs.36337		AA045587 Hs.82037	N51853 Hs.95822	AA872057 Hs.35080		AA029312 Hs.7200	AA424045 Hs.83384	W87533 Hs.94918
40404		855707 AA	431301 AA 782812 AA		392405 AA		111150 T8					416240 W8		509588 AA		1336262 AA		470144 AA	759948 AA	416978 W
S	GFZUI	GF203	GF203 GF201		GF203		GF200	GF201	GF200		GF201	GF201		GF200	GF201	GF203		GF201	GF200	GF202

	1 -2.077297	4 1.0568771				4 -1.653907				5 1.29557833	25				35 -2.4260758			2 -2.4326495			77			31 -1.5628706	m		32 -1.3389452		1.9034409
	454.4311	454.3614			454.348	454.2204			454.1604	454.1015	453.8852		453.6461	453.6433	453.6235	453.5463	453.5178	453.382			453.3307			453.3181	453.188		453.0392		452.8781
	KCNMB4				PTRF						ZNF211		RAF1									_			KIAA0937	DKFZP434F091			
potassium large conductance	calcium-activated channel;	ESTs	RNA POLYMERASE I AND	TRANSCRIPT RELEASE	FACTOR	ESTs	Homo sapiens mRNA; cDNA	DKFZp761E1824 (from clone	DKFZp761E1824); partial cds	ESTs	zinc finger protein 211	v-raf-1 murine leukemia viral	oncogene homolog 1	ESTs	ESTs	ESTs	ESTs	ESTs	Homo sapiens mRNA; cDNA	DKFZp434I1820 (from clone	DKFZp434I1820); partial cds	Human ring zinc-finger protein	(ZNF127-Xp) gene and 5	flanking sequence	KIAA0937 protein	DKFZP434F091 protein	EST	ESTs, Highly similar to INTERFERON-INDUCED	PROTEIN 1 [H.sapiens]
	He 46784	Hs.180546			Hs.29759	Hs.21568			Hs.28564	Hs.48614	Hs.15110		Hs.85181	Hs,17147	Hs.108771	Hs.102510	Hs.105421	Hs.88148			Hs.14235			Hs.7838	Hs.62264	Hs.30488	Hs.99739		Hs.92287
	A A 440000 Up 46704	Hs 43134			AA418829 Hs.90452	Hs.21568			Hs.56588	Hs.48614	Hs.77184		Hs.85181	AA482230 Hs.17147	Hs.108771	Hs.102510	AA456039 Hs.105421	AA256468 Hs.88148			AA455013 Hs.107738			4A669451 Hs.7838	AA029444 Hs.58037	Hs.30488	4A458943 Hs.99739		Hs.92287
	4 4 4 6 9 0 0	N22297			AA418829	H12264			T59678	N62724	W79396		N34117	AA482230	H96673	N59835	AA456039	AA256468			AA455013			AA66945	AA02944	H15274	AA458940		R78509
	000000	707707			267993	48277	i		80574	288995	346947		267634	840884	251877	289055	812161	682057			811612			884892	366821	49595	814427		144916
	000	GFZUS	1		GF203	GF203			GF201	GE202	GF201	;	GF200	GF202	GESOS	GF201	GF203	GF203			GF201			GF203	GF201	GF201	GF203		GF200

	-1.986071	1.04177984	1.15654382	-2.4735486	1.2513322 -1.8582467 1.1118205	-1.8386648 -1.8741513 -1.2931339 -2.0917691 -1.0820316
452.8205 452.6263 452.5118	452.487 452.4245	452.3257	452.317	452.3107 452.2847 452.2218	452.2013 452.071 452.0054	451.7605 451.6992 451.3515 451.3433 451.2689 451.1246
TIM ZNF131	KRAS2			HSU54999	CACNB1	CBLB
Homo sapiens cDNA FLJ1184 fis, clone PLACE1007507 Oncogene TIM zinc finger protein 131 (clone pHZ-10)	v-Ki-ras2 Kirsten rat sarcoma 2 viral oncogene homolog ESTs ESTs, Weakly similar to	Social of the control	H.sapiens] ESTs, Weakly similar to	PROTEIN 1 [M.musculus] ESTs LGN protein Human translation initiation factor elf-Zaloha mRNA.	3'UTR calcium channel, voltage- dependent, beta 1 subunit ESI's Cas-BrM (murine) ectropic	equivorumes sequence b ESTs ESTs ESTs ESTs ESTs ESTS ESTS
Hs.267446 Hs.334 C	Hs.184050 8	Hs.127294	Hs.23981	Hs.181161 Hs.42221 Hs.278338	Hs.151777 Hs.635 Hs.9788	Hs. 3144 Hs. 222654 Hs. 31433 Hs. 50743 Hs. 120306 Hs. 199014 Hs. 26653
AA135824 Hs.33214 AA001222 Hs.334 AA156030 Hs.78743	N95249 Hs.78150 AA005254 Hs.23565	Hs.127294	Hs.23981	Hs.65757 Hs.42221 Hs.82769	W60015 Hs.6485 H10665 Hs.100879 AA496123 Hs.107305	AA704729 Hs.3144 N77731 Hs.35012 H15089 Hs.13828 AA232206 Hs.50743 N49949 Hs.46991 N71714 Hs.50074 R59371 Hs.26653
AA13582 AA00122 AA15603	N95249 AA005254	R23246	R26693	H48099 N35080 W92011	W60015 H10665 AA496123	AA704729 N77731 H15089 AA232206 N49949 N71714 R59371
502891 362279 590148	307553 428828	131094	132524	193394 271686 415264	341942 46238 757173	450949 248020 49555 666359 282688 290654 38029
GF201 GF201 GF201	GF200 GF201	GF203	GF200	GF200 GF201 GF201	GF200 GF202 GF202	GF203 GF200 GF201 GF203 GF203 GF203

1.08582872 -1.7755255 1.17479357 -1.2498719	-1,444202 1,02066126 1,02066126 1,12999282 1,1577238	1.15011969	1.12704597 -1.3531096 -1.5436651
451.0735 451.0629 450.974 450.8956 450.8091	450.6855 450.5899 450.4583 450.4071 450.3787 450.3258 450.3258 450.3258 449.9897 449.9868	449.9642 449.8643 449.8144 449.8034	449.7464 449.7164 449.5743
ABP1 LDHC	ZNF76 PHB PHB CD81	KIAA0618 NPTX1	TOMM70A
amilioride binding protein 1 (amine oxidase (copper- containing)) ESTs ESTs lactate dehydrogenase C	ESTs, Highly similar to KIAA0772 protein [H.sapiens] ESTs zinc finger protein 76 (expressed in testis) ESTs ESTs ESTs ESTs ESTs CSTs CSTs prohibitin prohi	[D.melanogaster] KIAA0618 gene product neuronal pentraxin I ESTs translocase of outer	mitochondrial membrane 70 (yeast) homolog A ESTs EST
Hs.75741 Hs.82567 Hs.37372 Hs.99881 Hs.34244	Hs 28450 Hs 26793 Hs 2922 Hs 16439 Hs 79241 Hs 78283 Hs 75283 Hs 12283 Hs 12283 Hs 524457	Hs.243122 Hs.226223 Hs.84154 Hs.32659	Hs.21198 Hs.169624 Hs.99047
749924 Hs 75741 AA416724 Hs.82567 N52837 Hs.37372 AA453969 Hs.99881 AA026388 Hs.34244	H63865 Hs.28450 A4136612 Hs.95793 AA626012 Hs.29222 W86370 Hs.16439 H17804 Hs.79241 R60946 Hs.75923 R60946 Hs.19103 A4629554 Hs.12293 R22927 Hs.23438 AA486653 Hs.53457	R23254 Hs.23490 AA434187 Hs.90272 H22481 Hs.84154 AA457138 Hs.32659	AA088722 Hs.21198 AA398267 Hs.31520 AA446032 Hs.99047
70827 731218 244391 795178 366436	139892 490925 745003 416679 50354 342181 42313 42313 884388 130979	131099 770518 173674 810459	511257 726709 781029
GF200 GF202 GF200 GF200	GF203 GF201 GF201 GF201 GF201 GF200 GF200 GF200 GF200	GF203 GF201 GF200 GF201	GF202 GF203 GF202

Human DNA sequence from clone 989H11 on chromosome

-1,4686432	-1.1434161 -1.4072725	-2.1411951	-1.0126554	-1 4957606	-1.4237600	-1.5861725		-1.5526582 1.07245006	-1.0423887	0616706.1-	-1.197187 -2.0823166	-1.7068177
449.5495 449.4525	449.4478 449.3266	449.2678	449.2456 449.0493 448.7047	448.6771 448.6194	448.6106 448.4442	448.2214	448.2206 448.1874 448.1525	448.0626 447.9855	447.9654	447.7409	447.4601 447.4494	447.4017
MORF	CRA		CHS1	KIAA0250 DKFZP586I1023		IGSF1	FKBP6 KIAA0117		DKFZP586L0724	GNOND	EXT1	ACATN
22q13.1-13.2. Contains part of a novel gene, ESTs, GSSs and four putative CpG islands histone acetyltransferase	cisplatin resistance associated CRA ESTs Homo saniens mRNA for	KIAA1331 protein, partial cds complement component 1, r	subcomponent Chediak-Higashi syndrome 1 ESTs	KIAA0250 gene product DKFZP586I1023 protein	ESTs ESTs immunoglobulin superfamily,	member 1 FK506-binding protein 6	(36kD) ESTs KIAA0117 protein	EST ESTS	DKFZP586L0724 protein thymosin, beta, identified in	neuroblastoma cells ESTs	exostoses (multiple) 1 ESTs	acety-Coerzyme A transporter
Hs.129043 Hs.27590	Hs.166066 Hs.188993	Hs.3355	Hs.1279 Hs.36508 Hs.17757	Hs.15087 Hs.111515	Hs.28355 Hs.129467	Hs.22111	Hs.150490 Hs.43296 Hs.174135	Hs.93221 Hs.18160	Hs.26761	Hs.56145 Hs.37599	Hs.184161 Hs.98352	Hs.271907
R71669 Hs.129043 AA057313 Hs.27590	W77812 Hs.5370 AA701540 Hs.117357	9	T69603 Hs.1279 N74383 Hs.36508 N95011 Hs.17757		W80730 Hs.28355 AA135958 Hs.106915	AA780028 Hs.22111	AA460285 Hs.99521 N23009 Hs.43296 AA046204 Hs.101834	H57959 Hs.93221 AA707413 Hs.24267	_	N91887 HS.56145 AA009809 Hs.37599	AA487582 Hs.8789 AA421489 Hs.98352	H66943 Hs.91826
155532 381166	345858 435846	627112	83549 296198 305253	782428	415610 502721	462007	795736 266586 488839	204360 451557	825282	306771 429848	841698 731108	212180
GF203 GF200	GF200 GF203	GF202	GF201 GF200 GF201	GF201 GF201	GF203 GF201	GF203	GF201 GF201 GF201	GF200 GF203	GF203	GF200 GF201	GF200 GF202	GF200

		-1.1185942 -1.3989937	-1.8553419		1.56678643		-1.0137723		-1.1432388		-1.6517094	-1.6214316
•	447.3848	447.3321 447.3231	447.2804	447.2228	447.0706 447.0598	446 7511	446.7224	446.5534 446.5302 446.4504	446.4031 446.3771 446.3995	446.1808	446.1428	446.1002 446.0081 445.898
	KIAA0339		TOM34		SEMA7A	FARD3	FTH1		PEKCM		TCF7L2	EIF4B CTSO
APPENDIX A	KIAA0339 gene product Homo sapiens mRNA; cDNA	DKFZp586H051) ESTs	translocase of outer mitochondrial membrane 34 Homo sapiens cDNA	FLJ11294 fis, clone PLACE1009708 sema domain, immunoglobulin domain (lg), and GPI	membrane anchor, (semaphorin) 7A ESTs	fatty acid binding protein 3, muscle and heart (mammary-	ferritin, heavy polypeptide 1	ESTs ESTs ESTs	ESTs ESTs protein kinged mu	ESTs, Weakly similar to cleft lip and palate transmembrane protein 1 [H.sapienz]	cell specific, HMG-box) eukarvotic translation initiation	factor 4B cathepsin O ESTs
	Hs.112078	Hs.47986 Hs.89034	Hs.76927	Hs.48541	Hs.24640 Hs.73372	600	Hs.62954	Hs.58690 Hs.271837 Hs.95120	Hs.112751 Hs.26969 Hs.2691	ns.zos I Hs.11282	Hs.154485	Hs.93379 Hs.75262 Hs.171693
	AA459896 Hs.25707	AA435977 Hs.47986 AA282554 Hs.89034	AA457118 Hs.76927	N48582 Hs.40091	R33537 Hs.24640 AA176249 Hs.73372	A A 4 4 0 E 4 0 E 0 0 E 0 0 4	H73484 Hs.9601	W84750 Hs.58690 T54617 Hs.9764 AA025408 Hs.95120	AA071503 Hs.112751 H17509 Hs.26969 N52380 Hs.26961	_	AA417665 Hs.19582	AA704670 Hs.120849 N81036 Hs.91101 H91313 Hs.34577
	809410	730587 713026	810452	279253	135941 595813	404 550	232908	415764 73725 365706	366039 50513	249618	752652	383851 301082 241080
	GF201	GF202 GF203	GF200	GF201	GF200 GF202	50	GF200	GF201 GF201 GF201	GF202 GF201	GF201	GF200	GF203 GF200 GF201

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-1.9526656		1.00693806			-1.9862388	1.42735535	-1.2669948					-1.8218214	-2.3312388	1.25593532				1.01413683		-2.4094701		-1.43904	1.18841753			-1.0307654
445.8671 445.7142	445.5674	445.5565		445.4542	445.1606	444.9801	444.9726		444.9629			444.8611	444.8344	444.817				444.8031		444.7692		444.6804	444.675		444.6141	444.5334
TGIF	СРО	PRG6		CBFA2T1			MSLN													KIAA0165					KPNA3	MTMR4
TG-interacting factor (TALE family homeobox) ESTs	coproporphyrinogen oxidase (coproporphyria, harderoporphyria)	p53-responsive gene 6	core-binding factor, runt domain, alpha subunit 2;	related	ESTs	ESTs	mesothelin	Homo sapiens clone 23914	mRNA sequence	Homo sapiens cDNA	FLJ11058 fis, clone	PLACE1004736	ESTs	ESTs	ESTs, Weakly similar to !!!!	ALU SUBFAMILY SO	WARNING ENTRY !!!!	[H.sapiens]	extra spindle poles, S.	cerevisiae, homolog of	ESTs, Weakly similar to orf,	[S.cerevisiae]	ESTs	karyopherin alpha 3 (importin	alpha 4)	myotubularin related protein 4 MTMR4
Hs.90077 Hs.65307	Hs.89866	Hs.83135		Hs.31551	Hs.269373	Hs.163932	Hs.155981		Hs.177776			Hs.180817	Hs.117915	Hs.102756				Hs.17348		Hs.153479		Hs.98613	Hs.108653		Hs.3886	Hs.141727
R83270 Hs.90077 AA479135 Hs.65307	4A700808 Hs.89866	AA205393 Hs.83135		Hs.76929	4A488898 Hs.99646	Hs.50500	4A488406 Hs.83401		Hs.38861			Hs.10657	Hs.117915	Hs.82772				Hs.17348		AA948058 Hs.23215		Hs.98613	Hs.108653		Hs.3886	Hs.24843
R83270 AA479135	AA700808	AA205393		N75054	AA48898	W03052	AA488406		H69528			N63911	H61007	R31701				H69786		AA948058		N50948	H89713		AA668178 Hs.3886	H66232
194214 754194	436062	647767		299721	824889	296334	843028		212438			293830	208720	134783				210921		1416055		281125	240273		852829	234150
GF200 GF203	GF201	GF203		GF201	GF203	GF200	GF200		GF201			GF203	GF203	GF200				GF203		GF203		GF200	GF202		GF201	GF200

-1.3493954	1.4392526	-1.5543664 -1.2082642		-2.0088456	-2.5330527 -1.3336923		-1.1739658		-1.1621284			-1.0347865	-1.7936655		-1.2422293
- 444.5038	444.4826	444.1549			444.1179		444.022	443.9259	- 443.8019	443.7332		443.7024	443.6711	443.6238 443.5482	443.3629
SCCA1	NFATC3				KIAA1093		DLG4		RQCD1						STUB1
			ly similar oline 5- e isoform	•	X	ila)		_ pe)			t; cDNA m clone		rTS beta	:	
squamous cell carcinoma antigen 1 nuclear factor of activated T-	cells, cytoplasmic 3 ESTs	ESTs ESTs	Homo sapiens cDNA FLJ10646 fis, clone NT2RP2005773, highly similar to Homo sapiens pyrroline 5- carboxylate reductase isoform	mRNA	KIAA1093 protein ESTs	discs, large (Drosophila)	homolog 4 ESTs, Highly similar to	HSPC002 [H.sapiens] rcd1 (required for cell differentiation, S.pombe)	homolog 1	ESTs	Homo sapiens mRNA; cDNA DKFZp434H2218 (from clone	DKFZp434H2218) Homo sapiens cDNA FLJ11091 fis, clone	PLACE1005313 H.sapiens mRNA for rTS beta	protein ESTs	STIP1 nomology and O-box containing protein 1 ESTs
Hs.227948	Hs.172674 Hs.21435	Hs.58405 Hs.98422		Hs.274287	Hs.117333 Hs.34956		Hs.23731	Hs.76907	Hs.94211	Hs.99480		Hs.45114	Hs.33368	Hs.180433 Hs.47041	Hs.25197 Hs.186669
Hs.37104	Hs.12113 Hs.21435	Hs.58405 Hs.98422		AA044299 Hs.14214	4A699725 Hs.117333 V64671 Hs.34956		Hs.23731	Hs.54946	Hs.94211	Hs.99480		Hs.45114	Hs.33368	Hs.77358 Hs.47041	Hs.25197 Hs.89107
AA398883 Hs.37104	T72068 R59608	W74646 Hs.58405 AA425743 Hs.98422		AA044299	AA699725 N64671		R39954	N93438	AA488188 Hs.94211	AA485454 Hs.99480		AA102837 Hs.45114	AA206614 Hs.33368	N66132 Hs.77358 AA010210 Hs.47041	AA775749 Hs.25197 AA463960 Hs.89107
727147	85804 41913	346671		486348	433314		26021	307249	877651	811069		490606	645166	278483 430211	878200 810303
GF202	GF201 GF203	GF202		GF203	GF203 GF200		GF200	GF201	GF200	GF201		GF202	GF203	GF201 GF201	GF203 GF201

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-1.2035136	-1.4576612	1.11671317 -1.5129963			-1.0870417	1.33073123	-1.1203427	-1.3342307	1.20457161	1.25785374 -1.8522122
443.1347 -1	443.1217 -1	443.0679 1. 442.4024 -1	442.3752	N	442.275 442.275	442.1785 1. 442.107 441.9283	441.9211 -1		441.8138 1.	441.7049 1. 441.5988 -1
TFDP2	SCYA7	ТІММЭ		XPNPEP2	MACS AP14				KATNA1	EIF1AY
transcription factor Dp-2 (E2F dimerization partner 2) small inducible cytokine A7 (monocyte chemotactic protein	3) translocase of inner mitochondrial membrane 9	(yeast) homolog ESTs Homo sapiens mRNA: cDNA	DKFZp434E0528 (from clone DKFZp434E0528) X-prolyl aminopeptidase (aminopeptidase P) 2,	membrane-bound myristoylated alanine-rich protein kinase C substrate	(MARCKS, 80K-L) apoptosis inhibitor 4 (survivin) Homo sapiens mRNA; cDNA DKFZp586L081 (from clone	DKFZp586L081) ESTs ESTs	ESTs Homo sapiens cDNA FLJ10377 fis, clone NTZFM2001989, weakly similar to NUCLEOLAR	PROTEIN NOP4 katanin p60 (ATPase-	containing) subunit A 1	eukaryon, transtation initiation factor 1A, Y chromosome ESTs
Hs.19131	Hs.251526	Hs.271934 Hs.97505	Hs.256398	Hs.57922	Hs.75607 Hs.1578	Hs.8078 Hs.23009 Hs.108275	Hs.117262	Hs.274263	Hs.180859	Hs.155103 Hs.72713
AA400200 Hs.19131	AA040170 Hs.70390	AA195449 Hs.32456 AA398121 Hs.97505	Hs.39997	AA040387 Hs.57922	AA482328 Hs.75607 AA460685 Hs.1578	Hs.8078 Hs.23009 Hs.108275	AA682522 Hs.117262	AA426037 Hs.39725	Hs.15730	AA047039 Hs.40546 AA167540 Hs.72713
AA400200	AA040170	AA195449 AA39812	N59441	AA04038	AA482328 AA460689	R93715 H11730 N66847	AA68252	AA42603.	H94050	AA047039 AA16754
742806	485989	627154 726572	284541	376080	840865 796694	197765 47793 295601	431219	773421	242820	380394 609161
GF202	GF200	GF202 GF203	GF201	GF201	GF200 GF201	GF200 GF201 GF201	GF203	GF202	GF200	GF200 GF202

-1.1700906	1.4054711	-1.3877712	1.17012742	-1.1782875	-1.0108308	-1.8675004		-2.7293616			-1.2459148			-1.8577033		-1.5920145	-1.9012034	-1.2712419	-2.2092651		-1.5712802		1.66909091		1.04167658			1.25113137				-1.8539926
441.4704	441.3577	441.0874	440.9249	440.8901	440.8506	440.843	440.8327	440.7982	440.7071		440.6257	440.5867	440.5559	440.5274		440.5139	440.3434	440.3222	440.2504		440.2458		440.238	440.173	440.062			440.061		440.0161		439.9892
	CPNE1	DKFZp564C047	FALZ	LOC51249	GAS6	LOC51580			YDD19		LOC51696	EP300		ARF5							STAR		SRP72							CDK5R1		
ESTs	copine I	hypothetical protein	fetal Alzheimer antigen	hypothetical protein	growth arrest-specific 6	H-2K binding factor-2	ESTs	ESTs	YDD19 protein	hHDC for homolog of	Drosophila headcase	E1A binding protein p300	ESTs	ADP-ribosylation factor 5	Homo sapiens clone 24411	mRNA sequence	ESTs	ESTs	ESTs	steroidogenic acute regulatory	protein	signal recognition particle	72kD	ESTs	ESTs	Homo sapiens cDNA	FLJ20376 fis, clone	HUV01087	cyclin-dependent kinase 5,	regulatory subunit 1 (p35)	Homo sapiens mHNA; culvA DKFZp586L1722 (from clone	DKFZp586L1722)
Hs.97961	Hs.166887	Hs.17200	Hs.99872	Hs.184456	Hs.78501	Hs.278573	Hs.169160	Hs.21618	Hs.25615		Hs.6679	Hs.25272	Hs.22137	Hs.77541		Hs.20952	Hs.41324	Hs.84630	Hs.99376		Hs.3132		Hs.237825	Hs.19872	Hs.190013			Hs.29106		Hs.2869		Hs.8518
AA406048 Hs.97961	AA485922 Hs.75856	AA489211 Hs.105227	N91172 Hs.109652	AA455040 Hs.80924	AA461427 Hs.78501	R19314 Hs.11802	AA421488 Hs.18803	AA447768 Hs.21618	R26172 Hs.106123		AA115400 Hs.6679	N94428 Hs.25272	W86586 Hs.22137	AA629584 Hs.77541		N75064 Hs.20952	AA455933 Hs.41324	H21892 Hs.84630	N		AA679454 Hs.3132		AA443177 Hs.5171	W89128 Hs.19872	AA436158 Hs.104404			H91337 Hs.29106		AA442853 Hs.2869		W46632 Hs.109900
742830	843139	825041	301836	812240	796181	32996	731106	813671	132165		511388	309591	416659	884743		299737	813284	160192	811883		829828		811842	417318	754367			240748		757873		324154
GF202	GF200	GF203	GF202	GF203	GF200	GF200	GF201	GF203	GF201		GF202	GF201	GF201	GF203		GF200	GF203	GF203	GF203		GF203		GF200	GF201	GF203			GF200		GF201		GF202

1.25565186	-1.0880759	-1.1156753 -1.827541 -1.5834266 -1.3410251 -2.0176486	1.26092574 1.29592922	-1.4867017 -2.1847176	-1.3065325 1.33614067 -1.5044539 -1.572965 -1.578835 -1.578835 -1.578835 -1.578835
439.8443	439.7794 439.6983	439.4774 439.4518 439.2344 439.1821 439.1004	439.0754 438.9841	438.9102 438.9 438.7343	438.611 438.5543 438.5652 438.41 438.41 438.2771 438.2763 438.1919 438.1323 438.036 438.036 438.036
	PSME2		NEBL	LOC51765 BASP1	C10RF2 THBS1 DKTZP564M182 TIGB8 CEP1 CLONE-23970
flomo sapiens cDNA =LJ11349 fis, clone PLACE4000650, weakly similar to TUBERIN prodessome (prosome, prodessome (prosome, prodessome (prosome, procoani) activator subunit 2		NT2PP2002769 ESTs ESTs ESTs ESTs	otte Abrocopino protoin Linaso		Homo sapiens cDNA FLIZA435 fis, clone KAT03864 Informacione 1 open reading frame 2 Informationsprondin 1 Informationsprondin Informationspronding Informations
HS.15978	Hs.179774 Hs.18653 H	Hs.265960 Hs.265960 Hs.269551 E Hs.101654 Hs.102630 Hs.26579 Hs.26530 Hs.26579 Hs.26		Hs.23643 Hs.79516 Hs.201064	Hs.11408 Hs.19554 Hs.20760 Hs.20760 Hs.20760 Hs.207808 Hs.27808 Hs.79244 Hs.79244 Hs.79244 Hs.79244 Hs.79244 Hs.79244 Hs.79244
Hs.22017	Hs.77022 Hs.18653	763197 Hs.4046 AA701475 Hs.124701 106497 Hs.101654 AA495984 Hs.102630	W67309 Hs.44997 AA398340 Hs.111893	V22323 Hs.23643 AA488676 Hs.79516 H82104 Hs.40348	111464 Hs.19564 AA757604 Hs.19564 AA757604 Hs.19366 AA009615 Hs.62523 R16872 Hs.114146 AA009615 Hs.60299 W65709 Hs.832 AA673847 Hs.79244 H66030 Hs.97437 AA673893 Hs.87157
H60351	H65395 H89637	R63197 AA701475 H06497 AA495984	W67309 AA398340	N22323 AA488676 H82104	T64216 H11464 AA052061 AA002061 R10872 AA009615 W56709 AA428474 H66030 AA485893 W74673
207649	210405 240199	138021 435432 44377 768495	343167 726817	254029 843098 220244	80226 47665 395625 428048 12998 36551 340644 771165 210610 1325615 344721
GF200	GF200 GF200	GF200 GF203 GF203 GF203	GF200 GF203	GF202 GF202 GF201	GF201 GF201 GF203 GF202 GF202 GF200 GF200 GF200 GF200

1.2410924	1.2770432	1.24600108 -1.3689576	-2.3913345	1.35042427	-1.4136416	1.85512064 -1.805142	-1.4473506 1.28961406 -1.3390279	-1.162373	1.72063026	-1.2629801 -1.5440672
438.0525	437.9778	437.6899	437.4749	437.4112	437.4102	437.3753 437.3176	437.2569 437.2165 437.1721	437.1505	437.1404	437.0733 437.0283
		KIAA0601	HMGCR	DSCR1L1	NAB1	PTK9				UBE2D2 DKFZP586I1023
ESTs, Highly similar to notch protein homolog TAN-1 precursor [H.sapiens] Homo sapiens oDNA LE20037 fis, clone	COLLOOS 14 Homo sapiens cDNA FLJ20551 fis, clone KAT11656	ESTs, Moderately similar to proliferation potential-related protein [M.musculus] KIAA0601 protein	3-hydroxy-3-methylglutaryl- Coenzyme A reductase	Down syndrome candidate region 1-like 1	(ERG1 binding protein 1) Homo sapiens mRNA; cDNA DKFZp761E212 (from clone	DKFZp761E212) protein tyrosine kinase 9 ESTs, Highly similar to	unknown [H.sapiens] ESTs ESTs	ESTs Homo sapiens mRNA; cDNA DKFZp434J039 (from clone	DKFZp434J039); partial cds ubiquitin-conjugating enzyme E2D 2 (homologous to yeast	UBC4/5) DKFZP586I1023 protein
Hs.129053	HS.10784 Hs.7994	Hs.91065 Hs.174174	Hs.11899	Hs.156007	Hs.107474	Hs.110702 Hs.82643	Hs.145643 Hs.268927	Hs.101760	Hs.8737	Hs.108332 Hs.111515
AA733033 Hs.129053	HS.10784 Hs.7994	Hs.16939 Hs.6447	AA779417 Hs.11899	Hs.75368	Hs.107474	AA251026 Hs.110702 AA019459 Hs.82643	Hs.18184 Hs.37304	Hs.101760	Hs.8737	AA159600 Hs.32690 AA447681 Hs.25501
AA733033	H/1124	R88741 H73731	AA779417	H19439	N91896	AA251026 AA019459	T97910 H56424	H20747	H93814	AA159600 AA447681
399115	142944	194986	896949	51408	306798	684539 362853	121558 203805	51433	241988	593164 813608
GF203	GF200	GF200	GF203	GF200	GF203	GF203 GF200	GF200 GF200	GF202	GF200	GF202 GF203

1.56286441	-2.663016	-1.2616916	-1.1602722		-1.3774381	-1.474683 -1.19083384 -1.0564001	1.08332875
436.9032	436.7954 436.7587 436.6106	436.4572	436.1445 435.9868	435.9181	435.8958	435.7915 435.7018 435.6612	435.5806 435.5349 435.4633 435.373
	BET3 ACLY	E46L ARF1	ULK1		CHAF1B	000000	RDGBB CENPF
Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG islands similar to yeast BET3 (S. similar to yeast BET3 (S.	cerevisiae) ATP citrate lyase Ecte	like mouse brain protein E46 ADP-ribosylation factor 1	Groot (Crossagan), modern finase 1 ESTs Homo sapiens mRNA; cDNA DKF70434K1326 (from clone	DKFZp434K1326) Homo sapiens cDNA FLJ20188 fis, clone	COLF0561 chromatin assembly factor 1, subunit B (p60)	KIAAUCSO protein Homo sapiens mRNA; cDNA DKFZp434L1850 (from clone DKFZp434L1850); partial cds ESTs	ESTs ESTs Centromere protein F (350/400kD, mitosin)
Hs.8084	Hs.24391 Hs.174140 Hs.180732	Hs.13493 Hs.74571	Hs.47061 Hs.25560	Hs.47125	Hs.12439 Hs.75238	HS.13421 HS.250517 HS.5122 Hs. 268641	Hs.77204 Hs.7204 Hs.9286 Hs.77204
AA504250 Hs.8084	N71050 Hs.90490 AA136054 Hs.22390	R02710 Hs.70144	AA455505 Hs.47061 R51946 Hs.25560	W74133 Hs.47125	R32875 Hs.12439 AA425120 Hs.75238	AA430545 HS.13421 N78092 HS.15972 AA465386 HS.5122 TOEGET US.17550	47.01
825394	294580 502622	32889 124090	809727 154214	346308	135561	770066 248288 814117	364173 428192 71730 435076
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1.62294541		1.76654903		-2.8263277	-1.3308053	-1.1833154	-1.1084018		-1.1906429	1.13224967			1.40208326	-1.1335444				-1.0515689		1.3019626		-1.6010022
435.3659		435.1996		435.1612	435.1263	435.1247	435.114		435.0844	435.0692		435.0664	435.063	434.9878			434.8712	434.7411		434.4/25		434.3237 434.2492
		ETFA				ITPR1	TPP2		MTVR	ACTL6							SCYD1	RHAG				APLP2 LOC51318
Homo sapiens cDNA FLJ20782 fis, clone	electron-transfer-flavoprotein, alpha polypeptide (glutaric	aciduria II) ESTs, Highly similar to	tyrosine phosphatase-like protein homolog hSTYXb	[H.sapiens]	EST inocital 1.4 E. triphoenhate	recentor, type 1	tripeptidyl peptidase II	Mouse Mammary Turmor	Virus Receptor homolog	actin-like 6	ESTs, Weakly similar to HYPOTHETICAL PROTEIN	ZAP128 [H.sapiens]	ESTS	ESTs	small inducible cytokine	member 1 (fractalkine,	neurotactin) Rhesus blood group-	associated glycoprotein	Homo sapiens mRNA for TSC.	22-like protein ESTs	amyloid beta (A4) precursor-	like protein 2 hypothetical protein
H-	200	Hs.169919		Hs.50283	Hs.26679	Hs 198443	Hs.1117		Hs.18686	Hs.274350		Hs 49433	Hs 192868	Hs.47378			Hs.80420	Hs.169536		Hs.193398		Hs.64797 Hs.93814
99	200	Hs.86499		Hs.50283	Hs.26679	A A D 35450 Hs 78433	Hs.1117		Hs.18686	AA410394 Hs.31768		A A D 4 6 4 9 4 3 3	20020 Hs 51798	AA406348 Hs.47378			Hs.80420	Hs.77321		W58000 Hs.102447		H89664 Hs.64797 AA120816 Hs.110252
100	200	T58002		N73506	R59601	AAO3545C	T77959		W93891	AA410394		A A O 4 6 4 2 2	BOOSO	AA406348			R66139	T48949		W58000		H89664 AA120816
03057	000	71672		295880	41905	471795	24085		357450	753400		488202	122063	753198			140574	70489		341269		240249 490147
500	GFZUZ	GF200		GF203	GF203	00000	GF200		GF202	GF202		CE201	00210	GF203			GF201	GF200		GF200	3	GF200 GF201

	1 017565	4 44 7 7 0 0 0	-1.112/009	2.38189166				-1.9748234	1.12238944	-1.2510175			-1.6790928				-2.3488512						-2.0236194	-2.9205124		040070	1.01325978			-1.817533
	434.2151	454.1905	434.0228	434.0071			433.9173	433.8772	433.8226	433.8209			433.6743				433.4646	433.4184		433.3989			433.3051	433.0473	100 001	432.8354	432.7859		432.702	432.673
	TCF2			DKFZP586P2220														NOL4		BIG1						TAX1BP1			MAFG	•
transcription factor 2, hepatic; LF-B3; variant hepatic nuclear	factor	ESIS	ESTs	DKFZP586P2220 protein	ESTs, Moderately similar to	CaM-KII inhibitory protein	[R.norvegicus]	ESTs	ESTs	ESTs	Homo sapiens mRNA; cDNA	DKFZp434D0218 (from clone	DKFZp434D0218); partial cds	ESTs, Weakly similar to	REGULATOR OF MITOTIC	SPINDLE ASSEMBLY 1	[H.sapiens]	nucleolar protein 4	brefeldin A-inhibited guanine	nucleotide-exchange protein 1	ESTs, Weakly similar to !!!!	WARNING ENTRY !!!!	[H.sapiens]	EST	Tax1 (human T-cell leukemia	virus type I) binding protein 1	EST	v-maf musculoaponeurotic	oncodene family, protein G	ESTs
	Hs.169853	Hs.271958	Hs.32204	Hs.15832			Hs.107767	Hs.94862	Hs.46903	Hs.182234			Hs.15797				Hs.8881	Hs.6414		Hs.94631			Hs.68647	Hs.101567		Hs.5437	Hs.97334		He 252229	Hs.97327
	AA699573 Hs.74104	4	R93719 Hs.32204	H81940 Hs.15832			AA131299 Hs.106855	R33482 Hs.94862		AA169202 Hs.44444			T84965 Hs.15797				AA774503 Hs.8881	AA430033 Hs.6414		W89187 Hs.25125			R96804 Hs.68647	R78576 Hs.101567		AA149174 Hs.22513	AA401695 Hs.97334		AA045436 He 100358	AA398338 Hs.97327
	433481	768254	197775	239958			503602	136324	280233	594323			111765				399270	781091		417327			200307	144861		504691	727275		107061	726836
	GF201	GF203	GF200	GF200			GF201	GF203	GF203	GF202			GF200				GF203	GF201		GF201			GF200	GF200		GF201	GF203		500	GF203

-1.2805707	1.15386402	-1.787523 -1.9635837 -1.4059837	-1.9597279 -1.0267928 -2.2743079	1.142197 -1.5725282 -2.5042734	-1,0631316
432.6272 432.6151 432.6052	432.5289	432.3991 432.3522 432.3061 432.2292	432.1895 432.1542 432.0971 432.0543	432.0379 431.9602 431.9187 431.8533 431.8289 431.7595	431.6309
KIAA0313 AARS	PTGS2 PNN	<u> </u>	NAP1L2	IPLA2(GAMMA) MAC30 MAC30	GOT2
PDZ domain containing guanine nucleotide exchange tactor(GEF)1; FA(Ras/Rap1A- associating)-GEF alamyl-tRNA synthetase ESTs	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) PTGS2 pinin, desmosome associated pinin, desmosome PNOS protein	ESTs, Highly similar to CGI- ESTs ESTs ESTs	nucleosome assembly protein 1-like 2 ESTS ESTS ESTS ESTS Intracellular membrane- sassociated calcium- ind-concrient in hoshing-sa A2	incoperation prosping and a series of the prosping and a series of the protein protein protein ESTs	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) GOT2
Hs.154545 Hs.75102 Hs.43455	Hs.196384 Hs.274459	Hs.18885 Hs.34174 Hs.170065 Hs.153472	Hs.66180 Hs.117747 Hs.185739 Hs.135292	Hs. 44198 Hs. 58068 Hs. 199695 Hs. 113663 Hs. 269892 Hs. 20039	Hs.170197
AA488969 Hs.22656 AA156571 Hs.75102 N23858 Hs.43455	Hs.735 Hs 5567	M00102 HS:3307 AA459002 HS:18885 AA157017 HS:103415 AA418003 HS:23141 BE5934 HS:8562	AA156109 Hs.66180 AA678047 Hs.117747 AA417759 Hs.60287 195839 Hs.17684	AA489199 Hs. 44198 A70147 Hs.58068 A79230 Hs. 4187 A79230 Hs. 13663 R63908 Hs. 113663 A91398 Hs. 107842 A91880 Hs. 20039	AA487739 Hs.79365
AA488969 AA156571 N23858	R80217	AA459002 AA157017 AA418003 BE2934	AA156109 AA678047 AA417759 T95839	AA489199 W70147 N79230 N79230 R63908 R91398 W91880	AA48773
824895 588829 254533	147050	416316 814271 502561 767459	589853 431840 746235 120390	825005 344308 292388 292388 139667 195975	841370
GF200 GF201 GF202	GF201	GF203 GF201 GF203 GF203	GF202 GF203 GF203 GF201	GF203 GF201 GF200 GF200 GF203 GF201	GF200

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-1.3887772	-1.6380164 -1.8152412 1.51768677	-1.164188 -1.8376716 1.34602291 -1.5300514 -1.2803052	1.07859245	-1.3118135 -1.0179607		1.17607118
431.5486 431.3963	431.2195 431.2194 1	431.0658 431.0439 430.936 430.8575 430.865 430.6643 430.6643	430.5602 429.8122 429.7986 129.7651	429.7383	429.5734	429.5697 429.5665
		API1	PTPN21 EBI3 KIAA0923	PABPN1		CSH1 SELENBP1
ESTs ESTs	ESTs, Moderately similar to RB18A protein [H.sapiens] ESTs ESTs Homosapiens mRNA; cDNA Homosapiens mRNA; cDNA	DKFZp6481264 (from clone DKFZp6481264) ESTs ESTs ESTs Appoptosis inhibitor 1	protein tyrosine phosphatase, non-receptor type 21 Epstein-Barr virus induced gene 3 ESTs ESTs		ESTs, Weakly similar to HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I "B FORM" PRECURSOR [H.sapiens]	chorionic somatomamnotropin hormone 1 (placental lactogen) selenium binding protein 1
Hs.189825 ES Hs.96908 ES	ES Hs.219382 RB Hs.9451 ES Hs.7016 ES	DK Hs.76550 DK Hs.32553 ES Hs.99391 ES Hs.99391 ES Hs.75263 ap Hs.76095 ES	ри Hs.155693 no Ep Hs.185705 ge Hs.13775 ES Hs.22587 KL	Hs.117176 nu Hs.46519 E8	ES AF IN FC FC HS.266331 PF	ct sc Hs.75984 1 Hs.7833 se
T72535 Hs.12563 AA453796 Hs.96908	N47954 Hs.91991 H63394 Hs.9451 AA405754 Hs.7016	AA453783 Hs.76550 AA029441 Hs.32553 AA429398 Hs.106594 AA445077 Hs.90391 AA702174 RG.57 H51648 Hs.106095 R60807 Hs.11700	H03504 Hs.89834 AA425028 Hs.75995 AA504137 Hs.13775 H20847 Hs.20986	AA040742 Hs.117176 N48689 Hs.46519	Hs.42866	AA482325 Hs.74130 T65736 Hs.7833
T72535 AA45379	N47954 H63394 AA4057	AA45378 AA02944 AA42939 AA45507 AA70217 H51848 R60807	H03504 AA425028 AA504137 H20847	AA04074 N48689	N71796	AA4823. T65736
21922	280270 208981 742094	813730 366830 771128 812261 448190 194031	151449 768496 825223 51460	486186 279372	290749	840882 80338
GF201 GF203	GF202 GF203 GF203	GF202 GF201 GF201 GF203 GF200 GF200	GF201 GF200 GF203 GF201	GF203 GF202	GF201	GF200 GF202

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	A0946	4 4 2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5		423 423 423	24 22 24 24 24 24 24 24 24 24 24 24 24 2		<u> </u>
	LOC51773 DKFZP566A0946		CHN2 LOC51058		ERG	GABRG2	PGF
APPENDIX A	EST HBV pX associated protein-8 DKFZP566A0946 protein ESTs	Homo sapiens mRNA; cDNA DKFZp434A2410 (from clone DKFZp434A2410); partial cds ESTs	ESTs chimerin (chimaerin) 2 ESTs hypothetical protein	ESTS EST EST ESTS	Homo sapiens cDNA FLJ20479 fis, clone KAT07382 ESTs ESTs v-ets avian erythroblastosis virus ES6 oncogene related	gamma-aminobutyric acid (GARA) A receptor, gamma 2 ESTs, Moderately similar to orphan neurotransmitter transporter NTT5 IH sanlensi	EST placental growth factor, vascular endothelial growth factor-related protein Homo sapiens mRNA for KIAA1122 protein, partial cds ESTs
	Hs.167660 Hs.20509 Hs.78006 Hs.93552	Hs.25897 Hs.97745	Hs.269395 Hs.15202 Hs.269568 Hs.20879	Hs.193074 Hs.34550 Hs.129810 Hs.20152	Hs.23990 Hs.188835 Hs.268711 Hs.45514	Hs.7195 Hs.59260	Hs.97587 Hs.2894 Hs.21356 Hs.49895
	Hs.42670 Hs.56273 Hs.78006 Hs.93552	W61323 Hs.25897 AA400101 Hs.97745	N55355 Hs.94062 H89912 Hs.24821 AA703378 Hs.59980 AA053665 Hs.20879	411968 Hs.106942 AA002153 Hs.34550 AA486281 Hs.105237 W88497 Hs.20152	AA485675 Hs.23990 AA463643 Hs.104956 R44999 Hs.78716 R01304 Hs.45514	R40790 Hs.7195	AA398209 Hs.97587 AA130714 Hs.2894 R59694 Hs.21356 N70608 Hs.49895
	H99362 AA280381 R39924 H97508	W61323 AA400101	N55355 H89912 AA703378 AA053665	H11968 AA002153 AA486281 W88497	AA485675 AA463643 R44999 R01304	R40790	AA398205 AA398205 AA130714 R59694 N70608
k et al.	262262 712230 25664 251961	342399 742706	245886 221256 450031 510369	47916 427657 842848 417730	811097 811845 34302 123755	28218	726621 586803 42776 298603
Westbrook et al	GF202 GF203 GF203 GF202	GF201 GF202	GF201 GF203 GF203 GF202	GF203 GF201 GF202 GF201	GF201 GF203 GF200 GF200	GF200	GF203 GF201 GF202 GF202

-2.1549785 -1.3822076 -1.7078418 1.29183855	1.27307562	-1.6024228	-1.3936296	-1.0503946
			•	·
427.978 427.9606 427.9406 427.8619	427.861 427.8592 427.8213 427.7614	427.5068 427.4456 427.4448	427.4446	427.3462 427.3462 427.2737
KIAA0450 HIRIP5	C110RF8 ZYG	C110RF4		
KIAA0450 gene product HIRIPS protein EST EST reprosome 11 open reading	frame 8 Trans 8 Trans 8 Trans 8 Trans 8 Trans 9 Trans	hitmonsome 11 open reading frame 4 Homo sapiens cDNA Homo sapiens cDNA LL20783 fis, clone COL03108 ESTs. Weakly similar to ESTs, Weakly similar to Green/sise incling with assurance protein 1 ong with assurance protein 1	C.elegans] Homo sapiens mRNA for KIAA1146 protein, partial cds Homo sapiens mRNA; cDNA DKFZp434N1721 (from clone	NK-Z494N1721) SSTs Homo sapiens cDNA Homo sapiens cDNA HOLE/120148 is, clone COL08022, highly similar to HOLE/HUMAN HOLE/HOLE/HUMAN RIBONUCLEOPROTEIN I.
KIAAQ450 gene product HIRIPS protein EST EST chromosome 11 open re	organization of promise 8 ZYG homolog ESTs, Highly similar to modulator recognition f H. sapiens) Homo sapiens cig5 mF partial sequence	chromosome 11 open i trame 4 Homo sapiens cDNA FLL20788 fis, clone CCL03108 ESTs. Weakly similar to similar to 5. cerevisiae longevity-assurance pro longevity-assurance pro longevity-assurance pro longevity-assurance pro	[C.elegans] Homo sapier KIAA1146 p Homo sapier	DK-Zp434N1721) ESTS Homo sapiens cDNA FLJ20148 fis, clone COL08032, highly sin ROL-HUMAN HETEROGENEOUS NUCLEAR
Hs.170156 Hs.17368 Hs.22303 Hs.42622	Hs.46638 Hs.29285 Hs.15864 Hs.269274 Hs.17518	Hs.75859 Hs.246885 Hs.180024	Hs.11896 Hs.153489	Hs. 99141 Hs. 99141 Hs. 91684
AA757847 Hs.121533 AA625581 Hs.17368 R43009 Hs.22303 H99079 Hs.42622	AA020011 Hs.46638 AA489714 Hs.29285 T97699 Hs.15864 AA136616 Hs.71587 T95113 Hs.17518	197899 Hs.27721 AA126862 Hs.16001 T82948 Hs.15089	AA025779 Hs.11896 T68710 Hs.11894	AA022472 Hs.78624 AA447744 Hs.99141 H95141 Hs.102354
AA757847 AA625581 R43009 H99079	AA020011 AA489714 T97699 AA135616	T97899 AA126862 T82948	AA025779 T68710	AA022477 AA447744 H95141
396229 745314 31760 262061	363597 824393 121540 501540	121533 502165 110912	366341	364324 813641 256515
GF203 GF203 GF203 GF202	GF200 GF201 GF201 GF201	GF200 GF201 GF200	GF200	GF202 GF203 GF201

Westbrook et al.	k et al.				APPENDIX A		Atty	Atty Docket No. 21 / 26/9
GF202	629498	AA192765	AA192765 Hs.65818	Hs.65818	ESTs		427.2707	1.61381266
GF200	700302	AA283693	AA283693 Hs.95821	Hs.95821	osteoclast stimulating factor 1 OSTF1	OSTF1	427.1953	-1.4318917
GF203	287558	N62110	Hs.25413	Hs.25413	ESTs		427.1589	-1.3561731
GF203	752837	AA436384	AA436384 Hs.13766	Hs.13766	ESTs		427.0734	-1.9327639
GF200	342994	W68009	Hs.12273	Hs.25615	YDD19 protein	YDD19	426.9064	1.18110357
GF201	84141	T71042	Hs.12066	Hs.12066	ESTs		426.7996	
					chaperonin containing TCP1,			
GF200	897880	AA598637	AA598637 Hs.79150	Hs.79150	subunit 4 (delta)	CCT4	426.5423	1.47862379
GF201	40229	R53064	Hs.22249	Hs.22249	ESTs		426.4935	
					Homo sapiens mRNA full			
					length insert cDNA clone			
GF201	259374	N31952	Hs.34223	Hs.167531	EUROIMAGE 195423		426.3241	
GF201	92299	T67088	Hs.111573	Hs.13034	ESTs		426.2751	
GF202	343256	W67372	Hs.94780	Hs.8929	ESTs		426.198	-1.1142331
GF202	212698	H70491	Hs.114231	Hs.114231	C-type lectin-like receptor-2	LOC51266	426.0317	-1.181052
GF201	281371	N47886	Hs.14304	Hs.14304	ESTs		425.9541	
GF202	502603	AA134570	AA134570 Hs.94769	Hs.94769	RAB23 protein	LOC51715	425.8669	-1.264664
GF201	124575	R01941	Hs.88219	Hs.88219	zinc finger protein 200	ZNF200	425.8317	
GF202	743405	AA609338	4A609338 Hs.112694	Hs.112694	ESTs		425.5891	-2.5888304
GF201	346583	W74533	Hs.24212	Hs.24212	latrophilin	KIAA0786	425,4901	
					5-hydroxytryptamine			
GF203	280371	N47111	Hs.46362	Hs.46362	(serotonin) receptor 2C	HTR2C	425.3172	-1.5108354
GF202	376086	AA040389	4A040389 Hs.61993	Hs.61993	ESTs		425.3089	-1.9716231
GF203	825809	AA505135	4A505135 Hs.44037	Hs.44037	ESTs		425.2544	-1.2785108
					tumor suppressing			
GF201	212115	H68885	Hs.8130	Hs.154036	subtransferable candidate 3	TSSC3	425.0947	
					protein phosphatase 2			
					(formerly 2A), catalytic subunit,	_ `		000
GF200	823876	AA490696	AA490696 Hs.80350	Hs.80350	beta isoform	PPP2CB	425.0537	-1.5195231
GF201	487141	AA045340	AA045340 Hs.106515	Hs.25615	YDD19 protein	YDD19	425.0479	
					cyclin-dependent kinase	C PICTOR	100	
GF201	854668	AA630082 Hs.3561	Hs.3561	HS.238990	Innibitor 15 (pz/, np.1) phosphatidylinositol-4-	CONNIB	423,0364	
					phosphate 5-kinase, type I,			
GF201	24918	R39069	Hs.78406	Hs.78406	beta	PIP5K1B	425.0228	

-2.1371049	-1.0884869	-1.2484237 1.04536331 -2.8097113	-1.5072035	-1,1010466 1,20026044	-1.4207792 1.23701413	-1.4412916	1.0917625 -1.8817174 1.19341544
424.9977 424.8871 424.8447	424.7299	424.57 424.5603 424.4773	424.4366 424.3073	424.1836 424.1823 424.1323	423.9684 423.912	423.8774	423.4593 423.3766 423.3659 423.264
RDX KIAA0291	GAR22	KIAA0549 KIAA0903	KIAA0399	DKFZP58611023 PLS1	KIAA0020	DJ742C19.2 EIF4B	LTBH ITGA7
radixin KIAA0291 protein EST	422-18448-01 Citionicoonic 22 ESTS, Highly similar to STEROL REGULATORY FLEMENT BINDING	PROTEIN-2 [H.sapiens] KIAA0549 protein KIAA0903 protein Homo sapiens capiens	PLACE10'8', viole PLACE1008122 KIAA0399 protein Homo sapiens mRNA; cDNA	DKFZP544174 (1011 cone) DKFZP58611023 protein plastin 1 (1 isoform) ESTs, Weakly similar to	[C.elegans] [C.elegans] KIAA0020 gene product phorbolin (similar to apolipoprolein B mRNA editing	protein) eukaryotic translation initiation factor 4B	lymphotoxin beta receptor (TNFR superfamily, member 3 LTBR EST integrin, alpha 7 ESTs
Hs.250613 Hs.104717 Hs.101263	Hs.15346	Hs.3074 Hs.154248 Hs.16218	Hs.40337 Hs.100955	Hs.191268 Hs.111515 Hs.430	Hs.106534 Hs.2471	Hs.226307 Hs.93379	Hs.1116 Hs.31925 Hs.74369 Hs.117796
AA477165 Hs.1028 H15662 Hs.104717 R59977 Hs.101263	Hs.15346	AA463469 Hs.3074 R99407 Hs.12890 AA456284 Hs.43437	Hs.40460 Hs.100955	H00313 Hs.28666 T87139 Hs.16075 AA017379 Hs.430	AA677531 Hs.106534 AA454662 Hs.2471	Hs.206 Hs.10444	AA465150 Hs.5857 H24018 Hs.31925 AA055979 Hs.74369 H56152 Hs.117796
AA47716 H15662 R59977	R35292	AA46346 R99407 AA45628	H83123 R26143	H00313 T87139 AA01737	AA6775 AA4546	T64880 T58729	AA46515 H24018 AA05597 H56152
740554 49502 42485	37449	811808 201274 813144	199027 133118	149596 112865 361122	460395 811930	66718	815017 51485 377671 203858
GF200 GF201 GF203	GF200	GF202 GF200 GF203	GF203 GF201	GF203 GF200 GF201	GF203 GF200	GF200	GF203 GF202 GF201 GF203

-1.274444	1.02475779	1.20884862	1.12391778	-1.6932777	-1.2660925	-1 8382083	-1.2747291		-1.2158728	-1.1934133		-2.9095012	-2.6221736
423.2446	423.2368 423.1498	423.0674	422.9102 422.9102	422.8896	422.8799 422.827	400 7414	422.7337		422.4985 422.493	422.4595	422.3361	422.3148	422.2449 422.0755
SPTBN2	ECM2		PHB PHB	HPGD	KIAA0584	2	TEC		KIAA0549	RBM4	0	-	SPINK5
spectrin, beta, non-erythrocytic 2 extracellular matrix protein 2,	female organ and adipocyte specific ESTs	ESTs, Weakly similar to contains similarity to bacterial mutT proteins [C.elegans]	prohibitin prohibitin	hydroxyprostaglandin dehydrogenase 15-(NAD)	KIAA0584 protein ESTs	pinin, desmosome associated	protein tec protein tyrosine kinase	ESTs, Moderately similar to HPV16 E1 protein binding	protein [H.sapiens] KIAA0549 protein	RNA binding motif protein 4	Human DNA sequence from clone 633020 on chromosome 20q11.23-12 Contains 5' end of a gene similar to Bos taurus P14 protein, ESTs, CA repeat(D20S859), STSs and GSSs	ESTs serine protease inhibitor, Kaza	type, 5 ESTs
8 Hs.26915	Hs.35094 8 Hs.113200 B	Hs.269527			Hs.106794 Hs.104930		HS.274459 HS.89656		Hs.59159 Hs.154248			Hs.136005	Hs.5476 Hs.24643
Hs.26915	Hs.35094 Hs.113200	AA678092 Hs.119680	Hs.75323 Hs.119103	4A775223 Hs.77348	H08862 Hs.26999 AA435997 Hs.104930	000	AA707321 Hs.44499 AA779321 Hs.89656		AA010000 Hs.59159 AA150183 Hs.8792	AA456271 Hs.6106	AA458464 Hs.78389	Hs.102421	Hs.36802 Hs.24643
H30688	N79778 R10279	AA678092	R60946	AA775223	H08862 AA435997		AA707321 AA779321		AA010000 Hs.5915 AA150183 Hs.8792	AA456271	AA458464	N26008	H53602 N59827
184038	300323 128948	430709	42313	868838	45852 730737		451504 454048		430073	811911	809437	268837	202814 289027
GF200	GF201 GF203	GF203	GF200	GF203	GF201 GF202		GF203 GF203		GF201	GF200	GF201	GF203	GF201 GF203

Attv Docket No. 21726		1.29064209 -2.1390516 1.27811998	-1.214677 -2.1884587 1.22557246 -1.2155059 1.8569964	-1.2489859	1.15928915	1.00275357	1.27897587		-1.0537309
Attv		422.0157 421.9514 421.9253	421,9078 421,6183 421,5938 421,4263 421,4065	421.2964	421.1563 421.1501	421.1018 421.0875	421.0645	421.0283	420.8492
0000		DSP RHO7			MBD4	RAGA	SERP1		CEACAM1
09847798.070201	APPENDIX A	desmoplakin (DPI, DPII) GTP-binding protein Rho7 ESTs	Homo sapiens cDNA FLJ20394 fis, clone KAIA5035 ESTs ESTs ESTS ESTS	ESTs, Highly similar to NADH- UBIQUINONE OXIDOREDUCTASE 51 KD SUBUNIT PRECURSOR IH.sapiens	methyl-CpG binding domain protein 4 EST	Ras-related GTP-binding protein EST	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4 Homo sapiens HMT-1 mRNA Thomacoulthandense	complete cds	carcinoembryonic antigen- related cell adhesion molecule 1 (biliary glycoprotein)
		Hs.74316 Hs.99034 Hs.17441	Hs.252748 Hs.145527 Hs.223380 Hs.269208 Hs.247123	Hs 24075	Hs.35947 Hs.117030	Hs.57304 Hs.275068	Hs.76698	Hs.44592	Hs.50964
		N72540 Hs.64541 AA700934 Hs.99034 T94848 Hs.17441	N50936 Hs.9858 AA443712 Hs.99019 N51830 Hs.47348 AA708248 Hs.120102 H68724 Hs.118053		AA011232 Hs.35947 AA677085 Hs.117030	AA411640 Hs.57304 R98487 Hs.70335	N91117 Hs.54684	AA464702 Hs.44592	AA411757 Hs.50964
	91 al.	245585 383898 119403	281114 784032 281847 397620	805300	359411 454196	753700 201172	302955	810225	753301
:	Westdrook et al.	GF200 GF203 GF202	GF202 GF202 GF202 GF203	S 60	GF200 GF203	GF200 GF201	GF203	GF201	GF200

1.0635827	1.01989367	-1.7114003	-1.8986287	-1.1838779	-1 1681558				1.243055/1				1.19079295	-2.4004607	-1.271739			-1.2014331					-2.7563079	1.19275118		-1.0477426		
420.6694	420.6606	420.6562	420.5264	420.3806	420.367			420.0864	419.9297	419.9165	419.856	419.8292	419.8262	419.7702	419.7684		1	419.5115	419.4816	419.4335		419.3238	419.2291	419.0807	419.0599	419.0567	410 0400	410.3432
PXMP3	NBS1	AREG											DPYS					CRSP9		PREP		C22ORF5					7 10 07 10	FINISZL4
peroxisomal membrane protein 3 (35kD, Zellweger syndrome)	_		ESTS	EST	ESTs	ESIS	DKFZp434E0121 (from clone	DKFZp434E0121)	ESTs	ESTs	ESTs		opyrimidinase	ESTs	ESTs	cofactor required for Sp1	tivation,	t 9 (33kD)			chromosome 22 open reading	frame 5	ESTs	ESTs	ESTs	ESTs	postmeiotic segregation	increased 2-like 4
Hs.180612	Hs.25812	Hs.270833	HS.17557	Hs.209754	Hs.71124	HS.50/53		Hs.65135	Hs.37456	Hs.98288	Hs.97383	Hs.42681	Hs.10755	Hs.97726	Hs.97318			Hs.262823	Hs.106095	Hs.86978		Hs.182626	Hs.87194	Hs.29667	Hs.269123	Hs.142736	:	Hs.278468
AA452566 Hs.75240	AA463450 Hs.25495	4A857163 Hs.1257	AA/582/1 HS.1215// R72290 Hs 117557	~	4A427621 Hs.71124	AA058533 HS.60753		AA443585 Hs.65135	_			9 Hs.42681		AA401380 Hs.97726	AA398295 Hs.97318				8 Hs.23190	AA664056 Hs.86978		4A429477 Hs.4751	AA233932 Hs.87194	6 Hs.29667		8 Hs.19195		0 Hs.113853
	AA463	_			_	•		_	H58001	N58022	AA447992	N24579	H74004	-	-			W37993		-		_	-	N59766		R01608		H25510
788518	811761	1410444	396886	433230	770789	380943		771260	204444	247381	782736	267252	232933	742702	726800			322218	130078	855800		771172	666755	248535	209176	123932		161373
GF200	GF203	GF203	GF203	GF203	GF201	GF203		GF201	GF200	GF201	GF201	GF201	GF200	GF202	GF203			GF203	GF201	GF201		GF201	GF203	GF200	GF201	GF200		GF201

Westbrook et al.

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	-1.1403792	1.27311164 -1.166522 -1.0460131	-2.4123693 -1.4766415	-1.420579 1.22695834 -1.2652147 1.05987363	-1,4532388 -1,0542938 -1,3556243 1,10011795
418.8625 418.8417	418.5933	418.3963 418.3784 418.3765	418.2977 418.0304 418.0255 417.9429	417.776 417.7176 417.6848 417.5139	417.4273 417.3681 417.3499 417.3153 417.2396
		HP10390	HUMHOXY1 DSP KIAA0134 COL4A1	TCEA1	i TCOF1 KIAA0986
Homo sapiens cDNA FLJ20355 fis, clone FHPT S604, highly similar to AF121883 Homo sapiens sorting nexin 14 ESTs, Moderately similar to hypothetical protein	[H.sapiens] ESTs, Moderately similar to pim-1 protein [H.sapiens] putative tyne II membrane	protein ESTs ESTs zinc-finaer DNA-binding	Profesion ESTs desmoplakin (DPI, DPII) KIAA0134 gene product collagen, type IV, alpha 1	Homo sapiens mRNA for KIAA1345 protein, partial cds EST transcription elongation factor A (SII), 1 ESTS, Weakly similar to TRANSCRIPTION FACTOR	SOX-9 [H.sapiens] Treacher Collins-Franceschetti syndrome 1 ESTs ESTs ESTs KIAA0986 protein
Hs.46801 Hs.47668	Hs.234972 Hs.5326	Hs.8752 Hs.43712 Hs.86227	Hs.26719 Hs.107692 Hs.74316 Hs.151706 Hs.119129	Hs.146085 Hs.237307 Hs.23542 Hs.78869	Hs.97984 Hs.172727 Hs.35992 Hs.21921 Hs.27379 Hs.53542
Hs.82705 Hs.47668	AA598781 Hs.3435 AA487203 Hs.5326	R22439 Hs.100924 N25936 Hs.43712 AA206050 Hs.86227	N56349 Hs.94707 R86267 Hs.107692 R33456 Hs.113360 H25547 Hs.106380 AA150402 Hs.119129	Hs.34994 Hs.35306 Hs.23542 Hs.78869	AA427400 Hs.97984 AA457050 Hs.73166 R98905 Hs.35992 AA437094 Hs.104942 H17455 Hs.27379 H85547 Hs.53542
N63097 W72231	AA59878 AA48728	R22439 N25936 AA20605	W56349 R85267 R33456 H25547 AA15040	N49231 R94601 R59615 H27379	AA427400 AA457050 R98905 AA437094 H17455 H85547
284792 345145	898076	130610 268711 647661	340673 180321 135975 161458 491692	280122 198026 42018 163174	770979 815535 206882 757327 50060 222006
GF201	GF202 GF201	GF200 GF202 GF203	GF201 GF203 GF203 GF201 GF201	GF200 GF200 GF203 GF200	GF201 GF203 GF200 GF202 GF201 GF203

	-1.2651526	-1.2819713					1.65425801	1.16468614		-2.0463459	1.18036843				-1.2613106			1.01426716				-1.0613969				-1.3610162 -2.0071287
	417.1875	417.1636	417.0046	416.8209	416.764		416.4377	416.3863		416.227	416.083			415.9863	415.9837	415.8691		415.8541	415.7184			415.7098		415.6201		415.6021 415.5239
			FRZB				DYRK3				DKFZP564A122			DBY				COL3A1				GALNT1				PROSC YDD19
ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!	[H.sapiens] Human clone 23721 mRNA		d-related protein	ESTs	ESTs	dual-specificity tyrosine-(Y)- phosphorylation regulated		ESTs	ESTs, Weakly similar to	unknown [H.sapiens]	DKFZP564A122 protein	DEAD/H (Asp-Glu-Ala-	Asp/His) box polypeptide, Y	chromosome I	ESTs	ESTs	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type		ESTs	UDP-N-acetyl-alpha-D-	galactosamine:polypeptide N-	acetyigalactosariiii iyiirarisieras e 1 (GalNAc-T1)	Homo sapiens clone 23687	mRNA sequence	proline synthetase co- transcribed (bacterial	homolog) YDD19 protein
	Hs.210706	Hs.83572	Hs.153684	Hs.9992	Hs.196701		Hs.38018	Hs.101370		Hs.98608	Hs.187991			Hs.99120	Hs.43429	Hs.271635		Hs.119571	Hs.237689			Hs.80120		Hs.12513		Hs.210749 Hs.25615
	N64494 Hs.24164	AA465603 Hs.83572	Hs.78116	Hs.9992	AA055829 Hs.16345		Hs.38018	AA287261 Hs.101370		AA428655 Hs.98608	Hs.111652			Hs.94696	Hs.43429	Hs.34250		Hs.5417	Hs.40969			Hs.124276		Hs.12513		AA456325 Hs.24705 R25614 Hs.23910
	N64494	AA465603	R65782	T56056	AA055829		H62028	AA287261		AA428655	N59690			W37634	N23708	R89104		AA670351 Hs.5417	N79989			N31898		H28997		AA456325 R25614
	290337	814776	140071	73310	377587		209224	700854		781460	246661			321885	255277	195801		878420	302180			271865		49719		8131 8 9 132708
	GF203	GF200	GF201	GF201	GF201		GF200	GF203		GF202	GF200			GF201	GF202	GF201		GF203	GF201			GF203		GF201		GF203 GF200

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APPENDIX A

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-1.0756595			1.12120321	-1.2364563	-1.2364563	-1.008052	-2.0749666		1.39851342				-1.3082027	-2.1040116				-1.4078889	-1.3441612	4 0440000	-2 2286948	
415.5174	415.5054	415.3516	415.2958	415.2125	415.2125	415.0095	415.0089	1	414.723		414.6296		414.4989	414 4431			414.4004	414.3265	414.3143	44.0470	414.2172	413.8452
DDIT3	UBE2E3			MNPEP	MNPEP	DKF-ZP564B14/	CUL4A	מחלה	SUCRP		LOC51226		ATP5E	SOX30						à	V 10V	+700
DNA-damage-inducible transcript 3	E2E 3 (homologous to yeast UBC4/5) Homo sapiens cDNA	COL00364 ESTs. Weakly similar to	C26E6.11 [C.elegans] methionine aminopeptidase;	eIF-2-associated p67 methionine aminopeptidase;	eIF-2-associated p67	DKFZP564B147 protein	cullin 4A	retinoid X receptor, garrima	(explorin)	COPZ2 for nonclathrin coat	protein zeta-COP	transporting, mitochondrial F1	complex, epsilon subunit	SHY (sex determining region	ESTS, Weakly similar to	sodium-hydrogen exchanger 6	[H.sapiens]	ESTs	ESTS	ESTS, Weakly Similar to CARS	Cyp [H.sapiens]	ADP-fibosylation lactor-line 4 ESTs
Hs.129913	Hs.4890	Hs.267448	Hs.12106	Hs.78935	Hs.78935	Hs.151945	Hs.183874	Hs.26550	0000	US.0100	Hs.37482		Hs.177530	102005	HS. 197 603		Hs.188665	Hs.19193	Hs.16069		Hs.32234	Hs.2016/2 Hs.104607
AA015892 Hs.129913	AA459868 Hs.4890	AA448268 Hs.61546	AA703387 Hs.12106	AA487589 Hs.78935		N74662 Hs.102832		W96099 Hs.26550	0010	AA456109 IIS.6160	W70230 Hs.37482		AA700688 Hs.84205	11250	AA400263 IIS.87744		AA099386 Hs.61495	AA460234 Hs.19193	N76858 Hs.16069		R83355 Hs.32234	AA779165 Hs.63195 R37696 Hs.20904
361456	795809	782832	450050	841691	841691	298648	898317	358433	0010	813533	343990		434968		/4263/		489640	796495	245742		186626	453005 25520
GF202	GF201	GF201	GF203	GF200	GF200	GF203	GF200	GF201	200	GFZ00	GF201		GF203		GF202		GF201	GF203	GF200		GF203	GF203 GF201

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-1.5470671		-1.0053283	1.0251139		-1.3735011	-1.2570898	-1.0994515	-1.3726841				-1.0816598						-1.4733564				1.15049997				1.15049997	-1.2000031	-1.5581373		-1.2055485	
413.691 413.6555 413.6516		413.6036	413.382		413.2749	413.1552	413.041	413.0204	412.7723	412.752		412.5713			412.5066			412.2994				412.2051				412.2051	412.1111	412.0051		411.9928	
UGP2			KIAA0321		WARS2	SYNJ1		GLRX				DGCR2										DDX11				DDX11					
UDP-glucose pyrophosphorylase 2 ESTs ESTs	Homo sapiens cDNA FLJ20189 fis, clone	COLF0657	KIAA0321 protein	tryptophanyl tRNA synthetase	2 (mitochondrial)	synaptojanin 1	ESTs	glutaredoxin (thioltransferase)	ESTs	ESTs	DiGeorge syndrome critical	region gene 2	Homo sapiens cDNA	FLJ10641 fis, clone	NT2RP2005748	ESTs, Weakly similar to HEAT	SHOCK 70 KD PROTEIN 6	[H.sapiens]	DEAD/H (Asp-Glu-Ala-	Asp/His) box polypeptide 11	(S.cerevisiae CHL1-like	helicase)	DEAD/H (Asp-Glu-Ala-	Asp/His) box polypeptide 11	(S.cerevisiae CHL1-like	helicase)	ESTs	ESTs	ESTs, Weakly similar to	T15B7.2 [C.elegans]	
Hs.77837 Hs.13268 Hs.208238		Hs.29052	Hs.8663		Hs.227274	Hs.127416	Hs.10653	Hs.28988	Hs.269068	Hs.55238		Hs.2491			Hs.265891			Hs.44581				Hs.27424				Hs.27424	Hs.24654	Hs.22232		Hs.114062	
AA044390 Hs.77837 AA456087 Hs.13268 155340 Hs.70034		370005 Hs.29052			AA251354 Hs.111342	105085 Hs.127416	102039 Hs.10653	AA291163 Hs.28988	452771 Hs.46788	AA284270 Hs.55238		AA598861 Hs.2491			AA055170 Hs.82660			AA455653 Hs.44581				AA402879 Hs.27424				4A402879 Hs.117894	334012 Hs.24654			AA701448 Hs.114062	
486436 AA 813518 AA 77371 T5		142442 B7	_		684582 AA	_	151067 HG	_	283396 N5	327299 AA		AA 897978			377194 AA			813999 AA				741841 AA				741841 A	_	Ī		435063 A/	
GF201 GF203 GF202		GF200	GF200		GF203	GF203	GF203	GF200	GF201	GF201		GF203			GF201			GF203				GF200				GF200	GF200	GF203		GF203	

-1.4139093 -1.401567 1.18219597	1.10602735	1.82510404 -2.8028128 -1.351136	-2.8388832	1.23974523	1.03831306 -2.1043617 1.03954872 -2.5967517 -1.4920054
411.9882 411.9285 411.7254	411.7215 411.7195	411.6983 411.6834 411.652 411.6065	411.4176	411.3585	411.3218 411.2617 411.2527 411.1916 411.1405
EHOCC1	ERCC3 IL14	GRSF1 CC1.3 H1F2	COL5A3	IL16	FALA NMI KIAA0449 KIAA0076
excision repair cross- complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) ESTS ESTS excision repair cross- complementing rodent repair deficiency, complementation group 3 (storderma	complementing) interleukin 14	Garter may sequence binding factor 1 ESTs splicing factor (CC1.3) Histone family, member 2	ES1s Pro-(apha)3(V) collagen ESTs, Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII [H.sapiens]	interleukin 16 (lymphocyte chemoattractant factor) v-ral simian leukemia viral oncogene homolog A (ras	related) N-myc (and STAT) interactor KIAA0449 protein ESTs KIAA0076 gene product
Hs.59544 Hs.34576 Hs.50535	Hs.77929 Hs.83004	Hs.79295 Hs.103238 Hs.145696 Hs.7644	HS.48439 HS.235368 HS.44259	Hs.82127	Hs.6906 Hs.54483 Hs.169182 Hs.110156 Hs.51039
Hs.59544 Hs.34576 Hs.50535	Hs.77929 Hs.38838		N59839 Hs. 48439 R52038 Hs. 25469 AA088214 Hs. 44259	AA454784 Hs.82127	H97948 Hs. 6906 AAZ79601 Hs. 54483 H14513 Hs. 77995 AA699565 Hs. 110156 AA479771 Hs. 51039
T95289 R92362 W00946	H20908 N34055	AA485773 W90520 AA193573 T66816	N59839 R52038 A408821	AA45478	H97948 AA279601 H14513 AA699565 AA479771
120468 196168 296454	51666 244077	840384 417908 666038 66317	289096 154173 488271	809776	260768 704532 48530 433484 740122
GF203 GF203 GF200	GF200 GF200	GF200 GF201 GF203 GF200	GF203 GF203 GF201	GF200	GF202 GF200 GF200 GF203 GF203

-1.4876095	-1.4876095	-2.9021233 2.82430974		-1.4089735		-1.0571377		-1.3298808	3			1.41152827	1.07663136	1.37982677
410.868	410.868	410.8668 410.8224	410.7896	410.7558	410.6897	410.6842	410.5287	410.4931	410.2584	410.2153		410.1038	410.0928	409.9522 409.8694
SP11	SPI1	<u>.</u>	TNRC5		SRP46	LOC51696	ADH4	GNG5	70B2			TIMM8B	EPB41L2 YDD19	SMARCD1
spleen focus forming virus (SFFV) proviral integration oncogene spi1 Spleen focus forming virus		se), alpha-1-antitrypsin	rinucieotue repeat containing 5 ESTs, Weakly similar to	hotekin [M.musculus] Splicing factor, arginine/serine-	rich, 46kD	9e 4	(class II), pi polypeptide	-	upiquitin carrier protein EZ-O transducer of ERBB2, 2	ESTs FSTs	ranslocase of inner nitochondrial membrane 8	(yeast) homolog B erythrocyte membrane protein		associated, actin dependent associated, actin dependent subjact of chromatin, subjamily d, member 1 ESTs
sple (SF Hs.157441 ond sple	(SF Hs.157441 ond	Hs.75621 elasta: Hs.77554 ESTs	Hs.56828 5 ES'	Hs.58559 rho Spl	Hs.155160 rich	Hs.6679 Dro	Hs.1219 (cla		Hs.93002 ubi	Hs.74052 ES		Hs.268561 (ye	Hs.7857 bal Hs.25615 YD	ass Rec Rec Rec Rec Rec Rec Rec Rec Rec Rec
Hs.89843	RG.28	Hs.118040 Hs.77554	Hs.56828	Hs.58559	Hs.18257	AA283024 Hs.125111	Hs.1219	Hs.5322	Hs.93002 Hs.4994	Hs.74052	0000	Hs.7499	Hs.33987 Hs.43199	Hs.79335 Hs.1092
N66572	N66572	H58926 H72591	AA454691 Hs.56828	W79834	W87714 Hs.18257	AA283024	H63124	H72187	AA430504 Hs.93002 AA486088 Hs.4994	N93721	00000	AA629910 Hs.7499	W88572 Hs.33987 AA489194 Hs.43199	H91691 T81033
278808	278808	207735	809682	346889	416951	713273	208542	213577	769921 840775	307138	203240	884657	417426 825012	241736 109265
GF200	GF200	GF203 GF200	GF201	GF202	GF201	GF203	GF201	GF200	GF200	GF201	10215	GF203	GF201 GF203	GF201 GF200

1.27445186	1.23790542	-1,2446059		-1.6843089	-1.3459119				-1.6830018							-1.4828659	-1.6804957	-1.6804957		-1.1281971		-1.2695333	1 1505001	100000
409.7357	409.7116 409.7008	409.6077	409.5025	409.4857	409.3351		409.3241		409.3111	409.0844		408.8324		408.7638	408.7346	408.7261	408.6164	408.6164		408.6072		408.3062	400 0070	400.2073
TSC501	KIAA0105 P311	YDD19	NRXN4	BK1191B2.3.1			ATF4			DKFZP586D0919		C140RF1		GLE1L	KIAA0534					MST1R		EIF2S3	בינות ב	ILIORA
kidney- and liver-specific gene TSC501 gene predicted from cDNA with a complete coding	sequence P311 protein	in ontactin	associated protein)	putative acyltransferase Homo sapiens cDNA	NT2BP4001207	activating transcription factor 4 (tax-responsive enhancer	element B67)	Homo sapiens cDNA	FLJ20533 fis, clone KAT10931	DKFZP586D0919 protein	chromosome 14 open reading	frame 1	GLE1 (yeast homolog)-like,	RNA export mediator	KIAA0534 protein	ESTs	H.sapiens seb4D mRNA	H.sapiens seb4D mRNA	macrophage stimulating 1 receptor (c-met-related	nitiation	factor 2, subunit 3 (gamma,	52kD)	Interieukiri 13 receptor, alpha	interieukin 15 receptor, alpria
Hs.14637	Hs.119 Hs 142827	Hs.25615	Hs.31622	Hs.7436	He 13109	2	Hs.181243		Hs.106650	Hs.49378		Hs.15106		Hs.169363	Hs.196012	Hs.221698	Hs.236361	Hs.236361		Hs.2942		Hs.211539	HS.12503	Hs.12503
N58170 Hs.14637	4A598802 Hs.119	AA054135 Hs.23924	4A028905 Hs.31622	N72217 Hs.7436	AA 105041 He 104101	100000000000000000000000000000000000000	AA600217 Hs.75094		4A406580 Hs.106650	4A150199 Hs.49378		N70492 Hs.100294		341973 Hs.22175	416736 Hs.91627	AA455659 Hs.103233	AA459588 Hs.78193	4A459588 Hs.104642		AA129089 RG.61		V66197 Hs.70182	4A053285 HS.11853/	4A053285 Hs.12503
247660 N	898095 A	- `	470279 A	291272 N	V 605333		949971 A		753320 A	491313 A		298384 N		31740 R	_	m		814526 A		586698 A		_	•	488019 A
GF200	GF200	GF203	GF201	GF203	0000	GI-203	GF201		GF203	GF201		GF201		GF201	GF201	GF203	GF200	GF200		GF200		GF203	GF200	GF200

VT2RP1000348, weakly

Homo sapiens cDNA similar to REDUCED

=LJ10427 fis, clone

1.06290848 1.12216082 -1.3165463 -1.6262419 -2.2707527 1.0774037 -1.1905825 -1.1854285 -1.2838512 -1.2953588 -1.0776512 -2.6282661 -1,310381 407.4372 407.4346 407.4187 408.2406 408.0102 407,9555 407.8302 407.5075 407.4872 407,4658 108.1865 407.6127 108.262 407.462 407.49 AKR1C1 APACD 3333 P112 IRF4 Homo sapiens chromosome 9. dehydrogenase 1; 20-alpha (3aldo-keto reductase family 1, STARVATION PROTEIN 161 interferon regulatory factor 4 ESTs, Moderately similar to ESTs, Moderately similar to aryl hydrocarbon receptor member C1 (dihydrodiol nner membrane protein, mitochondrial (mitofilin) alpha)-hydroxysteroid Indulin 2 [H.sapiens] Homo sapiens cDNA Homo sapiens cDNA protease inhibitor 12 nuclear translocator ATP binding protein FLJ10205 fis, clone associated with cell FLJ10652 fis. clone /IABILITY UPON HEMBA1004954 dehydrogenase) VT2RP2005886 ALR [H.sapiens] P1 clone 11659 orain protein 13 (neuroserpin) differentiation ESTS STS Hs.108396 Hs.275374 Hs.166172 Hs.153884 -ls.236844 Hs.107293 Hs.82132 Hs.68090 4s.78504 Hs.85044 Hs.75922 Hs.78589 Hs.6226 Hs.40061 Hs.99403 N91302 Hs.108396 Hs.68783 AA447997 Hs.68090 AA676907 Hs.23999 AA857716 Hs.78504 AA152461 Hs.85044 AA670434 Hs.75922 AA115876 Hs.78589 AA825491 Hs.82132 Hs.40061 AA456048 Hs.99403 Hs.78183 Hs.15885 W92795 Hs.6559 AA043254 Hs.6226 H79772 R11398 N80741 R93124 1358229 1435300 486179 196992 129563 782748 292512 878846 564621 812184 588430 300590 455204 118394 GF200 GF200 GF200 GF203 GF201 GF203 GF202 GF200 GF203 GF203 GF203 GF200 GF203 GF200 3F201

1.02892324 -1.5122362	-1.5119344 -1.3375048	7771777	-1.1309719	-1.2033226	-1.1203001	-1.8132835	1.50453059 -1.7438748	-1.2978725	-1.6185563	
407.3895 407.3067	407.2717 407.0527 406.7937 406.7462	406.697	406.3814 406.3814	406.0966	405.9401 405.8393 405.8378	405.7527 405.7117	405.6723 405.5788	405.5441	405.452	405.127
FLNB	IGFBP2	MAPRE3	ALDH6 NRXN1		LIG1	PPP1R10 GALE	PRKAG1	KHSRP		
filamin B, beta (actin-binding protein-278) ESTs insulin-like growth factor	oinding protein 2 (36KD) ESTs ESTs	unyacyprinicated into 2 microtubule-associated protein, RP/EB family, member 3	aldehyde dehydrogenase 6 neurexin I ESTs, Highly similar to	precursor polypeptide [H.sapiens]	ligase I, DNA, ATP-dependent LIG1 ESTs ESTs	protein phosphatase 1, regulatory subunit 10 galactose-4-epimerase, UDP-	protein kinase, AMP-activated, gamma 1 non-catalytic subunit PRKAG1 EST KH-type splicing regulatory	protein (FUSE-binding protein 2) ESTs, Moderately similar to	CGI-67 protein [H.sapiens] ESTs, Moderately similar to	Ku70-binding protein [H.sapiens]
Hs.81008 Hs.9394	Hs.162 Hs.47135 Hs.167814 Hs.173381			Hs.169079	Hs.1770 Hs.133525 Hs.13960	Hs.106019 Hs.278580	Hs.3136 Hs.261626	Hs.91142	Hs.26765	Hs.61188
AA486238 Hs.81008 AA495926 Hs.9394	H79047 Hs.162 AA788970 Hs.47135 N68738 Hs.108270 D2606 Hc.6075	5	AA455235 Hs.75746 R43532 Hs.22998	W68291 Hs.83968	AA291715 Hs.1770 H66710 Hs.108281 AA777379 Hs.13960	AA071526 Hs.100330 AA281030 Hs.76057	AA070381 Hs.79099 AA447679 Hs.99133	T99639 Hs.91142	N26928 Hs.26765	AA453588 Hs.61188
840818 768433	233721 1240220 293097	39977	450660 814798 32573	342721	725266 211865 449020	366105 711768	531028 813604	123400	257323	795207
GF200 GF203	GF200 GF203 GF201	GF201	GF201 GF203 GF203	GF200	GF200 GF201 GF203	GF201 GF200	GF200	GF200	GF203	GF201

	1.20652448	-2.1060125 -1.1410564	-1.0089682 1.40112815			1.1518449 1.07417185	1371763	-1.9334825	-1.0687478 1.27215144 -1.0129636
405.1075	404.9957	404.9348 404.92	404.7642 404.7462	404 6918	404.6864	404.3798 404.2548 404.2532	404	404.1336	403.9056 403.9015
	LGALS7	TXK			PTGS2	KIAA0992		NFIC	!
ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]	soluble, 7 (galectin 7) Homo sapiens mRNA for	NICE-5 protein TXK tyrosine kinase	ESTs EST	Horro Horro FLJ10622 fis, clone NT2RP2005509, highly similar to Homo sapiens CGI-45	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase 2 (prostaglandin G/H synthase and cyclooxygenase) PTGS2	ESTs KIAA0992 protein ESTs	ESTS, Moderately similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!!	[H.sapiens] nuclear factor I/C (CCAAT- binding transcription factor)	ESTS ESTS ESTS
Hs.108979	Hs.99923	Hs.23410 Hs.29877	Hs.77703 Hs.34011	71.05.01 800.02.01	Hs.196384	Hs.258812 Hs.6496	600000	HS.190356 Hs 184771	Hs.23260 Hs.42873 Hs.34192
N34345 Hs.108979	AA011057 Hs.99923	748169 Hs.107538 112312 Hs.29877	AA147338 Hs.77703 H48115 Hs.34011	M05063 Hs 110178	AA644211 Hs.92309	H54701 Hs.29798 T67663 Hs.94143 R41754 Hs.6496	2001-001	AA/U1108 HS.119/38	
270997 N	359747 Av	153743 R- 148421 H		230000 AV		203268 H 66774 TG 31825 R		397555 A	
GF201	GF200	GF200 GF200	GF202 GF200		GF201	GF203 GF200 GF201	ם מבונה	GF203	GF203 GF203 GF200

	1.56422267	1.19160091	1.39896126	0 5444045	2.2441913	-1.0820.T-	-1.4540849	-1.109673		-1.6971347		-1.5373703			1.00933609	-2.2109973		-1.6249788					-1.0997391	-1.60640/		-2.7062697		-1.1717023		1.12648289	
	403.8155	403.7552	403.7142	400 6400	403.0193	403.5569	403.3888	403.2839	403.1689	403.0974		403.0944	403.0634		403.0115	402.9775		402.8634			402.6128		402.5934	402.541		402.4794	402.4665	402.4391		402.4221	
		FACL2			CHU3	KIAA0677				CBLN1		AMPD2			NFE2L1			PRP4					PTPRN				ADORA2B			SUCLA2	
ESTs, Weakly similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	[H.sapiens] fatty-acid-Coenzyme A ligase,	long-chain 2	ESTs	Chromodoniain helicase DIVA	binding protein 3	KIAA0677 gene product	ESTs	ESTs	ESTs	cerebellin 1 precursor	adenosine monophosphate	deaminase 2 (isoform L)	ESTs	nuclear factor (enythroid-	derived 2)-like 1	ESTs	serine/threonine-protein	kinase PRP4 homolog	Homo sapiens cDNA	FLJ10308 fis, clone	NT2RM2000260	protein tyrosine phosphatase,	receptor type, N	ESTs	ESTs, Weakly similar to	ratariii pou suburiii [H.sapiens]	adenosine A2b receptor	ESTs	succinate-CoA ligase, ADP-	forming, beta subunit	
	Hs.120949	Hs.154890	Hs.191184		Hs.25601	Hs.155983	Hs.172843	Hs.26270	Hs.269039	Hs.662		Hs.82927	Hs.27804		Hs.83469	Hs.269382		Hs.198891			Hs.14169		Hs.89655	Hs.33905		Hs.5152	Hs,45743	Hs.23197		Hs.182217	
	Hs.17753	Hs.34	Hs.97393		4A454980 Hs.34886	4A620458 Hs.32725	AA424910 Hs.31744	Hs.26270	Hs.40753	AA495901 Hs.662		AA485376 Hs.82927	Hs.27804		AA496576 Hs.83469	AA287090 Hs.87558		AA598779 Hs.119139			AA431716 Hs.14169		Hs.89655	AA495819 Hs.33905		Hs.5152	C	Hs.23197		AA282208 Hs.40820	
	T96215	173556	T97917		AA45498	AA62045	AA42491	R49555	N31588	AA49590		AA48537	H29308		AA49657	AA28709		AA59877			AA43171		R45941	AA49581		H50655	AA05535	N66205		AA28220	
	120973	82734	121559		811893	951091	768229	38344	271750	768357		811013	52725		755821	701690		898070			782246		33941	768395		194318	377252	278644		712888	
	GF200	GF200	GF200		GF203	GF202	GF203	GF203	GF201	GF200		GF203	GF201		GF200	GF203		GF202			GF201		GF200	GF203		GF203	GF201	GF203		GF203	

Attv Docket No. 2172			-1.2183586	1.03057407	-1,0115952	1.09466093		-1.734928 -1.2703603	-1.6914738				-1.5380694 -1.3759994	-1.2054506
Affv		402.3539	402.2308 402.2299	402.2243	402.2233	402.1735	402.1226	402.1132 401.9862	401.6289	401.6169	401.6147	401.4744	401.4436 401.4255	401.3779 401.364 401.2135
00001		GSBS	SUDD	GPX2	PCK1			HRMT1L1	GNA12	UMPK	ISYNA1		RNASE1 ASGR1	PPP1R2
105857758 .070201	APPENDIX A	G-substrate	sudD (suppressor of bimD6, Aspergillus nidulans) homolog ESTs	glutathione peroxidase 2 (gastrointestinal)	pnospnoenolpyruvate carboxykinase 1 (soluble) Homo sapiens mRNA; cDNA	DKFZp434E1212 (from clone DKFZp434E1212) ESTs, Weakly similar to !!!!	ALC SOBFAMIL 1 5 WARNING ENTRY !!!! [H.saplens] HMT1 (hnRNP	methyltransferase, S. cerevisiae)-like 1 EST	guanine nucleotide binding protein (G protein) alpha 12	uridine monophosphate kinase UMPK	synthase A1	mRNA clone 1046:1-1	1 (pancreatic) asialoglycoprotein receptor 1	protein phosphatase 1, regulatory (inhibitor) subunit 2 PPP1R2 ESTs ESTs
		Hs.227011	Hs.209061 Hs.193379	Hs.2704	Hs.1872	Hs.120439	Hs.33439	Hs.235887 Hs.40172	Hs.182874	Hs.75939	Hs.264414	Hs.210783	Hs.78224 Hs.12056	Hs.267819 Hs.32995 Hs.48487
		Hs.27581	Hs.92389 Hs.33707	AA135289 Hs.2704	AA405769 Hs.1872	AA598956 Hs.111571	Hs.33439	AA778346 Hs.105365 H80724 Hs.40172	Hs.119040	Hs.75939	AA454554 Hs.24746	AA487262 Hs.100922	AA487797 Hs.78224 H58255 Hs.12056	AA428749 Hs.91585 AA398412 Hs.32995 N62213 Hs.48487
		H09573	R35649 N57936	AA13528	AA40576	AA59895(R87650	AA77834 H80724	R83896	90669W	AA45455	AA48726	AA48779 H58255	AA42874 AA39841: N62213
7	g B	46041	136998 247233	587847	742082	898055	194607	379309 241507	186623	344243	809508	841495	840493 204541	769657 726878 290182
Monthson to the	NA CONTRACTOR	GF201	GF201 GF200	GF200	. GF200	GF203	GF201	GF203 GF200	GF203	GF201	GF201	GF201	GF200 GF200	GF200 GF203 GF201

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Atty Docket No. 2172	401.1427 -2.5448645					400.4762 1.03999951				400.4598 -2.4282744		400.4495 1.03618796		400.4495 1.03618796	400.3479	400.26					399.8993 -1./6690/6		399.8377	8282 000	399.1210	_			399.3351 -2.2934745		399.3146		399.313
										MGAT4A		MSF		MSF	THY1					HOXA9					Faire	CEE			RING1				-
APPENDIX A	ESTs	ESTS	ESTs	ESTs	ESTs	EST	mannosyl (alpha-1,3-)-	glycoprotein beta-1,4-N-	acetylglucosaminyltransferase,	isoenzyme A	megakaryocyte stimulating	factor	megakaryocyte stimulating	factor	Thy-1 cell surface antigen	ESTs	Homo sapiens mRNA; cDNA	DKFZp566P2346 (from clone	DKFZp566P2346)	homeo box A9	ESTs	ESTs, Weakly similar to	KIAA0984 protein [H.sapiens]	ES Is, Highly similar to CGI-	121 protein [H.sapiens]	postsynaptic protein CRIP1	ESTs	ESTs	ring finger protein 1	Homo sapiens clone 23664	and 23905 mRNA sequence	Homo sapiens cDNA	FLJ20642 fis, clone KAT02751
	Hs.112757	HS.Z41/Z Hs.71922	Hs.180391	Hs.166783	Hs.60797	Hs.260516				Hs.177576		Hs.218791		Hs.218791	Hs.125359	Hs.206469			Hs.183770	Hs.127428	Hs.33470		Hs.108118		Hs.26706	Hs.39733	Hs.268672	Hs.91870	Hs.35384		Hs.180737		Hs.13801
	AA609744 Hs.112757	AA101954 HS:24172 AA148417 HS:71922	AA490255 Hs.105254	AA453287 Hs.26198	AA021132 Hs.60797	H25907 Hs.32202				R66290 Hs.28715		AA280514 Hs.100096		AA280514 Hs.80749	AA496283 Hs.74563	H29276 Hs.6666			AA150895 Hs.12361	AA497085 Hs.105397	R86845 Hs.33470		N52651 Hs.33969		AA284291 Hs.26706	AA401475 Hs.39733	R10108 Hs.113073	AA448855 Hs.91870	AA425254 Hs.35384		T61475 Hs.6803		AA453271 Hs.13801
k et al.	1031907	510668	823771	795395	364098	162161				140759		712641		712641	769686	49953			505062	897497	165824		245039		327245	742610	128894	786154	773246		79935		795367
Westbrook et al.	GF202	GF202	GF203	GF202	GF203	GF200				GF200		GF200		GF200	GF201	GF201	i		GF201	GF200	GF203		GF201		GF201	GF201	GF203	GF203	GF200		GF201		GF201

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-1.2715537	-1.1812753	-1.0206727	-1.3444751	-1.6516851	1.00721331	1.09680786	-1.0027582		-1.2242105		1.26807197		-2.8267811					-1.8413177			-1.3912573		-1.6623567	1.32741895	-1.1760565		!	1.22718407	
399.1783	399.0525	398.8794	398.7571	398.7514	398,7417	398.6907	398.6659		398.6353	398.4416	398.3378		398.2892		398.2661		398.2639	398.0245	398.0189	398.0049	397.8749		397.8669	397.8635	397.8148	397.7708		397.7206	
SPTAN1	PSMA2		CL640	KIAA0081							NUP153						SLC12A7						MPDU1		DGUOK	KIAA1098		PTE1	
spectrin, alpha, non- erythrocytic 1 (alpha-fodrin) proteasome (prosome, macropain) subunit, alpha	type, 2	EST	hypothetical protein	KIAA0081 protein	ESTs	ESTs	ESTs	Homo sapiens clone 24416	mRNA sequence	ESTs	nucleoporin 153kD	Homo sapiens mRNA; cDNA DKFZp43401519 (from clone	DKFZp434O1519); partial cds	Homo sapiens cDNA FLJ10193 fis, clone	HEMBA1004763	solute carrier family 12 (potassium/chloride	transporters), member 7	ESTs	ESTs	ESTs	ESTs	mannose-P-dolichol utilitzation	defect 1	ESTs	deoxyguanosine kinase	KIAA1098 protein	peroxisomal acyl-CoA	thioesterase	
Hs.77196	Hs.181309	Hs.230219	Hs.44563	Hs.78871	Hs.226925	Hs.189878	Hs.269659		Hs.5957	Hs.78980	Hs.211608		Hs.102541		Hs.235195		Hs.172613	Hs.5930	Hs.49806	Hs.251879	Hs.22222		Hs.6710	Hs.269662	Hs.77494	Hs.137732		Hs.69575	
Hs.62313	Hs.78080	4A682479 Hs.117257	V62617 Hs.44563	AA284495 Hs.78871	AA016245 Hs.60697	AA701662 Hs.114072	AA700867 Hs.114068		4A417761 Hs.5957	AA284288 Hs.102962	Hs.75336		Hs.102541		Hs.3757		AA427732 Hs.12579	Hs.5930	AA429484 Hs.49806	Hs.107069	AA213667 Hs.22222		Hs.6710	Hs.126693	Hs.77494	Hs.82605		AA447824 Hs.69575	
T60235	R71913	AA682479	N62617	AA284495	AA016245	AA701662	AA700867		AA417761	AA284288	R12905		R76614		H29513		AA427732	H61276	AA429484	N62251	AA213667		R77432	H99467	R07560	N53505		AA447824	
76362	155434	450642	288888	713653	360747	433590	452354		746245	327085	27548		143661		52635		770838	236279	771177	287770	683274		145132	262342	125722	284139		813591	
GF200	GF200	GF203	GF203	GF200	GF203	GF203	GF203		GF203	GF201	GF200		GF200		GF201		GF201	GF203	GF201	GF201	GF203		GF200	GF203	GF200	GF201		GF200	

	1.09465909		-2.3227744		-2.1740039	-2.2762883	-1.3436331	1.17453907	-2.3076875	-1.1150952
397.6858	397.677 397.6469	397.5197	397.5193	397.4581	397.1772 397.0719 397.0623	397.0466 396.9671 396.8884	396.8066	396.7825 396.726	396.7243 396.7122 396.6373	396,5842
ZNF174	MTF1 PDCD2	PNN	CD47						CREM LSP1 KIAA0036	CASP1
zinc finger protein 174	factor 1 programmed cell death 2	printi, destriosonire associated protein (Bh-related	antigen, integrin-associated signal transducer)	Homo sapiens cDNA FLJ20431 fis, clone KAT03722 ESTs, Weakly similar to	hypothetical protein [H.sapiens] ESTs ESTs	ESTs, Moderately similar to KIAA0007 [H.sapiens] ESTs ESTs	Homo sapiens cDNA FLJ1312 fis, clone PLACE1010105, weakly similar to RING CANAL PROTEIN	Homo sapiens mRNA for KIAA1184 protein, partial cds ESTs	cAMP responsive element modulator lymphocyte-specific protein 1 KIAA0036 gene product	caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase)
Hs.155204	Hs.211581 Hs.41639	Hs.274459	Hs.82685	Hs.80162	Hs.12296 Hs.58595 Hs.271651	Hs.191526 Hs.32565 Hs.46616	Hs 198711	Hs.100747 Hs.34396	Hs.155924 Hs.56729 Hs.169387	Hs.2490
AA700196 Hs.26872	AA676322 Hs.74080 AA521466 Hs.41639	Hs.83389	AA455448 Hs.82685	Hs.12054	N48293 Hs.12296 AA025246 Hs.58595 N23753 Hs.36519	AA460557 Hs.90315 AA495814 Hs.32565 N64790 Hs.46616	A A 482 594 Hs 62 684	Hs.100747 Hs.34396	AA464861 Hs.79106 R74253 Hs.107202 N35079 Hs.89729	Hs.2490
AA700196	AA676322 AA521466	W57983	AA455448	T70901	N48293 AA025246 N23753	AA460557 AA495814 N64790	AA482594	R01094 R91258	AA464861 R74253 N35079	T95052
453147	430427 826211	341051	813552	84022	279575 365425 268000	796674 768406 284601	746080	124447	789383 143306 271684	120106
GF201	GF201 GF200	GF201	GF200	GF201	GF203 GF201 GF201	GF201 GF203 GF201	66503	GF201 GF200	GF201 GF200 GF201	GF200

					stromal cell derived factor			
GF203	767983	AA418825 Hs.7365	Hs.7365	Hs.6354	receptor 1	SDFR1	396.5546	-2.6410376
GF203	396111	AA757732	AA757732 Hs.121534	Hs.190408	ESTs		396.5015	-1.129685
					p75NTR-associated cell death			
					executor; ovarian granulosa			
GF200	138775	R63543	Hs.17775	Hs.17775	cell protein (13kD)	DXS6984E	396.4144	-1.047487
GF201	283268	N45301	Hs.46501	Hs.201591	ESTs		396.1459	
					cell growth regulatory with ring			
GF201	417361	W89211	Hs.103236	Hs.59106	finger domain	CGR19	396.0854	
GF201	309233	N98336	Hs.54811	Hs.54811	ESTs		396.0503	
					response (cyclin-			
GF200	38763	R51052	Hs.85270	Hs.250595	related)	SPHAR	396.002	-2.1182051
					S-phase response (cyclin-			
GF200	38763	R51052	RG.49	Hs.250595	related)	SPHAR	396.002	-2.1182051
					Homo sapiens cDNA			
					FLJ11282 fis, clone			
					PLACE1009476, weakly			
					similar to PUTATIVE ATP-			
					DEPENDENT RNA			
					HELICASE T26G10.1 IN			
GF201	288667	N59197	Hs.107137	Hs.155049	CHROMOSOME III		395.9495	
					Nijmegen breakage syndrome			
GF203	261567	H98655	Hs.42548	Hs.25812	1 (nibrin)	NBS1	395.8637	1.04532669
GF201	810875	AA458983	AA458983 Hs.15911	Hs.15911	DKFZP586E1422 protein	DKFZP586E1422	395.774	
					general transcription factor IIH,			
GF200	811942	AA455003	AA455003 Hs.89578	Hs.89578	polypeptide 1 (62kD subunit)	GTF2H1	395.7492	1.09695889
				000707	Sel-1 (Supplessor of IIII-12,	÷ 1.0	0223	
GF201	8/218	165844	HS.11//8	HS.181300	C.elegans)-like Homo saniens mBNA for DIPB		393.0772	
GF201	795828	AA61495	AA461495 Hs 14512	Hs 14512	protein		395.677	
GESON	139818	B62373	Hs 52526	Hs 52526	KIAA0669 gene product	KIAA0669	395.6361	-1.8806249
0000	53048	B15748	He 21383	He 21383	ESTS		395.6261	-2.1377051
8	2000	2	20012:01		ESTs, Weakly similar to CGI-			
GF200	244974	N54932	Hs.8187	Hs.234156	128 protein [H.sapiens]		395.5599	-1.2124937

-1.9703554	1.36879983 -1.998578	1.01891231	-1.3731633	1.14043403	-1.5815303	-1.4773571
395.3637	395.2983 395.2879 395.1088	395.0753	394.9422 394.7626 394.6814 394.6381 394.6338	394.4789 394.4503 394.305 394.281	394.1952	393.9345 393.9188
	KDELR2 5T4	MTIF2	RYBP PMM2	TCF17 LTBP3		STS CREB3
ESTS, Weakly similar to IIII ALU CLASS B WAFNING THYT IIII [Histaplens] Homo sapiens mFNA; cDNA DKFZp564P116 (from clone DKFZp564P116)	andoplasmic reticulum protein retention receptor 2 5T4 oncofetal trophoblast glycoprotein ESTs	mitochondrial translational initiation factor 2	Ring1 and YY1 binding protein RYBP ESTs ESTs Homo sapiens clone 23570 Homo sapiens clone 23570 phosphomannomutase 2 PMM2	ES Is transcription factor 17 ESTs tatent transforming growth factor beta binding protein 3	Homo sapiens cDNA FLJ11015 fis, clone PLACE1003302, highly similar to ZINC FINGER PROTEIN 83	steroid sulfatase (microsomal), arylsulfatase C, isozyme S cAMP responsive element binding protein 3 (luman)
Hs.30237	Hs.118778 Hs.82128 Hs.77114	Hs.149894	10.	Hs.95835 Hs.100932 Hs.97276 Hs.238839	Hs.29147	Hs.79876 Hs.173422
H93217 Hs.30237 H10403 Hs.25832	AA626867 Hs.118778 AA428514 Hs.82128 T83551 Hs.77114	H18070 Hs.3823	AA454193 Hs.7910 N62077 Hs.48475 A424920 Hs.23799 AA459657 Hs.12311 N35888 Hs.44759	AA464688 Hs. 95835 R26082 Hs. 100932 AA464558 Hs. 97276 AA278842 Hs. 111396	AA166907 Hs.61518	H15215 Hs.79876 AA401477 Hs.65677
H93217	AA626867 AA428514 T83551	H18070	AA4541 N62077 AA4246 AA4596 N35886	AA4646 R26082 AA4646 AA2786	AA1669	H15218
241824	745214 773170 111122	50754	795453 289868 768953 795529 272529	810218 132144 810529 703827	595529	49591
GF200 GF201	GF201 GF200 GF200	GF200	GF201 GF201 GF203 GF201 GF201	GF201 GF203 GF201 GF203	GF202	GF200 GF201

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⋖	393.6087 393.317	393.3099	393.2906	393.2419	393.1416	393.0125	392.8519	392.838	392.7391	392.696	392.6434	392.4106	392,3838		392.1145	392.1039		391.7729		391.4425 391.4287	
	FLJ20040		CHEDG1		PBEF KIAA1249	KIAA0879		KIAA0602		CD3G	GABRE			~ _		GAS7		AGPAT1 KIAA1026		LAS	
APPENDIX A	EST hypothetical protein	ESTs, Weakly similar to open reading frame [M.musculus]	G protein-coupled sphingolipid receptor ESTs. Highly similar to	hypothetical protein [H.sapiens] pre-B-cell colony-enhancing	factor	KIAA0879 protein	ESTs	KIAA0602 protein	ESTS	CD3G antigen, gamma polypeptide (TIT3 complex)	gamma-aminobutyric acid (GABA) A receptor, epsilon	ESTs	ESTs	ESTs, Weakly similar to Weak similarity with the Ysv6 protein	[C.elegans]	growth arrest-specific 7 1-acylglycerol-3-phosphate O-	acyltransferase 1 (lysophosphatidic acid	acyltransferase, alpha) KIAA1026 protein	ESTs, Moderately similar to hematopoietic RING finger 1	[M.musculus] lipoic acid synthetase	
	Hs.119998 Hs.61960	Hs.19978	Hs.274488	Hs.40241	Hs.239138	Hs.54037	Hs.47587	Hs.37656	Hs.262544	Hs.2259	Hs.22785	Hs.120873	Hs.13812		Hs.11252	Hs.226133		Hs.240534 Hs 27742	!	Hs.37680 Hs.53531	
	AA707189 Hs.119998 AA429470 Hs.61960	AA707659 Hs.19978	R13546 Hs.1387	AA004878 Hs.40241	AA281932 Hs.6895		AA454982 Hs.47587	AA454581 Hs.37656	AA485080 Hs.86429	T66800 Hs.2259	H63934 Hs.22785	9	N40556 Hs.13812		AA598538 Hs.11252	R54060 Hs.91757		AA458922 Hs.6587 B63407 Hs 27742		N80989 Hs.38036 W72965 Hs.53531	
ok et al.	451925 771157	451707	26418	428570	712604	281737	811895	809525	815740	66322	209137	399081	276816		898162	39918		814409		292357 344825	
Westbrook et al.	GF203 GF201	GF203	GF200	GF201	GF200	GF203	GF203	GF201	GF203	GF200	GF200	GF203	GF203		GF203	GF203		GF200) j	GF200 GF201	

H61595 H8.37982 ESTS FIST H322868 H8.6726 H8.227630 Irach silencing transcription AEST 391.0609 H77554 H8.55416 ESTS SIST 390.8038 AAA73221 H8.74584 H8.151787 116 kD SIST 390.8038 AAA41812 H8.3777 H8.108479 H8.108479 H9.108479 H9.108479 NS2482 H8.108479 H8.108479 H8.108479 H9.108479 390.8038 AAA41812 H8.24867 H8.26805 ESTS SIMPLATATION SPECIFICITY FACTOR, 100	Westbrook et al. GF203 824260	AA491256	AA491256 Hs.97179	Hs.97179	APPENDIX A ESTs		Atriy 1 391.1919	Atty Docket No. 21726,
REST	32.0	H61595	Hs.37982	Hs.37982	ESTs RE1-silencing transcription		391.0609	-1.0596881
AA779221 Hs, 7484 Hs, 151787 116 kD U5-116 kD 390,283 AA448192 Hs, 37727 Hs, 128652 ESTs 390,7892 NEZ482 Hs, 108479 Hs, 108479 Hs, 108479 Hs, 108479 NEZHRA 10373 Hs, 128652 ESTs 390,7864 NTZPR 4007 86, weakly SPECIFICITY FACTOR, 100 SPECIFICITY FACTOR, 100 NZ5619 Hs, 42851 Hs, 28600 ESTs AA707871 Hs, 12813 US, 28000 ESTs AA707871 Hs, 12813 DKFZP43AJ214 protein DKFZP43AJ214 390,561 PK18269 Hs, 12813 DKFZP43AJ214 protein 390,6187 PK2004 Hs, 11369 Hs, 25615 VDD19 protein VDD19 N20054 Hs, 124779 ESTs, Moderately similar to ND19 N20054 Hs, 16876 ESTS SS0,3993 AA205403 Hs, 134779 Hs, 1857 Hs, 1857 Human clone 29629 mRNA SS0,393 SS0,393 AA69451 Hs, 49774 ESTS Human clone 29629 mRNA SS0,393 AA454618<	4 8	R32858 H77554	Hs.6726 Hs.35416	Hs.227630 Hs.35416	factor ESTs U5 snRNP-specific protein,	REST	391.0493 390.993	-1.2318362 -1.3812123
Homo sapiens cDNA FLUG97 is, conve FLUG97 is, convergence in the FLUG97 is, convergenc	ထက္က	AA779221 AA448192 N52482	I Hs.74584 2 Hs.97727 Hs.108479	Hs.151787 Hs.128652 Hs.108479	116 kD ESTs ESTs	U5-116KD	390.8038 390.7892 390.7064	-1.7454816
AA47959 Hs.15562 Hs.15562 Hs.2650 Hs.2650 Hs.2650 Hs.2650 Hs.2650 Hs.2650 Hs.2650 Hs.2650 Hs.2661 Hs.2661 Hs.2661 Hs.2661 Hs.2661 Hs.2661 Hs.2661 Hs.2660 Hs.2661 Hs.2662	,				Homo sapiens cDNA FLJ10871 fs, clone NT2RP4001696, weakly similar to CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100			
AA707871 Hs.12813 Hs.12813 DKFZP434J214 protein DKFZP434J214 380.5051 R41839 Hs.17248 Hs.154073 UDP-gallactose transporter UGTREL1 380.5008 T64004 Hs.1369 Hs.2615 YDD19 protein YDD19 380.5008 N20054 Hs.20325 Hs.20325 Hs.20325 Hs.20325 Hs.30471 AA05443 Hs.18576 Hs.18779 ESTS Molecular shall sha	2 5	AA447959 N25619	9 Hs.15562 Hs.42651	Hs.15562 Hs.269036	KD SUBUNIT ESTs		390.6941 390.6187	-1.0740673
Hard Hard Hard Hard Hard Hard Hard Hard	00	AA707871	l Hs.12813	Hs.12813	DKFZP434J214 protein UDP-galactose transporter	DKFZP434J214	390.5051	-1.6949145
Page		R41839 T64004	Hs.17248 Hs.11369	Hs.154073 Hs.25615	related YDD19 protein	UGTREL1 YDD19	390.5008 390.4934	-1.0015452
N63171 Hs.116834 Hs.11711 KIAA0329 gene product KIAA0329 390.0383 W21373 Hs.24930 1400lin-specific Chaperone a TBCA 390.0122 390.0122 R39602 Hs.30784 Himman clone 23629 mRNA 389.8794 389.8794 R39602 Hs.135687 sequence 389.8794 389.8794 Human clone 23629 mRNA STS 389.8499 389.8499 Ha.69714 Hs.69714 ESTS 389.8499 R4454618 Hs.12479 Hs.2479 SH3 domain of STAM 389.5335 AA454618 Hs.2479 Hs.2487 Homo sapiens mRNA for measured controlled co	990	N20054 AA205403 AA034179	Hs.20325 3 Hs.124779 9 Hs.18576	Hs.20325 Hs.124779 Hs.18576	ESTs, Moderately similar to pot. ORF V [H.sapiens] EST ESTs		390.4741 390.3093 390.1375	-1.0961828 -1.2919524
R39602 Hs.30799 He.135587 sequence 338.8734 A68945A; Hs.17726 Hs.6432 ESTs 389.8734 H40697 Hs.13906 Hs.49714 Hs.49714 Hs.49714 Hs.3971 A4454618 Hs.12479 Hs.12479 Hs.12479 Hs.13976 389.5335 AA457044 Hs.43729 Hs.20887 KIAA1212 protein, pantal ods 389.5217	100	N63171 W21373	Hs.116834 Hs.24930	Hs.11711 Hs.24930	KIAA0329 gene product tubulin-specific chaperone a Human clone 23629 mRNA	KIAA0329 TBCA	390.0383 390.0122	-2.0224272 1.79041629
N94060 Hs.49714 Hs.49714 ES18 389.586 AA454618 Hs.12479 Hs.12479 SH3 domain of STAM AMSH 389.5335 Homo sapilens mRNA for AA497044 Hs.43729 Hs.20887 KIAA1212 protein, partial ods 389.5217	° 53 24	R39602 AA699457 H40697	Hs.90799 7 Hs.117326 Hs.113906	Hs.135587 Hs.163432 Hs.25223	sequence ESTs ESTs		389.8794 389.8499 389.842	-2.407956
AA497044 Hs.43729 Hs.20887 KIAA1212 protein, partial cds 389.5217	2 8	N94060 AA454618	Hs.49714 3 Hs.12479	Hs.49714 Hs.12479	ests associated molecule with the SH3 domain of STAM Homo sapiens mRNA for	АМЅН	389.5335	GZZ6C90.1-
	22	AA49704	4 Hs.43729	Hs.20887	KIAA1212 protein, partial cds		389.5217	-1.3424034

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-1.0573423	-2.6860929	-1.2954897	-1.1420152		1.212864	000000000000000000000000000000000000000		1.40980249	-2.5313694	-1.2676124		-1.4338734	1 6600001	200000	1.17315158	1.12433985		-1.036678		1.33874764
389.5126 389.5078	389.4398 389.1726	388.941	388.9361		388.9029	388.6821		388.6227	388.4741	388.3385		388.182	900	300.014	388.0027	388.0008		387.9873		387.9777
STX11		ALB	GJA7		ERCC4			SSBP		YDD19		CASP9	2700.41	MARSKS	SPUVE	NUP88				DDX11
Homo sapiens mRNA; cDNA DKFZp4340071 (from clone PKTZp4340071) syntaxin 11 Homo sapiens cDNA FLJ11052 fis, clone	PLACE1004645 EST	albumin	gap junction protein, alpha 7, 45kD (connexin 45) excision repair cross-	complementing rodent repair deficiency, complementation	group 4	ESTs	single-stranded DNA-binding	protein	ESTs	YDD19 protein	caspase 9, apoptosis-related	cysteine protease	mitogen-activated protein	Kinase Kinase Kinase 5 serine protease, umbilical	endothelium	nucleoporin 88kD	ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!!	[H.sapiens]	Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like	helicase)
Hs.7089 Hs.118958	Hs.274136 Hs.119913	Hs.75442	Hs.138959		Hs.89296	HS.122810 HS.59077		Hs.923	Hs.184664	Hs.25615		Hs.100641	1	HS.151988	Hs.154737	Hs.172108		Hs.54073		Hs.27424
	W73592 Hs.103186 AA705684 Hs.119913	AA700758 Hs.58451	AA027964 Hs.61459		AA292809 Hs.89296	AA/06/78 HS.122810 AA001884 HS.59077		R05693 Hs.923	AA452545 Hs.61748	N66135 Hs.28731		AA281152 Hs.100641		AA151065 Hs.84149	R76394 Hs.29968	AA488609 Hs.90734		N78903 Hs.54073		AA032090 Hs.62461
111721	344056 435145	435371	469762		727210	431369		125183	788494	278496		705110	!	504877	143887	843070		300024		470930
GF200 GF200	GF201 GF203	GF203	GF200		GF200	GF203		GF200	GF203	GF203		GF200		GF200	GF200	GF200		GF202		GF200

-1.1622472 1.54126185	1.16507584 -1.294028 1.62117919	1.45381213	-1,3281091	-1.7750703
387.9425 387.9162 387.7411 387.6974	387.5467 387.5467 387.5394	387.5214 387.5052 387.4458	387.4365 387.2382 387.2315 387.1807 387.1496	386.8484 386.8484 386.8255
COP9 MAD4	HDCMC28P	RMSA1 FGFR1	PF21.2	CACNA1H
COP9 homolog ESTs ESTs Mad4 homolog Homo sapiens cDNA	COL09072 HDCMC28P protein ESTs, Weakly similar to cell fate specification homolog MAB2L1 [M.musculus]	assembly I dibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome)	endothelin converting enzyme nuclear factor (erythroid- denved 2)-like 2 ESTs, Highly smilar to OASIS protein [M. musculus] ESTs, Weakly similar to HRIHFED157 [H. sapiens] ESTs Human gene from PACs Aminior 10 SAMTA and 360E16	onformscorne A, similar to small G proteins, especially RAP-2A ESTs calcium channel, voltage-calcium channel, voltage-dependent, alpha IH subunit CACNAIH
Hs.75193 Hs.61857 Hs.35586 Hs.102402	Hs.23412 Hs.88820 Hs.35533	Hs.1010 Hs.748 Hs.40096	Hs.181406 Hs.155396 Hs.55898 Hs.9589 Hs.130843	Hs.225979 Hs.93125 Hs.122359
AA489699 Hs.75193 AA131862 Hs.61857 R96695 Hs.35586 AA447515 Hs.6563	AA485140 Hs.88820 AA485140 Hs.88820 R96208 Hs.35533	R77718 Hs.92278 R54846 Hs.748 AA398394 Hs.40096	H18427 Hs.18880 AA629687 Hs.78975 W49690 Hs.55898 AA488984 Hs.109966 AA011041 Hs.100051	AA022910 Hs.5159 AA022910 Hs.93125 AA779225 Hs.122359
824382 504081 199624 782578	686664 815772 197856	145513 154472 726790	50882 884438 325126 824719 359687	487929 364547 452676
GF200 GF201 GF200 GF201	GF203 GF203 GF200	GF200 GF201 GF201	GF201 GF201 GF201 GF203 GF203	GF201 GF201 GF203

				-1.0842525	-1.2240349		-1.0115178		-1.6210007							1.61464541	-1.4284204	-2.4448587	1.02877591	-1.0541606	-1.4521526		2.16361567						-1.4053723		-1.6166157
386.793	386.7556			386.7424	386.6971		386.2968		386.2567		385.9983					385.8548	385.8465	385,7813	385.71	385.6819	385.6713		385.654		385.5987			385.4219	385.1376		385.0598
GOLGA3					KIAA0210				COL14A1		UBE2B					OGT		ARF4	KIAA0225		DKFZP564B0769		ITGA4								
golgi autoantigen, golgin subfamily a, 3	ESTs	ESTs, Highly similar to	METALLOT MICINEIN-IB	[H.saplens]	KIAA0210 gene product	Homo sapiens clone 25186	mRNA sequence	collagen, type XIV, alpha 1;	undulin	ubiquitin-conjugating enzyme	E2B (RAD6 homolog)	O-linked N-acetylglucosamine	(GICNAc) transferase (UDP-N-	acetylqlucosamine:polypeptide-	N-acetylalucosaminyl	transferase)	ESTs	ADP-ribosylation factor 4	KIAA0225 protein	ESTs	DKFZP564B0769 protein	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of	VLA-4 receptor)	ESTs, Highly similar to	neuregulin-3 [M.musculus]	Homo sapiens mRNA; cDNA	DKFZp434E146 (from clone	DKFZp434E146)	ESTs	Human clone 23721 mRNA	sedneuce
Hs.4953	Hs.20188			Hs.36102	Hs.115740		Hs.5985		Hs.36131		Hs.811					Hs.100293	Hs.171585	Hs.75290	Hs.84790	Hs.32703	Hs.18368		Hs.40034		Hs.19515			Hs.6120	Hs.12097		Hs.83572
AA663910 Hs.4953	W94896 Hs.20188			Hs.36102	AA278840 Hs.79149		H48472 Hs.5985		AA167222 Hs.36131		Hs.79349					Hs.100293	Hs.31656	Hs.75290	4A600190 Hs.84790	AA018618 Hs.32703	Hs.18368		AA490846 Hs.81929		Hs.19515			4A457102 Hs.6120	Hs.12097		Hs.22868
AA663910	W94896			H72722	AA278840		H48472		AA16722		T88933					R40794	H20128	T71316	AA600190	AA018618	W92594		AA490846		H29781			AA457102	R99311		R45056
855684	415204			232772	703846		200599		609332		22428					28012	172403	85171	950369	362686	357970		823964		52754			810411	201264		34773
GF201	GF201			GF200	GF200		GF200		GF200		GF201					GF200	GF203	GF203	GF200	GF203	GF200		GF203		GF201			GF201	GF200		GF200

100007790,070001

7000000	1.35300535		-1.546679	-1.6201992			-1.1664372	-1.4587556						-2.7013892	-2.5837783		-1.2372285		1.03680782						-1.0148674		-1.9373804		-1.93/3804	-1.9591981		-1.3908603	
1000	364.9403	384.8042	384.6355	384.5792			384.4378	384.3044	384.2031			384.1925	384.1768	384.1212	384.0844		384.0788	383.9898	383.8782		383.7395		383.4923	383.4812	383.3531		383.3418		383.3418	383.295		383.2881	
		P2Y5		ALOX5								RES4-25	KIAA0417	AZGP1			CRYZL1	KIAA0979			CCT7			PIM1	TPM1		SPHAR		SPHAR				
Human clone 121711 defective mariner transposon	Hsmar2 mHNA sequence purineraic receptor (family A	group 5)	ESTs	arachidonate 5-lipoxygenase	Homo sapiens mRNA; cDNA	DKFZp434H092 (from clone	DKFZp434H092); partial cds	ESTs	ESTs	gene near HD on 4p16.3 with	homology to hypothetical S.	pombe gene	KIAA0417 gene product	alpha-2-glycoprotein 1, zinc	ESTs	crystallin, zeta (quinone	reductase)-like 1	KIAA0979 protein	ESTs	chaperonin containing TCP1,	subunit 7 (eta)	Homo sapiens clone 25088	mRNA sequence	pim-1 oncogene	tropomyosin 1 (alpha)	S-phase response (cyclin-	related)	S-phase response (cyclin-	related)	ESTs	Homo sapiens mRNA; cDNA	DKFZp564L0864); partial cds	
	Hs.153527	Hs.189999	Hs.269623	Hs.89499			Hs.28514	Hs.98873	Hs.221776			Hs.117487	Hs.12385	Hs.71	Hs.26000		Hs.25854	Hs.168625	Hs.38613		Hs.108809		Hs.4863	Hs.81170	Hs.77899		Hs.250595		Hs.250595	Hs.25023		Hs.21015	
	Hs.9564	Hs.101544	AA758454 Hs.121256	Hs.89499			Hs.28514	AA436456 Hs.98873	Hs.106832			4A699419 Hs.117487	Hs.12385	Hs.71	Hs.26000		4A459008 Hs.25854	H93424 Hs. 100190	AA704230 Hs.38613		AA676588 Hs.108809		AA149105 Hs.25347	AA455270 Hs.29131	Hs.77899		Hs.85270		RG.49	Hs.25023		AA700937 Hs.21015	
	T53022	N90783	AA758454	H51574			B64372	AA436456	T96107			AA699419	H17950	AA862465 Hs.71	R53101		AA459008	H93424	AA704230		AA676588		AA149105	AA455270	W58092		R51052		R51052	R77213		AA700937	
	68225	303109	396307	179890			139313	753028	120929			433256	50295	1456160	154379		814288	220700	450532		882484		504647	810036	341328		38763		38763	144762		383881	
	GF200	GF201	GF203	GF200	5		GE203	GF203	GF201			GF201	GF201	GF203	GF203		GF203	GE201	GF203	3	GF201		GF201	GF201	GF200		GF200		GF200	GF200		GE203	3

					the state of the s	1	383 9587	-1 3420068
GF203	856639	AA669318	AA669318 Hs.1166/4	HS.1166/4	non-metastatic cells 3, protein	71 141		
GF201	726658	AA398218 Hs.81687	Hs.81687	Hs.81687	expressed in	NME3	383.2433	
GF203	28654	R40574 Hs.42959	Hs.42959	Hs.42959	KIAA1012 protein	KIAA1012	383.1318	-1.3746884
GF201	360065	AA053815	Hs.23245	Hs.23245	ESTs		383.1225	
GF203	223121	H84130	Hs.114256	Hs.114256	ESTs		383.1022	-2.6892904
CE201	191866		Hs 33752	Hs 124977	ESTs		383.0201	
GF203	814235	2	Hs.4206	Hs.158688	translation initiation factor IF2	IF2	383.0054	-1.7576396
3					small nuclear			
					ribonucleoprotein polypeptide			
GF201	852913	AA668189	AA668189 Hs.105465	Hs.105465		SNRPF	382.9817	
5					3-hydroxy-3-methylglutaryl-			
					Coenzyme A synthase 1			
GF203	704519	AA279533 Hs.88635	Hs.88635	Hs.77910	(soluble)	HMGCS1	382.9485	-1.3294944
GF201	46611	H10009 Hs.23540	Hs.23540	Hs.23540	ESTs		382.8455	
GF203	823647	AA496984 Hs.9271	Hs.9271	Hs.9271	KIAA1071 protein	KIAA1071	382.8043	-1.3934056
GF202	625149	AA181927 Hs.29940	Hs.29940	Hs.34401	HT015 protein	LOC51312	382.796	-2.8944045
					suppression of tumorigenicity			
					13 (colon carcinoma) (Hsp70-			
GF200	210887	H65676	Hs.119222	Hs.119222	interacting protein)	ST13	382.7957	1.16840016
					suppression of tumorigenicity			
					13 (colon carcinoma) (Hsp70-			
GF200	210887	H65676	Hs.75971	Hs.119222	interacting protein)	ST13	382.7957	1.16840016
				7077	mayin containing	EMO	382 3047	1 07737762
GF200	376875	AA047666 Hs.1424	HS.1424	HS.1424	monooxygenase i	DWI-	202.3047	1 58464976
GF200	813818		Hs.5158	HS.5158	KIAAU4U9 protein	NIAA0408	302.2300	100000
GF203	151766	H04230	Hs.11517	Hs.11517	ESTs		382.2485	-1.2300303
GF201	429911	AA033985	4A033985 Hs.61714	Hs.61714	ESTs		381.8926	
GF203	788354	AA453021	AA453021 Hs.99298	Hs.99298	ESTs		381.8082	-1.6640422
GF200	206544	H59365	Hs.16995	Hs.238954	ESTs		381.7983	1.12789827
						ì	7705	
GF201	46213	H09636	Hs.90149	Hs.110713	DEK oncogene (DNA binding) ESTs, Weakly similar to III!	DEK	381.//95	
					ALU SUBFAMILY 3 WARNING ENTRY !!!!			
GF201	50587	H17620	Hs.22562	Hs.226429	[H.sapiens]		381.7646	

Westbrook et al	ık et al.				APPENDIX A		Ally	Ally Docket No. 21.
					CD44 antigen (homing function and Indian blood			
GF200	713145	AA282906 Hs.57649	Hs.57649	Hs.169610	group system) chondroitin sulfate	CD44	381.6196	1.37321374
GF201	301104	N81049	Hs.43979	Hs.45127	C)	CSPG5	381.5228	
GF203	859118	20	AA666255 Hs.25994	Hs.44131	KIAA0974 protein	KIAA0974	381.4277	-1.7541542
GF203	29030	R40377	Hs.26301	Hs.111515	DKFZP586I1023 protein	DKFZP58611023	381.3171	-1.2661011
GF200	128775	R10007	Hs.106008	Hs.194146	ESTs		381.3037	1.15676905
					DEAD/H (Asp-Glu-Ala-			
					Asp/His) box polypeptide 5			
GF200	162775	H27564	Hs.76053	Hs.76053	(RNA helicase, 68kD)	DDX5	380.9288	1.01572427
GF201	50299	H17954	Hs.6664	Hs.6664	ESTs		380.9024	
					nuclease sensitive element			
GF203	221212	H91845	Hs.117954	Hs.74497	binding protein 1	NSEP1	380.6719	1.15853943
GF202	742708	AA400102	4A400102 Hs.49051	Hs.49051	ESTs		380.6102	-2.0534605
GF201	434826	AA703116	AA703116 Hs.114169	Hs.229950	KIAA0415 gene product	KIAA0415	380.5867	
GF203	256981	N30224	Hs.114447	Hs.114447	ESTs		380.5639	-1.4454823
GF200	110791	T90641	Hs.15187	Hs.191164	ESTs		380.5449	-1.3280976
					Homo sapiens mRNA for			
GF201	809430	AA458453	AA458453 Hs.88737	Hs.153489	KIAA1146 protein, partial cds		380.5016	
GF200	768453	AA495944	AA495944 Hs.50740	Hs.50740	ESTs		380.4934	-1.3435217
					nuclear receptor binding			
GF203	128791	R16767	Hs.113310	Hs.272736	protein	NRBP	380.4924	-1.2359023
					pregnancy specific beta-1-			
GF201	132594	R26803	R26803 Hs.24002	Hs.272620	glycoprotein 9	PSG9	380.4657	
GF203	382643	AA069444	AA069444 Hs.79855	Hs.87889	helicase-moi	KIAA0928	380.379	-1.6978636
					spastic paraplegia 7,			
					paraplegin (pure and			
GF200	825335	AA504559	AA504559 Hs.78497	Hs.78497	recessive)	SPG7	380.3528	-1.6020733
GF201	201217	R99293	Hs.36111	Hs.220651	ESTs		380.1572	
					ESTs, Weakly similar to			
GF203	221695	H92642	Hs.41641	Hs.41641	CAGH4 [H.sapiens]		380.1266	-1.2177027

09897798.070201

syndecan 2 (heparan sulfate APPENDIX A

	1.07903287			1.08591255		-1.3234307		-1.5593084						1.43086384		-1.5145694							-1.2/1/444	1.35435232				-1.0655214	1.00810173		1.08803773	0070100	-1.0856132	-2.3002000	
	380.0978	380.0957		380.0518	380.01/4	379.68	379.6659	379.4499			379.4041	379.2342		379.23		379.2228	379.1447	*		379.0898	379.0734		378.6805	378.4831				378.2901	378.281		3/8.2666	107	3/8.140/	3/ 0.0000	
	SDC2				DKFZP586I1023	KIAA0352	HABP2							RAB5A			KIAA0087						오	DKFZP586F1318				KRT5			BMI1		RAF1		
proteoglycan 1, cell surface-	associated, fibroglycan)	ESTs	Homo sapiens mRNA for	KIAA1436 protein, partial cds	DKFZP586I1023 protein	KIAA0352 gene product	hyaluronan-binding protein 2	ESTs	Homo sapiens mRNA; cDNA	DKFZp76111912 (from clone	DKFZp761I1912)	ESTs	RAB5A, member RAS	oncogene family	ESTs, Highly similar to	R31341_1 [H.sapiens]	KIAA0087 gene product	Homo sapiens cDNA	FLJ20736 fis, clone	HEP08473	ESTs	huntingtin (Huntington	disease)	hypothetical protein	keratin 5 (epidermolysis	bullosa simplex, Dowling-	Meara/Kobner/Weber-	Cockayne types)	ESTs	murine leukemia viral (bmi-1)	oncogene homolog	v-rat-1 murine leukemia viral	oncogene homolog 1	ESIS	
	Hs.1501	Hs.13305		Hs.5459	Hs.111515	Hs.17262	Hs.241363	Hs.121574			Hs.22543	Hs.30819		Hs.73957		Hs.24983	Hs.69749			Hs.48712	Hs.193344		Hs.79391	Hs.25213				Hs.195850	Hs.23917		Hs.431		Hs.85181	Hs.17268	
	Hs.1501	Hs.13305		Hs.8989	Hs.9833	Hs.17262	AA180013 Hs.80796	AA758379 Hs.121574			N53378 Hs.22543	AA431434 Hs.30819		Hs.73957		AA481437 Hs.24983	AA001536 Hs.69749			Hs.101175	4A129724 Hs.61439		Hs.79391	Hs.25213				7 Hs.862	Hs.23917		3 Hs.431		RG.22	AA703524 Hs.17268	
	H64346	N91868		T87069	T54914	R80299	AA180013	AA758379			N53378	AA431434		H11564		AA481437	AA001536			R44357	AA129724		T64094	T77847				AA160507 Hs.862	R25641		AA478036 Hs.431		N25425	AA70352	
	210717	306726		113048	74114	146726	611407	396358			283995	782450		47559		756554	361996			34405	502123		79828	108422				592540	132848		740457		267634	450192	
	GF200	GF201		GF200	GF201	GF200	GF201	GF203			GF201	GF201		GF200		GF203	GF201			GF201	GF201		GF200	GF200				GF200	GF200		GF200		GF200	GF203	

Westbrook et al.	k et al.				P. WAN YOUR WAN YOUR TON YOUR YOUR YOUR YOUR YOUR YOUR YOUR YOUR	en faugh begin faugh Neget	Atty	Atty Docket No. 21726
GF200	757381	AA437139	AA437139 Hs.98938	Hs.98938	KIAA0345 gene product Homo sapiens mRNA; cDNA DKFZp586M0918 (from clone	KIAA0345	378.0808	1.35062743
GF203	855336	AA630376 Hs.8121	3 Hs.8121	Hs.8121	DKFZp586M0918)		377.8373	-1.0459477
GF201	230882	R95962	Hs.89506	Hs.89506	keratitis)	PAX6	377.8159	21 000001
GF200 GF203	109123 197651	T80978 R94504	Hs.36475 Hs.102000	Hs.36475 Hs.102000	ESTs		377.7081	-1.2864945
					ESTs, Highly similar to NY-		1073 770	1 000700
GF200 GF201	66354 488054	166840 AA053296	166840 Hs.1086/4 AA053296 Hs.63136	Hs.173684 Hs.63136	HEN-3/ antigen [n.saplens] ESTs		377.6683	1.320102
					RAB6, member RAS			
GF200	172440	H20138	Hs.107563	Hs.5636	oncogene family RAB6, member RAS	RAB6	377.614	1.18550988
GF200	172440	H20138	RG.8	Hs.5636	oncogene family	RAB6	377.614	1.18550988
					ESTs, Weakly similar to			
GF203	133341	R27193	Hs.28980	Hs.28980	fos39554_1 [H.sapiens]		377.5584	-2.4112819
GF203	270932	N29883	Hs.42788	Hs.42788	ESTs		377.486	1.21143366
					RAB11A, member RAS			
GF200	365060	AA025058	AA025058 Hs.75618	Hs.75618	oncogene family	RAB11A	377.4604	1.40991211
GF203	685381	AA243581	AA243581 Hs.94869	Hs.94869	ESTs		377.3595	-1.3067291
					basic transcription element			
GF200	302549	N80235	Hs.76521	Hs.150557	binding protein 1	BTEB1	3/7.02//	-1.6935/12
					carcinoembryonic antigen-			
					6 (non-specific cross reacting			
GF200	509823	AA054073	AA054073 Hs.73848	Hs.73848	antigen)	CEACAM6	376.8679	-1.0383843
					bullous pemphigoid antigen 1			
GF200	188036	H44784	Hs.620	Hs.620	(230/240kD)	BPAG1	376.6388	1.32466027
GF203	666159	AA233620	4A233620 Hs.23756	Hs.23756	ESTs		376.6382	-1.1745119
	!		:	:	activity-regulated cytoskeleton-		0023 920	
GF201	222457	H86117	Hs.40888	Hs.40888	associated protein	AHC	376.1078	-1.3455318
GFZU3	2113/0	060000	18:30/04	0.6002.80	discs, large (Drosophila)			
GF203	282893	N51225	Hs.24542	Hs.154294	homolog 1	DLG1	375.993	-1.4339482

-1.5208268 -1.2202698	-1.3574684	-1.6905331	-1.1346247	-2.7662283 -2.1040208		1.23098786	-2.3630393	-2.8823433										-1.3172432		-1.6923738 1.25391381
375.9594 375.85	375.843	375.8357	375.7921	375.6406 375.6349		375.5968	3/5.5/	3/5.503/									3/5.48/1	375,4568		375.3975 375.327
	COX7A2L		IDH1			CXORF5	HSPCZ24													GSTA2
ESTs, Highly similar to CGI-83 protein [H.sapiens] ESTs	oytochrome c oxidase subunit VIIa polypeptide 2 like Homo sapiens BAC 137K3 chromosome 8 map 8q24.3 containing part of gene for GGI 72 protein and part of	thyroglobulin gene, complete sequence isocitrate dehydrogenase 1	(NADP+), soluble ESTs, Weakly similar to 1-	evidence ESTs	chromosome X open reading	frame 5	transmembrane proteolipid	ESTS Human DNA sequence from	clone RP1-317E23 on	chromosome 1p36.13.	Contains the 3' end of a	putative novel gene, two novel	genes and a mannosyl-	oligosaccharide apina-1,2-	mannosidase pseudogene.	Collically Lots, olos, doos	and two putative CpG Islands ESTs, Moderately similar to	SERP1 [H.sapiens]	ESTs, Highly similar to NY-	REN-37 antigen [H.sapiens] glutathione S-transferase A2
Hs.118554 Hs.108551	Hs.30888	Hs.18341	Hs.11223	Hs.102441 Hs.268921		Hs.6483	Hs.15159	Hs.271432									Hs.11367	Hs.97993		Hs.173684 Hs.89552
AA682545 Hs.118554 H85536 Hs.108551	R10896 Hs.30888	AA064627 Hs.18341	AA666366 Hs.11223	N24538 Hs.102441 H57135 Hs.36885		N59716 Hs.6483	AA455042 Hs.15159	AA704278 Hs.131486									AA454564 Hs.11367	AA704945 Hs.97993		AA496963 Hs.8845 T73468 Hs.89552
431245 221976	129146	382451	859228	267541 204684		246703	812244	450997									809513	461403		823627 82710
GF203 GF203	GF200	GF203	GF203	GF203 GF200		GF200	GF203	GF203									GF201	GF203		GF203 GF200

GF201	430268	AA010559 Hs.18001	Hs.18001	Hs.18001	ESTs		375.2745	
GF203	211275	H68838	Hs.108301	Hs.108301		NR2C1	375.2665	1.0541481
GF200	51447	H20872	Hs.763	Hs.176663	Fc fragment of IgG, low affinity Illa, receptor for (CD16) Homo saniens clone 23781	FCGR3A	375.2148	1.08365113
GF203	454446	AA677309	AA677309 Hs.105343	Hs.25999	mRNA sequence Homo saniens clone 25129		374.9756	-1.1482108
GF203	752547	AA410893	AA410893 Hs.31834	Hs.31834	mRNA sequence		374.6582	-2.0439056 -1 8077358
GF201	40102	R54592	Hs.78878	Hs.127376	266 gene product	KIAA0266	374.3323 374.1968	
GFZUI	128/53	H19838	18.1303	HS. 1322 19	catenin (cadherin-associated		900	
GF200	364921	AA024656 Hs.5336 N73703 Hs 37446	AA024656 Hs.5336 N73703 Hs.37449	Hs.166011 Hs 111515	protein), delta 1 DKFZP58611023 protein	CTNND1 DKFZP586I1023	374.0204 374.0025	-1.4664758
GF203	451732	AA707671	4A707671 Hs.12351	Hs.64988	ESTs		373.9081	-1.5213492
GF203	449053	AA777413	4A777413 Hs.26315	Hs.180058	ESTs		373.8114	-1.1005244
					adipose differentiation-related			
GF201	435036	AA700054 Hs.3416	Hs.3416	Hs.3416	protein; adipophilin	ADFP	373.8055	
					fatty-acid-Coenzyme A ligase,			
GF203	858167	AA633818	4A633818 Hs.81452	Hs.81452	hain 4	FACL4	373.7805	-1.2442618
GF201	46730	H10302	Hs.20527	Hs.20527	ESTs		3/3.584/	
					PWP2 (periodic tryptophan		000	0,000
GF200 GF200	120306	H50886 T97204	Hs.79380 Hs.100709	Hs.79380 Hs.17998	protein, yeast) homolog ESTs	PWP2H	373.3834 373.0498	-1.2/24946 -1.0348411
					amylo-1,6-glucosidase, 4-			
					alpha-glucanotransferase			
					(giycogen deblandını) enzyme, diycogen storage			
GF201	853687	AA668425 Hs.904	Hs.904	Hs.904	disease type III)	AGL	373.0372	
					phytanoyl-CoA hydroxylase			,00000
GF200	293104	N91990	Hs.14958	Hs.172887	(Refsum disease)	РНҮН	372.9721	-1.4063384
GF201	430092	A A O O 9840	AA009840 Hs 57146	Hs.171889	synaptonemal complex protein 3	SYCP3	372.9547	
GF200	66335	T66831	Hs.12952	Hs.182712	ESTs		372.923	-1.2966149

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TOZOKO BEKKSEGO APPENDIXA

-1.2776736 1.03631772 1.95980046	-1.5381702 1.07013564 1.59091782	-1.3124105	-1.0769264		-1.0763985 -1.6463212 -2.2894763 1.17185275
2.1. 39.1.	-1.5 1.07	-1.3	-1.0		-1.0 -1.6 -2.2 -1.17
372.7935 372.7896 372.7515	372.7465 372.6482 372.604 372.5354 372.5266	372.4724 372.4359 372.3492 372.2497	372.2468	372.091 371.9069 371.8134	371.7263 371.6646 371.5857 371.5843 371.5815
FLNA	COL6A3	RES4-22 PEG3	APBA3 NDUFA10	ORSP2 DKFZP586E1621	SBB103
ESTs filamin A, alpha (actin-binding protein-280) EST	ESTs, Highly similar to KIAA0934 protein [H.sapiens] ESTs Collegen, type VI, alpha 3 ESTs ESTs	gene with multiple splice variants near HD locus on 4p16.3 paternally expressed gene 3 ESTs	amyloid beta (A4) precursor protein-binding, family A, member 3 (X11-like 2) NADH dehydrogenase Ubiquinone) 1 alpha subcomplex, 10 (42kD)	ESTs, Moderately similar to putative seven pass transmembrane protein [H.sapiens] colactor required for Sp1 transcriptional activation, subunit 2 (150kD) DKFZP586E1621 protein	ESTs ESTs ESTs hypothetical SBB103 protein ESTs
Hs.29258 Hs.195464 Hs.23151	Hs.47638 Hs.188554 Hs.80988 Hs.188795 Hs.19347	Hs.184411 Hs.139033 Hs.19603 Hs.118358	Hs.17528 Hs.198271	Hs.25274 Hs.21586 Hs.35861	Hs.10172 Hs.221490 Hs.181785 Hs.153639 Hs.186832
W37424 Hs.29258 AA598978 Hs.76279 R21232 Hs.23151	AA057073 Hs.47638 775884 Hs.25009 925003 Hs.80988 AA460026 Hs.97356 AA147837 Hs.19347	AA150741 Hs.100074 R68634 Hs.25095 AA001976 Hs.19603 AA678287 Hs.118358	Hs.17528 Hs.108119	ကတ	725213 Hs.10172 NG6877 Hs.127313 733353 Hs.33028 AA485443 Hs.6984 AA704589 Hs.119831
W37424 AA59897 R21232	AA05707 R75884 R62603 AA46002 AA14783	AA15074 R68634 AA00197 AA67828	W19429 H68542	N27280 AA15009 AA12706	R25213 N56877 R33353 AA48544 AA70458
322028 898281 130294	489031 143654 138991 795719 590298	504794 138496 427930 432039	303196	257634 504555 502664	132215 277480 135789 811066 450581
GF202 GF200 GF200	GF201 GF200 GF200 GF201 GF203	GF201 GF200 GF201 GF203	GF200 GF201	GF201 GF201 GF201	GF200 GF203 GF200 GF201 GF203

	3888 1.00356121	3049 -1.3318766		2152 -1.7471158	•	1536 1.19269013 1271 1.11582306	·	4 5040400					4017 -1.3100665		0788 -1.4849724		3/0.0556 -1.4123094	369.9515 -1.1942541		927 3943
	371.3888	371.3049	371.2258	371.2152	į	371.1536	371.0051	0000 020	370.773			370.6213	370.4017	370.1399	370.0788		3/0.0	3.69.6		369.927 369.8943
		NPM1	SEC24A	FETUB		HEVIN	CSE1L	9	N Y			MGAT2		TM9SF1						
ACIONISTA	ESTs nucleophosmin (nucleolar	numatrin) SEC24 (S. cerevisiae) related	gene family, member A	fetuin B Homo sapiens mBNA: cDNA	DKFZp586K1318 (from clone	DKFZp586K1318) hevin	chromosome segregation 1 (veast homolog)-like	nuclear transcription factor Y,	Deta ESTs	mannosyl (alpha_1 G.).	glycoprotein beta-1,2-N-	acetylglucosaminyltransferase MGAT2	EST transmembrane 9 superfamily	member 1	ESTs	ESTs, Highly similar to	KIAAU554 protein [H.sapiens] Homo sapiens clone 24655	mRNA sequence	ESTs, Weakly similar to BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN	[H.sapiens] ESTs
	Hs.205558	Hs.173205	Hs.211612	Hs.81073	:	Hs.62601 Hs 75445	Hs.90073	00070	HS.84928 Hs.163929			Hs.172195	Hs.236349	Hs.91586	Hs.183643		Hs.193830	Hs.179882		Hs.180178 Hs.94834
	AA015819 Hs.40949	Hs.77581	Hs.30294	Hs.81073		AA489033 Hs.62601 AA490694 Hs 75445	Hs.90073	0000	AA130846 HS.84928 AA701877 HS.114075			Hs.38897	Hs.26349	4A127685 Hs.91586	Hs.32777	:	Hs.4191/	Hs.6860		AA284268 Hs.25024 R15800 Hs.94834
	AA01581	N67007	R36592	N70226		AA48903 AA49069	N69204		AA13084 AA70187			H70099	R45970	AA12768	H94163		H93604	R97251		AA284268 R15800
	360644	295868	137296	296562		824936	292806		56/414 434783			212772	35681	490306	242700		242780	201483		327220 53203
	GF203	GF203	GF203	GF200	į	GF203	GF200	i co	GF203			GF200	GF203	GF200	GF200		GF 200	GF200		GF201 GF201

1.52976552	-1.3708512	-1.033543 -1.7113135 -1.9747631		1.51749903	-1.5363024	-1.0074483	-1.7863938
369.8316	369.8233	369.4316 369.4108 369.4021	369.236 369.1763	369.1349 369.1022	369.0786 369.0443	368.9895	368.9641 368.9439 368.9327 368.9044 368.8544
NSG-X	PPP3CC	1103	N33	ANXA11		SDHA	EVPL DKFZP564O2082
brain and nasopharyngeal carcinoma susceptibility protein protein phosphatase 3 (formerly 2B), catalytic subunit, camma isoform (raicineurin A	gamma) tetratriconentide reneat	contain 3 domain 3 ESTs ESTs Putative prostate cancer tumor	suppressor Homo sapiens clone 23728 mRNA sequence	Homo sapiens cDNA FLJ20655 fis, clone KAT01590 annexin A11	Homo sapiens cDNA FLJ20555 fis, clone KAT11822 ESTs succinate dehydrogenase	ar to !!!! :B2 !!!!	[H.sapiens] envoplakin ESTs DKFZP564O2082 protein ESTs
Hs.26937	Hs.75206	Hs.118174 Hs.120964 Hs.23762	Hs.71119 Hs.153106	Hs.239720 Hs.75510	Hs.126899 Hs.269034	Hs.469	Hs.54982 Hs.25482 Hs.167354 Hs.20013 Hs.14333
Hs.26937	Hs.75206	AA670134 Hs.75395 AA703519 Hs.120964 H98248 Hs.23762	Hs.109545 Hs.12481	Hs.15944 Hs.75510	Hs.126899 Hs.42550	Hs.469	AA455286 Hs.54982 AA029418 Hs.25482 AA182680 Hs.39163 H15429 Hs.20013 W81472 Hs.14333
06606Н	W17217 Hs.75206	AA670134 AA703519 H98248	H13424 R39555	T97675 Hs.15944 AA465051 Hs.75510	N50907 H98688	T70109	AA455286 AA029418 AA182680 H15429 W81472
240938	301976	844725 450111 261253	148800 23728	121700 810117	281053 2 6 2035	80915	810050 366834 624429 49546 347670
GF200	GF200	GF202 GF203 GF202	GF201 GF201	GF201 GF200	GF203 GF201	GF200	GF201 GF200 GF201 GF201 GF201

-1.5861708	1.19844387 -1.4168702	1.11191571	-1.3723903			1.17827331		1.34786126	1.17857941 1.0569935	1.06511501	1.21132681 1.25976109
368.8299 368.7231	368.7133 368.7115	368.6591	368.513 368.5119		368.3688	368.0884	368.0661	367.9608	367.9301 367.872	367.8159 367.5305	367.5257 367.4856
	PDHA1 KIAA0378	POMT1				NDUFA4			CSK	D6S52E	ANXA1 KIAA0308
ESTs, Highly similar to Similar to a C.elegans protein in cosmid C14H10 [H.sapiens] ESTs pyruvate dehydrogenase	(lipoamide) alpha 1 KIAA0378 protein	mannosyltransferase 1 Homo sapiens (clone S164)	mRNA, 3' end of cds ESTs	ESTs, Weakly similar to Similarity to Human ADP/ATP	carrier protein [C.elegans] NADH dehydrogenase (ubiquinone) 1 alpha	subcomplex, 4 (9kD, MLRQ) ESTs, Weakly similar to alternatively spliced product	using exon 13A [H.sapiens] ESTs, Weakly similar to !!!! ALU CLASS B WARNING	ENTRY !!!! [H.sapiens] Homo sapiens cDNA FLJ20159 fis, clone	COL08969 c-src tyrosine kinase	HLA-B associated transcript-3 D6S52E ESTs	annexin A1 KIAA0308 protein
Hs.165328 Hs.38489	Hs.1023 Hs.7006	Hs.99654	Hs.180789 Hs.269339		Hs.120994	Hs.108661	Hs.193651	Hs.8360	Hs.161554 Hs.77793	Hs.274348 Hs.191464	Hs.78225 Hs.10351
AA292714 Hs.96610 AA427722 Hs.38489	Hs.1023 Hs.7006	Hs.76689	Hs.12088 Hs.75442		æ	Hs.22338	Hs.90883	Hs.8360	R33273 Hs.24609 AA078778 Hs.77793	AA598629 Hs.79262 AA406046 Hs.63375	AA504162 Hs.61399 R81880 Hs.10351
AA2927 ⁻ AA4277	T65833 R52873	R37635	T71578 N68565		AA4535,	N70015	R84398	H50667	R33273 AA07877	AA59862 AA40604	AA50416 R81880
701790 771010	80374 41672	26566	85224 292613		795202	296177	194638	194342	136117 526282	898237 743057	825172 147630
GF203 GF201	GF200 GF200	GF200	GF201 GF200		GF201	GF200	GF201	GF200	GF200 GF200	GF200 GF202	GF203 GF200

	-1.3424644	-1.2820018	1.4765114	-1.8024448	-1.6579867 1.43006251	-1.1002795 1.1876103 1.84759926 -1.3453529	-1.5884423		-2.2783968	
367.4465	367.3372	367.275 367.275 367.1905	367.1817 367.1525	367.082	367.0552 367.0382	367.0362 367.0331 366.9273 366.9193	366.863	366.7602	366.7007	366.6249
		KIAA0422			ID2	EIF4G3 ZNF268 KIAA1007 KIAA0453	QGAP1		TPR2	
ESTs, Highly similar to atrophin-1 interacting protein 4 [H.sapiens]	NA le KAT05037	KIAA0422 protein KI ESTs ESTs Human clone 23948 mRNA	sequence ESTs, Weakly similar to	cytoskeletal [H.sapiens] inhibitor of DNA binding 2,	_		_ 	H.sapiens] nositol 1,4,5-triphosphate		NT2RP2001218
E al Hs.98074 [H		Hs.12373 K Hs.27788 E Hs.26133 E	Hs.159264 sr Hs.171618 E	Hs.47008	Hs.180919 h	Hs.25732 fe Hs.183291 zi Hs.181409 K Hs.194737 K	Hs.1742 a B E A A A A A A A A A A A A A A A A A A	Hs.27278 [F	Hs.238272 rr	Hs.93391 N
Hs.98074	H79241 Hs.16230 AA034040 Hs.48134	AA148045 Hs.12373 R89700 Hs.27788 V52186 Hs.26133	Hs.90802 Hs.34023	Hs.47008	Hs.76667 Hs.46981	Hs.25732 Hs.2481 Hs.108535 Hs.90865	Hs.1742	Hs.27278	Hs.21829	Hs.93391
AA448286 Hs.98074	H79241 AA034040	AA148045 R89700 N52186	H15114 H47863	N92712	H82706 N49899	N92469 T57959 T64885 R34492	AA598496 Hs.1742	W60647	R68021	AA010868 Hs.93391
782853	235070 429895	590591 167076 284263	49567 193724	306446	240151 243653	301849 71626 66711 136560	898148	341834	138304	359641
GF201	GF200 GF201	GF201 GF200 GF201	GF201 GF200	GF203	GF200 GF200	GF200 GF200 GF200 GF200	GF200	GF201	GF200	GF201

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1.18990385	-1.1823778 -1.1374198	-1.0487975								00070000	1.86994003		-1.6781088	1.15011154	-1.563348	-1.5816181			-1.6170598	-1.2256574	-1.5672624
366.5522	366.4229 366.3338	366.3314	366.2513		366.1042		366.0801	366.0797		1000	366.0287		365.9942	365.9579	365.9415	365.8752			365.8114	365.7868	365.5986
	NFIX	S 7FP161											CLDN5						MLLT7		
Homo sapiens mRNA; cDNA DKFZp56411916 (from clone DKFZp56411916)	binding transcription factor)	zinc finger protein homologous	KIAA1249 ESTs, Weakly similar to ACYL-	COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR	[H.sapiens]	ESTS, Highly Similar to ubiquitin-conjugating enzyme	[M.musculus]	ESTs	Homo sapiens mRNA from	chromosome odz I-zz,	clone:A3-A	claudin 5 (transmembrane protein deleted in	velocardiofacial syndrome)	ESTs	ESTs	ESTs	myeloid/lymphoid or mixed- lineage leukemia (trithorax	(Drosophila) homolog);	translocated to, 7	ESTs	ESTs
Hs.14920	Hs.35841 Hs.120026	He 156000	Hs.10669		Hs.7010		Hs.132880	Hs.269392			Hs.278391		Hs.110903	Hs.43854	Hs,20321	Hs.96840			Hs.239663	Hs.26079	Hs.44269
AA259151 Hs.14920	AA406269 Hs.99929 AA707550 Hs.120026	AA490537 Hs 16101	AA004862 Hs.15917		AA458956 Hs.7010			R69584 Hs.106120			R53891 Hs.26074		H94482 Hs.110903	N29590 Hs.43854	R09301 Hs.20321	AA521335 Hs.96840				R53917 Hs.26079	AA465090 Hs.44269
686733	754600 451664	824511	428936		810852		134265	141726		:	138141		243181	270665	127636	826130			70349	138210	814995
GF203	GF200 GF203	GESOO	GF201		GF201		GF201	GF201			GF200		GF203	GF203	GF200	GF203			GF200	GF200	GF203

365.5119 1.19214132 365.4476 1.13275112	365.4204 -1.4302146 365.318 -2.381643	365.1346 365.1188 -1.391119		365.0267 -1.1693753	364.9828 1.11793413	364,9149 -1.0055466		364.7031 1.54834351 364.4856 -1.3913709	364.3553 -1.2542418 383.8906 -1.8852019 383.8954 -1.0252723 383.6597 -1.189511
365.5	365.420. 365.318	365.1 365.1	365.1	365.0				364.7 DKFZP586I1023 364.2 364.3	83
nilar to utase-related ns]	imilar to Gag- M.musculus]	nRNA; cDNA (from clone	ly similar to B SUBUNIT sapiens] tegration site EVI5	nilar to n [H.sapiens]	sette, sub- member 4 ABCD4 icludes Ss	-	GYPB n RNF		nRN4; cDNA 33 (from clone 33) protein 1 TMEM1 in KIAA0483
ESTs, Highly similar to phosphoglucomutase-related protein [H.sapiens] ESTs	ESTs, Weakly similar to Gag- Pol polyprotein [M.musculus] EST	Homo sapiens mRNA; cDNA DKFZp564J142 (from clone DKFZp564J142) ESTs	ESTs, Moderately similar to CALCINEURIN B SUBUNIT ISOFORM 1 (H.sapiens) ecotropic viral integration site 5	ESTs, Highly similar to HSPC038 protein [H.sapiens]	A I P-binding cassette, sub- family D (ALD), member 4 glycophorin B (includes Ss	blood group) glycophorin B (includes Ss	blood group) ring finger protein	ESTs DKFZP586I1023 protein ESTs	Homo sapiens mRNA; cDNA DK-Ey761M0223 (from clone DKF2p761M0223) ESTS ESTS ESTS ESTS ESTS transmembrane protein 1 KIAAQ483 protein
2 Hs.167473 5 Hs.15155	16 Hs.187396 8 Hs.99258	0 Hs.227146 8 Hs.29008			6 Hs.94395	8 Hs.250653		9 Hs.26169 2 Hs.111515 4 Hs.15514	
H12279 Hs.22832 T83098 Hs.15155	AA626237 Hs.131716 AA451886 Hs.99258	AA142942 Hs.30540 AA402043 Hs.29008	AA431190 Hs.98580 H29292 Hs.27175		R02189 Hs.94395	AA455338 Hs.15798		H78368 Hs.26169 AA447974 Hs.21922 R94946 Hs.15514	g g
00 48182 00 110746	03 745514 03 786657	01 504678 03 741937			00 124753	00 812126		00 233547 01 782718 00 198605	12 60 1 1 1 1 1 1 1
GF200 GF200	GF203 GF203	GF201 GF203	GF201 GF201	GF200	GF200	GF200	GF200 GF200	GF200 GF201 GF200	GF201 GF203 GF203 GF200 GF200 GF200

-1.2182812	-1.0267445 -1.3823256	-1.2218976	-1.1727827 -1.6224715	-2.008864		-1.4289357	1.0344394	-1.6589816	1.56308757	-1.7543935 -1.2534509 -1.1352717	-1.99099
-1.5	2.1.	-1.5	1. 1.	-2.0		-1.	1.0	-1.6	1.5	777	-1.5
363.4875	363.4004 363.3723	363.0789	363.0115 362.9856	362.9046	362.8259	362.7488	362.6683 362.6597	362.503	362.3101	362.3074 362.1114 362.0121	362.0019
	MAP2K1 KIAA0943		CA150			PSEN2		ZNF183			
EST	mitogen-activated protein kinase kinase 1 KIAA0943 protein Homo sapiens cDNA El 190088 fie. chops	COLO3604	KIAA1164 protein, partial cds transcription factor CA150	ESTs, Weakly similar to weak similarity to collagens [C.elegans] Human carlherin-associated	protein-related (cap-r) mRNA, complete cds	disease 4)	Homo sapiens mHNA for KIAA1415 protein, partial cds ESTs	zinc finger protein 183 (RING finger, C3HC4 type) Homo sapiens mRNA; cDNA	DKFZp586N1323 (from clone DKFZp586N1323) ESTs, Highly similar to insulin	receptor substrate like protein [H.saplens] ESTs ESTs Homo saplens cDNA	FLJ10386 18, done NT2RM2002142, weakly similar to GASTRULATION SPECIFIC PROTEIN G12
Hs.101251	Hs.3446 Hs.76852	Hs.118964	Hs.40719 Hs.13063	Hs.127824	Hs.150917	Hs.25363	Hs.109315 Hs.268611	Hs.64794	Hs.24064	Hs.30827 Hs.89081 Hs.44024	Hs.236556
Hs.101251	R19938 Hs.3446 AA443886 Hs.76852	Hs.118964	AA018671 Hs.40719 AA045180 Hs.13063	AA127215 Hs.17056	Hs.78696	RG.48	Hs.40293 Hs.15905	AA132766 Hs.64794	Hs.24353	W85913 Hs.30827 AA282985 Hs.89081 AA788613 Hs.44024	Hs.7420
R59370	R19938 AA443886	H44838	AA018671 AA045180	AA127215	H45976	AA056325 RG.48	H81802 R12480	AA132766	R30941	W85913 AA282985 AA788613	R91137
38028	33826 756662	188422	362756 487761	502683	177772	380620	219929 128266	587525	134120	415696 713114 1240262	195051
GF203	GF200 GF203	GF203	GF203 GF203	GF203	GF201	GF200	GF203 GF201	GF200	GF200	GF203 GF203 GF203	GF200

-1.3196545		1.15079998		1.00357407	-1.1863525				-1.7660088				-1.3914125			1.4427033	-1.0768366			1.50861807						-1.1058633	1.36525566			1.13504305	,000,11	-1.1143361 1.52872328
361.9392		361.8446	361.7438	361.7173	361.6813			361.6447	361.5899		361.3897		361.274	361.2169		361.0699	361.0313			360.8278						360.7614	360.6402			360.6122		360.558 360.5289
GPRK5		GCSH	CTPS	STX3A									NPEPPS	ADD3		KIAA0917	KIAA0779									SEMA5A			·	TIA1	i	ELF4 PP
G protein-coupled receptor kinase 5	glycine cleavage system protein H (aminomethyl	carrier)	CTP synthase	syntaxin 3A	ESTs	Homo sapiens mRNA; cDNA	DKFZp434N1272 (from clone	DKFZp434N1272); partial cds	ESTs	ESTs, Highly similar to	KIAA0183 [H.sapiens]	aminopeptidase puromycin	sensitive	adducin 3 (gamma)	vesicle transport-related	protein	KIAA0779 protein	Homo sapiens mRNA; cDNA	DKFZp434M0420 (from clone	DKFZp434M0420)	sema domain, seven	thrombospondin repeats (type	1 and type 1-like),	transmembrane domain (TM)	and short cytoplasmic domain,	(semaphorin) 5A	ESTs	TIA1 cytotoxic granule-	associated RNA-binding	protein	E74-like factor 4 (ets domain	transcription factor) pyrophosphatase (inorganic)
Hs.211569		Hs.77631	Hs.251871	Hs.82240	Hs.8268			Hs.173871	Hs.26192		Hs.167889		Hs.132243	Hs.8110		Hs.27023	Hs.179507			Hs.273369						Hs.27621	Hs.169152			Hs.239489		Hs.151139 Hs.184011
1456120 AA862435 Hs.29297		Hs.96656	Hs.91663	AA436871 Hs.82240	4A774524 Hs.8268			Hs.22055	Hs.26192		AA001845 Hs.59969		Hs.85457	4A461325 Hs.8110		AA028034 Hs.27023	Hs.25203			Hs.122227						AA436152 Hs.27621	Hs.6403			AA775259 Hs.28207		Hs.17743 Hs.111534
AA86243		R71327	R66541	AA43687	AA77452			R42697	R54672		AA0018		R24894	AA46132		AA02803	N49403			R63497						AA4361	T64972			AA7752		H14359 H50229
1456120		143039	141234	757961	399302			32094	154483		428006		132012	796323		469704	277656			138693						754355	66829			878600		48614 179232
GF203		GF200	GF201	GF200	GF203			GF201	GF203		GF201		GF200	GF201		GF200	GF203			GF203						GF200	GF200			GF203		GF200 GF200

-1.136932		1.20808938		-1.4699941	-1.3950943					-1.0461537								-1.3290964		1.06859595									1.0933982	
360.3475		360.2084	360.1809	360.1691	360.131	360.1038	360.0757			359.9953		359.9884		359.9714			359.8073	359.7675		359.6427			0000	329.656	329.2399	359.3444		359.3041	359.2327	
		NAPG				KIAA0957				AKR1C3		GCDH		MTERF	ė					BHLHB2		Φ	0	MEF2C	DES			MICA	BTN3A3	
ESTs	N-ethylmaleimide-sensitive factor attachment protein,	gamma Homo sapiens cDNA FLJ10509 fis, clone	NT2RP2000617	ESTs	ESTs	KIAA0957 protein	aldo-keto reductase family 1;	member C3 (3-alpha	hydroxysteroid	dehydrogenase, type II)	glutaryl-Coenzyme A	dehydrogenase	transcription termination	factor, mitochondrial	ESTs, Weakly similar to fragile-	X-related protein 1 isoform f	[M.musculus]	ESTs	basic helix-loop-helix domain	containing, class B, 2	MADS box transcription	enhancer factor 2, polypeptide	C (III) OCYTE EIIII AII ICEI I ACTOI	SC)	desmin	ESTs	MHC class I polypeptide-	related sequence A	member A3	
Hs.177894		Hs.60415	Hs.274319	Hs.93678	Hs.62359	Hs.30991	HS.24222			Hs.78183	:	Hs.184141		Hs.97996			Hs.108345	Hs.34458		Hs.171825				HS./8995	Hs.171185	Hs.18564		Hs.90598	Hs.167741	
R10970 Hs.14935		AA010503 Hs.60415	R43271 Hs.9412	H03478 Hs.93678	ဖွ		W80808 HS.Z4ZZZ			AA916325 Hs.118605		R56638 Hs.63773		AA459396 Hs.97996			N73976 Hs.36272			T62084 Hs.8342				198/96 Hs.100/31	AA443098 Hs.77891	AA004652 Hs.18564		N71782 Hs.90598	AA478585 Hs.113894	
129177		359395	32517	151371	364022	47059	347293			1473304	!	41195		810951			296618	210622		85682				122288	809453	428749		290724	753587	
GF200		GF200	GF201	GF203	GF203	GF201	GFZUI			GF203		GF201		GF201			GF201	GF200		GF200				GF201	GF201	GF201		GF201	GF200	

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1.09374562 1.50044905 1.36384701 -1.8216603 1.26177473	-1.3374555 -2.671068079 -2.6710653 -1.3441649 -1.6585128	-1.3866471	-1.5344611
1.05 1.36 1.36 1.26 1.26	4.3 4.5 5.6 6.7 6.7	-1.3	
357.2206 357.1912 356.9845 356.9365 356.8521 356.8442	356.7304 356.7003 356.6399 356.6247 336.6211 356.4055	356.2479 356.2099 356.1969	355.8988 355.8988 355.885 355.885
ADSL	FXR1	3) ZNF20 MVD	DKFZP434P1750 PRKAR1A
ESTs adenylosuccinate lyase ESTs ESTs ESTs, waaky similar to fatty acid amide hydrolase [H.saplens]	ESTS, Weakly similar to KIAA0908 protein [H saptens] finaglie X mental relardation, autosomal homolog 1 ESTs Weakly similar to fivediction ESTs	zinc finger protein 20 (KOX 13) ZNF20 Homo sapiens cDNA FLJ10092 its, clone HEMB41002249 mevalonatie (diphospho) decarboxylase Homo sapiens mRNA; cDNA DKFZ9434B225 (from clone	DKFZp434B225) DKFZp434F750 protein protein kinase, cAMP- dependent, regulatory, type I, alpha (tissue specific extinguisher 1) ESTs
Hs.155807 Hs.75527 Hs.269009 Hs.178715 Hs.13181	Hs.26910 Hs.82712 Hs.193200 Hs.240763 Hs.268912 Hs.98480	Hs.110956 Hs.132972 Hs.3828	Hs.7274 Hs.7274 Hs.183037 Hs.21342
H68932 Hs.38758 AA456400 Hs.75527 H91673 Hs.114258 AA157112 Hs.63216 T70411 Hs.13181 H29873 Hs.9171	AA701491 Hs.26910 N79708 Hs.82712 AA460701 Hs.58571 AA489696 Hs.44816 R11505 Hs.20623 AA425131 Hs.98480	AA148578 Hs.110956 N52315 Hs.47461 N50834 Hs.3828	AA428603 Hs.4746 H52258 Hs.7274 AA630507 Hs.62039 N20322 Hs.21342
H68932 AA456400 H91673 AA157112 T70411 H29873	AA701491 N79708 AA460701 AA489696 R11505 AA425131	AA148578 N52315 N50834	AA428603 Hs.4746 H52258 Hs.7274 H5250 Hs.7274 AA630507 Hs.6203 N20322 Hs.2334
212098 813280 221151 589512 67033 190286	435447 289551 796709 824376 128228 768612	502988 284432 280934	781442 235923 854760 264575
GF200 GF200 GF203 GF202 GF200 GF200	GF203 GF200 GF202 GF203 GF201 GF203	GF202 GF201 GF203	GF201 GF203 GF201 GF201 GF203

1.09976377	-1.2507181	1.53440915				-1.8385339	1.04337527	1.04337527	1 6007440	24,0000	-1.2563293
355.6542	355.2241	355.0243 354.8995	354.8542	354.5958	354.5765	354.3391 354.3354	354.0586	354.0586	2000	353.72	353.444 353.3651
ABL1	KIAA0764				BLZF1		эрргса	PPP2CA	COUNTY I	1 700	FUT4
v-abl Abelson murine leukemia viral oncogene homolog 1 / FSTs. Weakly similar to zinc	protein [H.sapiens] 764 gene product	ESTS ESTS	ESTS, ESTS, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!!	[H.sapiens] basic leucine zipper nuclear	E	[H.sapiens] ESTs protein phosphatase 2	(formerly 2A), catalytic subunit, alpha isoform Protein phosphatase 2		mily,		TINF-III LOUGH III fucosyltransferase 4 (alpha (1,3) fucosyltransferase, myeloid-specific) ESTs
Ns.146355		Hs.19066 Hs.34274 Hs.38891		Hs.183253	Hs.158205 f	Hs.261734 Hs.21921 Hs.21921	Hs.91773	Hs.91773		60	HS.1739 HS.2173 HS.194589
RG.15	ന	Hs.19066 Hs.34274 Hs.38891	AA457150 Hs.92765	AA443125 Hs.15907	Hs.112176	Hs.23825 Hs.21921	AA599092 Hs.91773	AA599092 Hs.75624	TS:0000	AA029451 Hs.9656	AA190825 HS.17839 R28447 Hs.2173 AA156749 Hs.107813
H81821	N92478 AA50477	H18080 N33857 N51056	AA45715	AA44312	R43576	R27082 N68173	AA59909	AA59909	0077/N	AA02945	AA190823 R28447 AA156749
219976	301867	50768 272514 244267	810486	809489	23012	133331 292236	950445	950445	281345	366848	133213 502491
GF200	GF201 GF203	GF203 GF203 GF200	GF201	GF201	GF201	GF200 GF200	GF200	GF200	GF203	GF201	GF200 GF200 GF201

-2.0215879 -1.9419828 -1.6231964 -2.3621794 1.18662603	1,4793266 -2.8753282 -1,1010629 -2.2212484	-1.1945268 -1.4855109 -2.4536549 -1.6671309	-1.1770103	-1.0910968
353.3112 353.1996 353.149 353.125 353.1068 353.0302	353.0015 352.9579 352.7208 352.6659	352.6087 352.568 352.568 352.5067 352.4711	352.4226 352.3279 352.3088	352.1429
CUL1 PAPPA YDD19	PON3 DGKA TRAF4	RPMS12	CDC2L5	U2AF1
ESTs ESTs protein A YDD19 protein YESTs FESTs	paracyonase 3 diacylglycerol kinase, alpha (BOKD) TINF receptor-associated factor 4 ESTs	mHVA, cytoplasmic domain, partial cds ESTs ESTs ESTs minorana protein, mitochondrial, S12 Homo sapiens CNA FLLZ0763 fis, clone	Homo sapiens mFINA; cDNA DNE725680N 1223 (from chore DNE725680N 1223) cell division cycle 2-like 5 cell division cycle 2-like 5 (cholinesterase-related cell division controller) ESTS	auxillary tactor 1 (non- standard symbol)
Hs.14541 Hs.189107 Hs.75874 Hs.25615 Hs.49840 Hs.936512		Hs.256309 Hs.30096 Hs.99680 Hs.16177 Hs.9964 Hs.259774	Hs.24064 Hs.59498 Hs.237642	Hs.59271
AA486790 Hs.14541 AA70432 Hs.125622 AA609463 Hs.75874 R42864 Hs.23207 W04272 Hs.49840	AALGAGA TIS, 10302 R95740 Hs. 107966 AA677716 Hs. 113405 AA598826 Hs. 8375 N54911 Hs. 47884	W67174 Hs.74487 H03049 Hs.30096 AA286814 Hs.99680 AA001360 Hs.16177 R23752 Hs.9964 W37778 Hs.2440	R26417 Hs.24064 N35067 Hs.43686 AA450041 Hs.106919	W90506 Hs.59271
841093 AA 383706 AA: 743588 AA(31261 R4; 296901 W0		343072 151793 701272 427895 131653 1	132857 R20 271662 N3 788445 AA	418126
GF200 GF203 GF202 GF203 GF200	GF200 GF200 GF200 GF200	GF200 GF203 GF203 GF201 GF201	GF201 GF201 GF203	GF200

-1.0910968	-1.2915197	-1.0905482	-2.1232472	-2.0468757	-2.2935983	1.05716435	1.09977757		1.63665179
352.1429	352.068	352.0502 352.0336	351.9813 351.8944	351.79	351.6326	351.6252 351.51 351.4281	351.3251 351.2681	351.1859	351.1123 351.1105 351.075 351.0561
U2AF1	KIAA0110	GPR44	NOT4		PSMD8	TIAM2 CRYBA1	HIVEP1	MLLT6	COL4A3BP TPD52 KIAA0626
U2(RNU2) small nuclear RNA auxillary factor 1 (non-standard symbol)	with a complete coding sequence	G protein-coupled receptor 44 GPR44 ESTs	NOT4 (negative regulator of transcription 4, yeast) homolog NOT4 ESTs	transcript KIAA0491 proteasome (prosome,	macropain) 265 subunit, non- ATPase, 8 T-cell lymphoma inyasion and	metastasis 2 crystallin, beta A1 ESTs human immunodeficlency	virus type I enhancer-binding protein 1 ESTs myeloid/lymphoid or mixed- lineage leukemia (trithorax	translocated to, 6 collagen, type IV, alpha 3	(acouptains any anony probability and any anony protein DS2 KIAA0626 gene product ESTs
Hs.59271	Hs.124	Hs.4253 Hs.29904	Hs.20423 Hs.183789	Hs.136309	Hs.78466	Hs.12598 Hs.46275 Hs.14317	Hs.27354 Hs.27354	Hs.249194	Hs.21276 Hs.2384 Hs.178121 Hs.60162
W90506 Hs.118378	H67988 Hs.124	AA464202 Hs.4253 AA701232 Hs.29904	W93715 Hs.20423 AA701527 Hs.121069	N72138 Hs.4052	AA464557 Hs.78466	AA026692 Hs.98386 AA487614 Hs.46275 AA464531 Hs.14317	AA429769 Hs.306 W92772 Hs.16675	AA454610 Hs.96538	N62593 Hs.21276 AA459318 Hs.2384 N62737 Hs.30210 AA005236 Hs.60162
418126 WG	211206 H6	810403 AA 434864 AA	357363 W9 435817 AA	291103 NZ	810550 AA	366591 AA 839094 AA 810510 AA	758037 AA 418350 WG	811604 AA	288840 N6 814306 AA 289023 N6 428804 AA
GF200	GF200	GF201 GF203	GF201 GF203	GF203	GF203	GF201 GF200 GF201	GF200 GF201	GF201	GF203 GF200 GF201 GF201

1.16097579	1.26969255 -1.607056	-1.1104667	1.00953755 -1.3239923	-2.7240429	-1.6225507 1.23822814 1.04435983 1.81067024 -1.0166619	-1.2973792 -2.2312084 -1.4773174 -2.2292012
350.9999 350.8504	350.8082 350.6701 350.5754	350.5559	350.5179 350.4966	350.3695 350.3438 350.2807	350.2323 350.2189 350.1856 350.1762 350.1186 350.1151 349.6703	349.642 349.616 349.5764 349.5663
ADTB2 CYB5	GRIN1	NCBP1	Æ	ABCC3 NUP98	KIAA0871 CENPE KIAA0103 DKFZP564C1940	РТСН МЕОХ2
adaptor-related protein complex 2, beta 1 subunit cytochrome b-5	glutamate receptor, ionotropic, N-methyl D-aspartate 1 ESTs ESTs	nuclear cap binding protein 1, 80kD ESTs, Weakly similar to	ransglutaminase [H.sapiens] transglutaminase [H.sapiens] tumarate hydratase ATP-binding cassette, sub-	_	Fuzucki IIs, dune ESTs ESTs KAA0871 protein KAA0103 gene prodeut KIAA0103 gene product	patched (Drosophila) homolog PTCH ESTs mesendryme homeo box 2 growth arrest-specific homeo box) ESTs
Hs.74626 Hs.83834	Hs.105 Hs.220567 Hs.59974	Hs.89563	Hs.6127 t	Hs.90786 Hs.23244 Hs.112255	Hs.27267 Hs.23793 Hs.180291 Hs.7972 Hs.75573 Hs.154387 Hs.3804	Hs.159526 Hs.191910 Hs.77858 Hs.33718
Hs.102824 Hs.83834	R88267 Hs.105 AA707789 Hs.130753 AA411009 Hs.59974	AA278749 Hs.89563	T67279 Hs.6127 AA026917 Hs.75653	AA429895 Hs.90786 R49243 Hs.23244 AA148536 Hs.112255	N51612 Hs.27267 AA491292 Hs.32793 AA287009 Hs.96612 A94511 Hs.7972 AA402431 Hs.75573 AA181333 Hs.117 AA477663 Hs.3804	AA169807 Hs.54503 AA682876 Hs.119578 H25223 Hs.77858 N48003 Hs.33718
H54093 R92281	R88267 AA707789 AA411009	AA278749	T67279 AA026917	AA429895 R49243 AA148536	N51612 Hs.2726 AA491292 Hs.3279 AA287009 Hs.9681 B94511 Hs.7557 AA402431 Hs.7557 AA181333 Hs.117 AA427563 Hs.3804	AA169807 AA682876 H25223 N48003
202919 196189	166245 413080 752560	703739	66694 469412	781139 38808 491544	281597 824658 701547 197676 727526 624443	594540 450486 161172 281615
GF200 GF200	GF201 GF203 GF203	GF200	GF200 GF200	GF201 GF203 GF201	GF203 GF203 GF203 GF200 GF200 GF201	GF200 GF203 GF203 GF203

	-1.2139213		1.0783709	-1.2533785			-2.1147705	1.51350814		1.00222554	1.07169358	1000	-1.0654464				1.16915038	-2.0415849		-1.8268218	-1.1813681			1.02795478		0,10000	1.0236518	-1.6021402		1000000	-2.3238625	
	349.5351	349.3332	349.3265	349.0764		349.0082	348.7415	348.7094	:	348.5543	348.3/42	000	348.288		348.2867	348.2738	348.1178	348.1123		347.9222	347.8497	347.8291		347.7497			347.6169	347.6008			347.4683	347.4184
	NR1D2					LOC51759				HSF2BP	KIAA0244		PDE1A			BTG1				LZTR1				PDGFRL								REPS2
nuclear receptor subfamily 1,	group D, member 2	ESTs	ESTs	ESTs	hepatocellular carcinoma-	associated antigen 59	ESTs	ESTs	heat shock transcription factor	2 binding protein	KIAA0244 protein	phosphodiesterase 1A,	calmodulin-dependent	ESTs, Moderately similar to	located at OATL1 [H.sapiens] B-cell translocation gene 1,	anti-proliferative	ESTs	ESTs	leucine-zipper-like	transcriptional regulator, 1	ESTs	ESTs	platelet-derived growth factor	receptor-like	Homo sapiens mRNA; cDNA	UKFZp586l1524 (rrom clone	DKFZp58611524)	ESTs	ESTs, Moderately similar to	RNA helicase HDB/DICE1	[H.sapiens] RALBP1 associated Eps	domain containing 2
	Hs.37288	Hs.244639	Hs.172932	Hs.186651		Hs.278429	Hs.17649	Hs.35299		Hs.97624	Hs.78893		Hs.41717		Hs.192946	Hs.77054	Hs.36790	Hs.103411		Hs.78788	Hs.120911	Hs.54578		Hs.170040			Hs.274368	Hs.94002			Hs.15282	Hs.80667
	4A428473 Hs.37288	Hs.28302	Hs.24486	4A521307 Hs.104454		Hs.70608	4A460825 Hs.17649	Hs.35299		AA398410 Hs.97624	W95950 Hs.78893		AA393408 Hs.41717		AA476223 Hs.100307	Hs.77054	Hs.36790	AA703147 Hs.103411		Hs.78788	AA733027 Hs.120911	Hs.54578		AA455210 Hs.2459			_	Hs.94002			Hs.15282	Hs.80667
	AA42847	H10204	R31946	AA52130		W80591	AA46082	R94212		AA39841	W95950		AA39340		AA47622	N70463	H53556	AA70314		R38194	AA73302	W68162		AA45521			W60845	N50903			T99650	T72336
	773188	46907	134368	827196		415459	796262	198339		726874	358344		727792		771328	298268	202722	434845		23772	399101	343298		810010			341805	281043			123425	86160
	GF200	GF201	GF200	GF203		GF201	GF202	GF200		GF203	GF200		GF200		GF201	GF201	GF200	GF203		GF200	GF203	GF201		GF200			GF200	GF203			GF200	GF201

		-1.1588728	1.30481251		1.44016689	1 0100451	10.0401	-1.3071632		-1.1249872			-1.5838489	
347.2783 347.2002		347.0905	346.7078		346.5987	346 366	346.386	346.3745		346.3742	346.3562 346.2308		346.106	346.0741 346.0205
		NAIP	SRI			1410	VISI	2		SHC1	CYP27A1 KIAA0203			CEPT1 MYO9B
ESTs ESTs	neuronal apoptosis inhibitory	protein	sorcin	Novel human gene mapping to	chomosome 13	Wolfram syndrome 1	(Wolliamili)	ESTs	SHC (Src homology 2 domain- containing) transforming	protein 1	oytochrone PA50, subtamily XXVIII (steroid 27- XYOUNI (steroid 27-	Human DNA sequence from clone 51 FITE on chromosome clone 51 FITE on chromosome coding exon of the gene for PIS component of atminoacyl-RINA synthetase complex, part of an unknown gene downstream of a putative CpC siland, and an STS with a CA.	repeat poly choline/ethanolaminephosphot	ransferase myosin IXB
Hs.91389 E	_		Hs.117816 s	_	Hs.22174 C		HS.25077		0 , 0	Hs.81972	Hs.22568 x		Hs.88977	Hs.125031 Hs.159629
H11467 Hs.91389 AA400262 Hs.111909		AA621150 RG.2	N50843 Hs.24952		AA488718 Hs.22174		HS.26077			Hs.81972	N66957 Hs.82568 AA047435 Hs.77927		AA460543 Hs.88977	H67900 Hs.108292 AA702663 Hs.113199
H11467		AA6211	N50843		AA4887	0.00	H33810	R63971		T50633	N66957 AA0474		AA4605	H67900 AA7026
47671		1046522	280950		841695	00,000	138188	140018		77133	295843 488434		796652	229856 447365
GF201) 	GF200	GF203		GF200	C	00215	GF203		GF200	GF201 GF201		GF203	GF201 GF201

	-1.6971717	-1.6971717		-1.6281432			-1.404455	1.31593425		-1.3375884			-1.3681221				-1.1760672	-1.7746681	-1.3991839			-1.7879535	-2.1220373			-1,0911353		1.00854115	1.06160483	-2.9438682		1.20909073	
	345.933	345.933	345.7463	345.7366	345.6706	345.5525	345.4709	345.4207		345.4119			345.4002	345.1558	345.0222		344.9203	344.9074	344.8744			344.7473	344.5765	344.4695		344.4522		344.2808	344.263	344.1937		344.0403	
	POLR2K	POLR2K	ITGB8		PRSS16	TIM		RBL2					CRSP2	KIAA0255	CNIL		CDH5		KIAA0419					DKFZP434J154		RECOL		UBE2B		KIAA1058		HIBCH	
polymerase (RNA) II (DNA directed) polymentide K	(7.0kD) polymerase (RNA) II (DNA directed) polypeptide K	(7.0kD)	integrin, beta 8	ESTs	protease, serine, 16 (thymus)	Oncogene TIM	ESTs	retinoblastoma-like 2 (p130)	Homo sapiens clone 24583	mRNA sequence	cofactor required for Sp1	transcriptional activation,	subunit 2 (150kD)	KIAA0255 gene product	cornichon-like	cadherin 5, VE-cadherin	(vascular epithelium)	ESTs	KIAA0419 gene product	Homo sapiens cDNA	FLJ10641 fis, clone	NT2RP2005748	ESTs	DKFZP434J154 protein	RecQ protein-like (DNA	helicase Q1-like)	ubiquitin-conjugating enzyme	E2B (RAD6 homolog)	ESTs	KIAA1058 protein	3-hydroxyisobutyryl-Coenzyme	A hydrolase	
	Hs.150675	Hs.150675	Hs.184908	Hs.40334	Hs.274407	Hs.334	Hs.41434	Hs.79362		Hs.154336			Hs.21586	Hs.79305	Hs.201673		Hs.76206	Hs.192032	Hs.236828			Hs.265891	Hs.6126	Hs.226372		Hs.235069		Hs.811	Hs.25253	Hs.8021		Hs.236642	
	AA458646 Hs.102589	AA458646 Hs.10565	AA127965 Hs.62692	H99211 Hs.40334	N92924 Hs.54705	AA045822 Hs.91106	AA001665 Hs.41434	N50554 Hs.79362		AA488857 Hs.17398			R40567 Hs.21586	AA481480 Hs.79305	N72259 Hs.62420		T53626 Hs.76206	AA187979 Hs.123862	AA495938 Hs.9388			R86733 Hs.33391	AA464623 Hs.6126	AA464169 Hs.9372		AA456585 Hs.1536		AA598492 Hs.811	AA489636 Hs.25253	N70078 Hs.8021		AA521228 Hs.22938	
	813410	813410	501854	261852	307687	488645	428063	280752		824838			28444	756627	291348		69672	626548	768445			197300	812989	810353		809394		898138	823688	297940		827120	
	GF200	GF200	GF201	GF202	GF201	GF201	GF203	GF200		GF203			GF203	GF201	GF201		GF200	GF202	GF203			GF200	GF203	GF201		GF200		GF200	GF203	GF203		GF200	

-1.8338327 -2.2956291	1.07686748 1.2529962		1.0363391	1.07995386			-1.8546049	-1.0074485	1.38630553 -1.0506692 1.39044456	1.12375702 1.14729674 -1.0850297
343.9883 343.9673	343.7417 343.6837	343.6422 343.5176	343.3821 343.3821	343.1852	343.0251	343.0232	342.9769 342.8655	342.8392	342.7795 342.6461 342.6273	342.4336 342.3966 342.274
KIAA1096	69CO	SREBF1 BYSL	MNPEP	HPS		SMCX	STXBP3	GNG10	REV1	PRKCA
KIAA1096 protein ESTs CD69 antigon (A60 party T.	cell activation antigen) ESTs	binding transcription factor 1 bystin-like methionine aminopeptidase;	eIF-2-associated p67 methionine aminopeptidase; eIF-2-associated p67	Hermansky-Pudlak syndrome Homo sapiens mRNA; cDNA DKFZn434B231 (from clone	DKFZp434B231) SMC (mouse) homolog, X	chromosome Homo sapiens cDNA FLJ10264 fis, clone	HEMBB1001011, weady similar to ZINC FINGER PROTEIN 84 syntaxh binding protein 3 cuanine purcheritide binding	protein 10 Human clone A9A2BRB6 (CAC)n/(GTG)n repeat-	containing mRNA REV1 protein ESTs ESTs Maakly similar to	B0041.5 [C.elegans] protein kinase C, alpha ESTs
Hs.69559 Hs.92030	Hs.82401 Hs.25866	Hs.166 Hs.106880	Hs.78935 Hs.78935	Hs.83951	Hs.267445	Hs.55823	Hs.33268 Hs.8813	Hs.79126	Hs.169078 Hs.110347 Hs.32713	Hs.108812 Hs.169449 Hs.46670
AA186895 Hs.9525 AA707199 Hs.92030	AA279883 Hs.82401 AA600186 Hs.25866	AA425823 Hs.166 AA701929 Hs.106880	AA487589 Hs.78935 AA487589 Hs.16839	AA418773 Hs.83951	T94087 Hs.5956	H13688 Hs.55823	AA732917 Hs.33268 R20770 Hs.8813	AA460286 Hs.79126	T83828 Hs.119198 AA478442 Hs.25990 AA017167 Hs.32713	H98233 Hs.108812 AA030029 Hs.60762 N47091 Hs.46670
625924 452016	704459 950361	769571 435561	841691	767828	119133	148225	399444 26314	795738	113298 786234 361551	261219 469954 280331
GF202 GF203	GF200 GF202	GF201 GF201	GF200 GF200	GF200	GF201	GF201	GF203 GF200	GF200	GF200 GF203 GF203	GF202 GF200 GF203

1.5108449 1.2141156 1.2776882 -1.9076694 1.94337341 1.0370863

1,7802087

-1.1256184

-1.0417627

1.6077526 1.0279248 -2.0898288 -1.6573015

-1.2228037 -1.0522041

-1.8104838	-1.0801083 -1.6467011		-1.3703726	1.3633277	-2.0398524	-1.7393222	-1.1669291 1.47598641	-1.102825	1.3119598	-1.2624046	-1.6334806	-1.4478637
340.6638	340.6613 340.5847	0000	340.2639	340.2354	340.1688	340.0457	339.9431	339.6698	339.6046	339.5587 339.5149	339.3051	339.299
SELE	ID4 KIAA0982		ME1	ADPRTL1		ITGB4	97004	KIAA0456	KIAA1025	АМРН	ING1	ZNF144
selectin E (endothelial adhesion molecule 1) inhibitor of DNA binding 4, dominant negative helivalous.	helix protein KIAA0982 protein	Homo sapiens mRNA; cDNA DKFZp434G2222 (from clone	DKFZp434GZZZZ); partial cds malic enzyme 1, NADP(+)- dependent. cvtosolic	ADP-ribosyttransferase (NAD+; poly (ADP-ribose) polymerase)-like 1	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 362430	integrin, beta 4 ESTs, Moderately similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII	[H.sapiens]	KIAA0456 protein	KIAA1025 protein amphiphysin (Stiff-Mann syndrome with breast cancer	128kD autoantigen) ESTs inhibitor of growth family.	member 1 zinc finger protein 144 (Mel-	
Hs.89546	Hs.34853 Hs.27207		HS.35225 HS.14732	Hs.77225	Hs.32769	Hs.85266	Hs.50652 Hs 20196	Hs.5003	Hs.4084	Hs.173034 Hs.62774	Hs.46700	Hs.184669
Hs.89546	AA464856 Hs.34853 AA017133 Hs.27207		AA460149 HS.35225 N35825 HS.21043	AA478959 Hs.77225	AA001199 Hs.32769	AA485668 Hs.85266	Hs.50652	Hs.5003	Hs.13733	H06541 Hs.79045 AA114901 Hs.62774	Hs.46700	AA464421 Hs.25665
H39560	AA46485 AA01713		AA46014 N35825	AA47895	AA00118	AA48566	N91897	N31484	T72683	H06541 AA11490	N49419	AA46442
186132	789369 362628	100	795871	753987	362251	811096	306800	272155	108658	44164 491298	243358	809916
GF200	GF200 GF203	200	GF203	GF200	GF203	GF200	GF203	GF203	GF200	GF200 GF201	GF200	GF200

339.2793 1.24315062 339.2151 -2.4165821	339.1866 -1.8936758 339.0232 -1.1518888	338.8983 1.18119723	338.8846 -1.0374232 338.8383 -1.2420885	338.7209 1.061108 338.5662 -1.0188013	338.3337 1.043049 338.3311	338.2113 -1.609024 338.0354 -1.297307	337.932 -1.0653558	337.9112 337.758 1.00115393 337.6802 -1.0056151	337.6581 -1.3301415 337.6275 -1.141504 337.5755 1.17578187 337.5695 1.30319311
PABPC4	DOCK1	MPST	MAP3K8		АВНН	CXORF6 KIAA0071	PRIM1	APPBP1 MIG2	RYBP RDBP USP11
poly(A)-binding protein, cytoplasmic 4 (inducible form) PABPC4 ESTs Homo saniens mRNA for	spo 1		mitogen-activated protein Kinase Kinase Kinase 8 ESTs Homo saniens cDNA	FLJ10645 fis, clone NT2RP2005767, moderately similar to G.gallus PB1 gene ESTs		chromosome X open reading frame 6 KIAA0071 protein	primase, polypeptide 1 (49kD) PRIM1	amyloid beta precursor protein- binding protein 1, 59kD mitogen inducible 2 ESTs	Ring1 and YY1 binding protein RYBP ESTs RD RNA-binding protein RDBP ubiquitin specific protease 11 USP1
Hs.169900 Hs.167847	Hs.8117 Hs.47047 Hs.82295	Hs.74097	Hs.248 Hs.96487	Hs.179680 Hs.124230	Hs.109918 Hs.42599	Hs.20136 Hs.78398	Hs.82741	Hs.61828 Hs.75260 Hs.94012	Hs.7910 Hs.99745 Hs.106061 Hs.171501
AA486221 Hs.6867 T51004 Hs.111585	AA704323 Hs.119054 N52073 Hs.47047 W25727 Hs.82295	ťΩ	W56189 Hs.248 AA251733 Hs.96487	W01084 Hs.18460 N22824 Hs.124230	W38571 Hs.109918 N20968 Hs.42599	R08270 Hs.20136 AA456869 Hs.78398	AA025937 Hs.82741	AA126860 Hs.61828 AA490238 Hs.75260 N51589 Hs.94012	AA027856 Hs.111462 AA459114 Hs.99745 AA056390 Hs.106061 AA489498 Hs.103102
842820 76671	451055 282564 327150	000962	340630 684842	296883 265626	302591 265832	127197 815503	365641	502161 823756 280478	469685 814340 509484 843426
GF200 GF202	GF203 GF201 GF200	GF200	GF200 GF203	GF200 GF203	GF200 GF201	GF200 GF200	GF200	GF201 GF200 GF203	GF200 GF203 GF200 GF200

1.30319311	-1.5494977 -1.1408715	-1.600209 -2.6127292	-1.4899403	-2.5197438 1 27491512		1.32664067 -1.0547939 -1.530651	-1.0737625	1.02543941 -1.7395136 -1.8631666	-1.6301645
337.5695	337.5099 337.4732	337.4652 337.4445 337.4202	337.1717 337.1381 337.0874	336.7318	336.4449	336.4439 336.2057	336.1144	336.0306 335.9888 335.9727 335.9428	335.931
USP11	NCOR2	HSJ2	GUCA1A		GNAS1	KIAA0164	DEPP	PPP1CB HPR6.6 YDD19	-DLR
ubiquitin specific protease 11 (ONA Like		ate cyclase activator 1A	ESTs Homo sapiens mRNA; cDNA DKFZp761D0223 (from clone	_	sapiens cDNA 848 fis, clone 31732 164 gene product al protein induced by		ic subunit, beta isoform iterone binding protein protein	ow density lipoprotein receptor (familial hypercholesterolemia) LDLR
Hs.171501 ubiqu	Hs.120980 2 Hs.106200 ESTs	Hs.94 2 Hs.178398 ESTS Hs.171939 ESTS	•,	Hs.176674 ESTs Homo DKFZt DKFZt DKFZt	D.			Hs.21537 catalyt Hs.187555 ESTs Hs.90061 proges Hs.25615 YDD16	low o Hs.213289 (fam
AA489498 Hs.7832	T63031 Hs.76498 R63996 Hs.106200	AA490946 Hs.94 AA488871 Hs.99700 N51889 Hs.44671	φ φ	N33530 Hs.109085	AA035620 Hs.110382	R78505 Hs.20157 AA682624 Hs.54277 H21107 Hs.80338		726434 Hs.21537 AA701941 Hs.118361 359221 Hs.78801 361372 Hs.21824	AA489664 Hs.90593
843426 AA	80772 T6 139680 R6	824031 A/ 824856 A/ 282147 NE		270217 N3		143759 R7 431280 AA 173309 H2	_	132911 R2 435926 A/ 41698 RE 37980 R6	824332 A/
GF200	GF200 GF200	GF200 GF203 GF201	GF200 GF201 GF203	GF203	GF201	GF200 GF203 GF200	GF200	GF200 GF203 GF201 GF203	GF203

5	4.1	1004	C)	0	10.00	1	(1)	CO	0	0
APPE	2	×	_							

-2.2448084	-2.3423807	1.40398148	-1.9513612	-1.2603041 1.64369559			-1.6377473	1.26858706	-1.4159302	-1.2672962	-1.1740945	-1.5446427
335.919	335.8695	335.8608	335.837	335.8199 335.581	200 4700	335.47.08	335.4426 335.1865	335.0216	334.9686	334.9124 334.7766	334.6847	334.6642
KIAA0074			WNT2					LOC51061	VEGF	GYG2		
KIAA0074 protein Homo sapiens mRNA; cDNA DKF7n434M229 (from clone	DKFZp434M229) Homo sapiens HDCMD11P	mRNA, partial cds wingless-type MMTV internation site family member	ESTs, Weakly similar to !!!! ALU SUBFAMILY J	(H.sapiens)	Homo sapiens mRNA; cDNA DKFZp5640222 (from clone	ESTS, Weakly similar to LIPOAMDE ACYL TRANSFERASE COMPONENT PRECURSOR OF BRANCHED-CHAIN ALPHA-KETO ACID DEHYDROGENASE	COMPLEX [H.sapiens] ESTs	hypothetical protein vascular endothelial growth	factor	glycogenin 2	ESTs	ESTs
Hs.1192	Hs.31422	Hs.10724	Hs.89791	Hs.27542 Hs.269057		Hs.94795	Hs.36269 Hs.39982	Hs.275425	Hs.73793	Hs.58589	Hs.61272	Hs.24908
Hs.1192	AA417950 Hs.31422	Hs.10724	Hs.89791	Hs.27542 Hs.114388		Hs.94795	AA777399 Hs.36269 N29918 Hs.39982			Hs.58569	AA455099 Hs.61272	Hs.24908
N54344	AA41795	N52373	T99653	N68390 N35614		170352	AA777399 N29918	AA48904	R19956	W79445	AA45509	H77727
244767	767690	246041	122762	292392 272295		67067	449042	824943	34778	346997	812299	234617
GF200	GF203	GF200	GF200	GF200 GF203		GF201	GF203	GF203	GF200	GF202	GF203	GF200

1.56320192	1.56320192 1.20842806 -1.0449688 -1.9760456 1.06903752	-1.9774935	-1.3635126 1.25848808 1.36287747 -1.0774369	-1.0877317	1.00072871 -1.1326416 -2.1247791 1.48630341 -1.3531055 1.17711891
334.5027	334.5027 334.4089 334.0208 333.9528 333.8168	333.6586 333.6576	333.6535 333.495 333.4938 333.4431 333.3627	333.3349	333.2306 333.1401 333.1246 332.9388 332.9158 332.8392
DDX11	DDX11 KIAA0229 P40 MBP	PKM2	SNRPD1 KIAA1014	TMF1	TMF1 TBX3-iso HSPC207 FLJ20493
DEADM (Asp-Glu-Ala- Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) DEADM (Asp-Glu-Ala- Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like	helicase) KIAA0229 protein nucleolar protein p40 ESTs myelin basic protein	FULXIVES IN SOME KAT03458, Injuly similar to Z184, HUMAN ZINC FINGER PROTEIN 184 pyruvate kinase, muscle	Thornwareprotein Dr. Polypeptide (16KD) ESTs ESTs ENTman clone 23695 mRNA sequence KIAA1014 protein	ESTs TATA element modulatory factor 1 TATA element modulatory	factor 1 TBX3-iso protein ESTs EST hypothetical protein hypothetical protein
Hs.27424	Hs.27424 Hs.20060 Hs.74407 Hs.91147 Hs.69547	Hs.35820 Hs.198281	Hs.86948 Hs.34494 Hs.132956 Hs.90798 Hs.6834	Hs.176376 Hs.267632	Hs.267632 Hs.267182 Hs.98402 Hs.228019 Hs.75798 Hs.110916
AA402879 Hs.27424	AA402879 Hs.117894 N22435 Hs.20060 R45255 Hs.74407 AA700644 Hs.91147 H17696 Hs.69547	AA043772 Hs.35820 AA504507 Hs.6586	H16454 Hs.86948 H92176 Hs.34494 H56731 Hs.37244 R18935 Hs.90798 W57818 Hs.77369	AA678242 Hs.118870 AA252318 Hs.101580	AA252318 Hs.74985 738300 Hs.23352 AA425126 Hs.98402 168719 Hs.93297 V74340 Hs.75798 AA700090 Hs.110916
741841 +	741841 <i>F</i> 254625 <i>F</i> 22918 <i>F</i> 433538 <i>F</i> 50043 <i>F</i> 50043	486401 <i>F</i>	47542 H 195513 F 203910 H 33182 F 340949 V	431988 /	684940 137456 768602 211859 298716 7435415
GF200	GF200 GF200 GF200 GF203 GF200	GF203 GF203	GF200 GF200 GF200 GF200 GF200	GF203 GF200	GF200 GF200 GF203 GF200 GF203 GF203

1.18155734	-1.592902	-1.300185 -1.7259255	-2.5259158 -1.5017705	-1.5471688 -2.269691 -1.2360992 -1.1132149	-2.196244 -1.5601829 -1.7756054 1.0813244	-1.7134164 -1.179279
332.8167 332.7364	332.5322 332.4084 332.2326	332.2198 332.0592	331.9535 331.9376	331.9294 331.7133 331.5581 331.4967 331.4612	331.4502 331.3447 331.0244 330.8538	330.7858 330.5332
E		5G3	P 8	TNFRSF5 RENT1		
MNAT1 h BAD	9.	ATP5G3	EPHB4		Q a	e s
menage a trois 1 (CAK assembly factor) BCL2-antagonist of cell death ESTs, Moderately similar to	H. sapiens] ESTs ESTs ATP synthase, H+ transporting, mitochondrial F0	complex, subunit c (subunit s) isoform 3 ESTs Homo sapiens mRNA; cDNA DKFZA43461221 ffrom clone	DKFZp434G1221) EphB4	tumor necrosis factor receptor yeperfamily, member 5 ESTs ESTs ESTs regulator of nonsense transcripts 1 ESTs	Human Chromosome 16 BAC clone CIT987SK-A-101F10 ESTs ESTS EST EST Homo sapiens mRNA; cDNA Homo sapiens mRNA; cDNA	DKFZp434P1217 (from clone DKFZp434P1217); partial cds EST
Hs.82380 Hs.76366	Hs.234972 Hs.9403 Hs.25227	Hs.429 Hs.16727	Hs.23617 Hs.155227	Hs.25648 Hs.59821 Hs.31539 Hs.12719 Hs.165402	Hs.5320 Hs.44004 Hs.6700 Hs.122363	Hs.18271 Hs.117107
AA481759 Hs.82380 AA460291 Hs.76366	V73222 Hs.110295 T55592 Hs.9403 AA443920 Hs.25227	H47080 Hs.429 AA452244 Hs.16727	AA677212 Hs.23617 T51895 Hs.464	H98636 Hs.25648 AA054441 Hs.59821 AA676422 Hs.117508 AA156342 Hs.12719 AA677901 Hs.117092	N53445 Hs.47662 N29624 Hs.44004 H77398 Hs.6700 AA788641 Hs.122363	R63022 Hs.18271 AA678162 Hs.117107
AA4817 AA4602	N73222 T55592 AA44393	H47080 AA45224	AA67721 T51895	H98636 AA054441 AA676422 AA156342	N53445 N29624 H77398 AA78864	R63022 AA678162
810791 795729	246449 73561 756731	193106 786561	454128 75009	261519 381058 431597 590727	245273 257312 233183 1240283	139113 431948
GF200 GF201	GF200 GF201 GF203	GF200 GF203	GF203 GF200	GF200 GF203 GF203 GF201 GF201	GF200 GF203 GF200 GF203	GF200 GF203

1000	-1.5459166	-1 3886338	-1.0436787	2.57586109		1.31711121		-1.2047683	1.09149448	-1.6693157					1.19379537	-1.23/443/				-1.1120034	-1.6063048			-2.1870847	-1.0113669			-1.2274802
900	330.3315	330 3097	330.2207	330.0313		330.025	329.994	329.9629	329.9423	329.8495					329.7495	329.5171			329.5157	329.403	329.3634			329.2538	329.132	329.107		328.8453
			MTM1			LAMP2		DKFZP586I1023	HSU79252	PIBF1									CACNA1C		KIAA0650				LMNA			MAPK1
Homo sapiens cDNA FLJ20153 fis, clone COL08656, highly similar to AJ001381 Homo sapiens ncomplete CDNA for a	mutated allele ESTs	ESTs, Weakly similar to		ESTs	ysosomal-associated	rane protein 2	ESTs	OKFZP58611023 protein [hypothetical protein		Homo sapiens cDNA	FLJ10441 fis, clone	NI2RP1000/33, highly similar	O HUMAN MHINA IOL GOPTII-	TK protein	ESTs	calcium channel, voltage-	dependent, L type, alpha 1C	subunit	ESTs		Homo sapiens mRNA; cDNA	DKFZp43410812 (from clone	410812); partial cds	_ 	ESTs	mitogen-activated protein	kinase 1
	Hs.109805 m Hs.29282 E	E E		_	7	_	Hs.5170 E	Hs.111515 D	Hs.240062 h	_	_	ш:	Z ;	2	-	Hs.117323 E	O	0	Hs.89925 s	Hs.47447 E	Hs.8118 K	_	_	_	_	Hs.27857 E	_	Hs.66151 k
	Hs.109805 Hs.29282	110 24600	AA135133 HS./ 1622 AA491225 Hs 75302	Hs.52897		Hs.8262	Hs.5170	4A486836 Hs.44430	Hs.58151	Hs.43913					W94438 Hs.59523	AA699429 Hs.117323			AA136049 Hs.84987	V52151 Hs.47447	Hs.8118			Hs.5100	AA489582 Hs.77886	Hs.27857		Hs.75708
	W95682 R72632	44400100	AA130133 AA491225	H63760		N77754	N46427	AA486836	R85562	N59340					W94438	AA699429			AA136049	N52151	AA706967 Hs.8118			AA479781 Hs.5100	AA489582	H24327		W45690
	358333 156343	0,000	262249	208904		289615	279407	841278	180244	289939					358736	433257			502593	284383	451905			740554	897544	51747		323506
	GF200 GF203	000	GESON	GF200		GF200	GF201	GF200	GF200	GF203					GF200	GF203			GF201	GF203	GF203			GF200	GF200	GF201		GF200

-1.2274802	-1.6667281 -2.7418885		-1.3373596	1.12017433	1.11022292	-1.1306962	1.51815752	-1.1670587	-1.1519797	-2.3315579		1.11480111 -1.9034311 -1.2003668
328.8453	328.8326 328.8129	328.8004	328.5826	328.5049 328.4642	328.4393	328.2568 328.1669	327.9577	327.9428	327.8656	327.812	327.8108	327.6765 327.4646 327.4625
MAPK1		·		RFXAP DKFZP564A032		AC01		KIAA0753	MARS	BCL7A	GBF1	TFRC IFIT1 KIAA0989
mitogen-activated protein kinase 1 ESTs, Weakly similar to similar to acetyltransferases	[C.elegans] ESTs	ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHlorf? protein [C.elegans]	ESTs, Moderately similar to HERV-E integrase [H.sapiens] regulatory factor X-associated	protein DKFZP564A032 protein Homo sapiens cDNA FLJ20300 ffs, clone	HEP06465 Homo sapiens cDNA FLJ11082 fis, clone	PLACE1005206 aconitase 1, soluble	ESTs	KIAA0753 gene product	ESTs	B-cell CLL/lymphoma 7A golgi-specific brefeldin A-	resistance factor 1 transferrin receptor (p90,	CD71) interferon-induced protein 56 KIAA0989 protein
Hs.66151	Hs.20220 Hs.22279	Hs.14337	Hs.271956	Hs.24422 Hs.23889	Hs.106825	Hs.31792 Hs.154721	Hs.59729	Hs.28070	HS.119503 Hs.81474	Hs.211563	Hs.155499	Hs.77356 Hs.20315 Hs.92186
W45690 Hs.66151	AA488893 Hs.20220 R41782 Hs.22279	R17096 Hs.14337	AA699931 Hs.117356	AA057436 Hs.110267 AA421603 Hs.23889	AA700680 Hs.106825	H45192 Hs.31792 AA156988 Hs.82653	AA732915 Hs.59729	10	N51665 Hs.81474	AA281583 Hs.79060	AA102089 Hs.118827	N5981 Hs.118098 AA489743 Hs.85121 H93486 Hs.57423
323506	824896 30986	129862	435319	381067 739094	434952	176817 502355	399440	746069	280564	712426	489810	289652 823696 230274
GF200	GF203 GF203	GF201	GF203	GF200 GF203	GF203	GF203 GF201	GF203	GF203	GF203	GF203	GF201	GF203 GF200 GF200

-1.3665784	-1.8385212 1.0137693 -1.2712668 -1.3749111	-1.9744182	1.41200944	-1.7068595	-1.1502563	1.04212175	-1.0948459	1,43229944 -1,6566069 1,0053193
327.4458 327.3136	327.2578 327.169 327.1561 327.1399	326.8713	326.7985	326.723	326.6086 326.5859	326.1938	326.1769 325.9755	325.9655 325.8181 325.7513
PTPRT	VTI2	TCFL1 TRIP8	KLF1					GCSH
protein tyrosine phosphatase, receptor type, T ESTs vesicle-associated soluble NSF attachment protein	of S. cerevisiae VTI1) ESTs ESTs	transcription factor-like 1 thyroid hormone receptor interactor 8	Kruppel-like factor 1 (erythroid) KLF1 Homo sapiens mRNA; cDNA DKFZb43400227 (from clone	DKFZp434O0227) ESTs, Highly similar to retinoic acid-induced protein	[H.saplens] ESTs Homo sapiens cDNA FLJ10485 ffs. clone	NT2RP2000195 ESTs, Weakly similar to CELL-CYCLE NUCLEAR ALTOANTIGEN SG2NA	[H.sapiens] ESTs glycine cleavage system	carrier) ESTs ESTs
Hs.225952 Hs.6612	Hs.169206 Hs.18989 Hs.22829 Hs.233502	Hs.2430	Hs.37860	Hs.44787	Hs.49597 Hs.188620	Hs.107528	Hs.124199	Hs.77631 Hs.119059 Hs.90790
Hs.91603 Hs.6612	AA704511 Hs.129793 300826 Hs.18989 359960 Hs.22829 487795 Hs.114270	AA443950 Hs.2430 152320 Hs.9417	Hs.37860	Hs.44787	AA128005 Hs.49597 AA703114 Hs.114233	Hs.56750	Hs.108665 Hs.94966	728294 Hs.77631 4A676441 Hs.119059 722334 Hs.90790
R52794 H17135	AA704511 R00826 R59960 H87795	AA443950 T52320	H65733	N59295	AA128005 AA703114	T67558	H90964 W94105	R28294 AA676441 R22334
41647 51078	451098 123578 43009 220658	757165	211216	289794	501868 434822	22699	240702 358673	134748 431646 130895
GF201 GF203	GF203 GF200 GF203 GF203	GF203	GF200	GF203	GF201 GF203	GF200	GF200 GF200	GF200 GF203 GF200

	-1.0920814	-1,3718841		1.40805074		1.17986748	-1.1361/2	-1,3118235	1.22961704	1.48483166	1.1267121	1.22403845	1.31554904 -2.2004427	-1.0391147
325.6825	325.6791	325.5685	325.463	325.2229	325.1544	325.1408	325.0344 325.0144	324.8734	324.6422	324.594	324.5697	324.438	324.4336 324.3757	324.2555 324.0549
SLC22A1	POMT1	NUBP2	B4GALT1		M6PR	CHD2	BM-002	TLK1		PYCS	NRG1	ADARB1	TGA10	NDUFB4 CGI-02
solute carrier family 22 (organic cation transporter), member 1	ı-O- ısyttransferase 1	ESTS nucleotide binding protein 2 F coli MinD like)	:NAc beta 1,4- rase,		eceptor (cation dependent) N chromodomain helicase DNA		nypothetical protein ESTs	J-like kinase 1	ESTs, Highly similar to CGI- 128 protein [H.sapiens]	pyrroline-5-carboxylate synthetase (glutamate gamma- semialdehyde synthetase)		specific, B1 (homolog of rat RED1) Homo sapiens mRNA for	spo	(ubiquinone) 1 beta subcomplex, 4 (15KD, B15) N CGI-02 protein
8) HS.117367		HS.268886 1		. – –		~	Hs.5862 Hs 20787	_	Hs.9825	Hs 114366		Hs.85302	Hs.71109 Hs.158237	Hs.227750 Hs.33979
AA702013 Hs.117367	Hs.99654	H48389 HS.//802 AA427415 He 91619	4A284292 Hs 80881	Hs.35810	Hs.111507	Hs.81820	Hs.5862 Hs 20787		Hs.9825	AA143509 Hs 13048	Hs.434	AA489331 Hs.85302	Hs.94217 Hs.33182	AA704675 Hs.12283 V22901 Hs.33979
AA702013	R13777	H48389	AA284292	H94571	H96213	N75346	N73536 H94058	AA113429	AA490522 Hs.9825	AA143509	R72075	AA489331	R86953 H44722	AA704675 N22901
436135	26566	206986	327247	243194	251351	298833	295923	563451	824510	588500	155716	842939	197413 188388	450896 266712
GF201	GF200	GF200	GF201	GF200	GF201	GF200	GF200	GF200	GF203	GESOO	GF200	GF200	GF200 GF200	GF203 GF203

-1.1244941	-1.2613957	-1.1094745	-1.2549645 -1 7396664	-2.6175028		-1.351567		-1.1445679	1 0406004	-1.0406004	-1.1703551		-1.1471933	-1.1064264	-1.3200885	10000406	1.10000420	-1.418/300
324.0544	323.8864	323.8036	323.7712	323.5642		323.5433	323.3733	323.2602	0020	322.9798	322.9129	322.8582	322.7504	322.598/	322.588	322.5651	322.3280	322.0096
RGS7	PCMT1	F13A1	DPYD					RAD23A			FGB	1 IL13RA1	CD79A			ASGR2	L L S	
regulator of G-protein signalling 7 protein-L-isoasparlate (D- asparlate) O-	methyltransferase coagulation factor XIII, A1	polypeptide dihydropyrimidine	dehydrogenase	ESTs	Homo sapiens clone 23620	mRNA sequence Homo sapiens clone 25237	mRNA sequence RAD23 (S. cerevisiae)	homolog A	Homo sapiens cDNA EL11282 fis, clone PLACE1009476, weakly similar to PUTATIVE ATP- DEPENDENT RNA HELICASE TSEGIO1 IN	CHROMOSOME	fibrinogen, B beta polypeptide	interleukin 13 receptor, alpha 1 IL13RA1 CD79A antigen (immunoglobulin-associated	alpha)	ESIS	FOS-like antigen 2	asialoglycoprotein receptor 2	Interieron gamma receptor i	- G
Hs.79348	Hs.79137	Hs.80424	Hs.1602 Hs.178904	Hs.131711		Hs.90797	Hs.21902	Hs.180455	5	HS.155049	Hs.7645	Hs.250911	Hs.79630	HS.10300	Hs.155210	Hs.1259	HS.180866	HS.228601
Hs.79348	Hs.79137	AA448599 Hs.80424	AA428170 Hs.1602	Hs.131711		Hs.90797	Hs.21902	Hs.13172	200	AA/5/41/ Hs.24235	Hs.7645	AA443127 Hs.101445	Hs.79630	HS.10300	Hs.10461	Hs.1259	HS.//0//	HS.4/464
H23046	T68518	AA448599	AA428170 Hs.1602	W90575		R40970	H29227	N63941	7	AA/5/41/	H91815	AA443127	T87012	15/848	T58932	R98050	H11482	N5233/
51746	83363	785975	770957	417957		29063	52704	293921	5	39541/	241788	809495	115281	80699	77577	206795	4/900	28445/
GF200	GF200	GF200	GF200	GF203		GF200	GF201	GF200	,	GF203	GF200	GF201	GF200	GFZOZ	GF200	GF201	00215	GF202

-1.3288383	1.29412214	1.1922897	1.1922897		-1.1617331	-2.164705	70086801-	1.07063518		-1.3370471	1.46454981	-1.2001528	1.19606527			1.31729479		1.31729479	-1.9532504	-2.7792029		-1.6177653			-2.6091181		-1.7113575
321.8571	321.8111	321.7479	321.7479	321.6771 321.6756	321.6234	321.6147	321.6024	321.4497	321.4329	320.5196	320.3773	320.1796	320.1417	320.1024		320.0425		320.0425	319.9634	319.9292		319.7522	319.7291	319.5202	319.5002	319.4567	319.3114
TBXA2R	COX11	BTN3A3	BTN3A3				UKF2F434IZ16			KIAA0125		TDG		ARR3		EEA1		EEA1				VCAM1		HAT1		SID6-306	
thromboxane A2 receptor COX11 (yeast) homolog, cylochrome c oxidase	assembly protein	member A3	butyrophilin, subtamily 3, member A3	gene sequence	ESTs	ESTs	DRFZF434IZ IS protein Homo saniens mRNA for	KIAA1320 protein, partial cds	ESTs	KIAA0125 gene product	ESTs	thymine-DNA glycosylase	ESTs	arrestin 3, retinal (X-arrestin)	early endosome antigen 1,	162kD	early endosome antigen 1,	162kD	EST	ESTs	vascular cell adhesion	molecule 1	ESTs	histone acetyltransferase 1	ESTs	inorganic pyrophosphatase	ESTs
Hs.89887	Hs.241515	Hs.167741	Hs.167741	Hs.82837 Hs.105133	Hs.23625	Hs.63224	HS.49/25	Hs.117414	Hs.16374	Hs.38365	Hs.20103	Hs.173824	Hs.14453	Hs.308		Hs.2864		Hs.2864	Hs.23829	Hs.101007		Hs.109225	Hs.42585	Hs.13340	Hs.27519	Hs.5123	Hs.268686
AA039932 Hs.89887	AA457644 Hs.79392	AA478585 Hs.113894	AA478585 Hs.87497	H98812 Hs.111770 AA476221 Hs.97874	R35245 Hs.23625	AA055807 Hs.63224	AA39/906 HS.49/25	R22315 Hs.22942	9	H65343 Hs.38365	R08141 Hs.20103	AA490546 Hs.79023	N62269 Hs.14453	H86518 Hs.308		N66043 Hs.117783		N66043 Hs.2864	R27329 Hs.23829	AA707081 Hs.101007		H16637 Hs.75404	N35892 Hs.42585	AA625662 Hs.13340	R83161 Hs.80720	AA487586 Hs.5123	R37887 Hs.23859
485744	838716	753587	753587	262053	136772	510532	/26508	130868	428136	210368	127147	823614	290230	223274		293940		293940	132358	451598		49164	272548	745360	194399	841685	137653
GF200	GF200	GF200	GF200	GF201	GF200	GF202	GF203	GF200	GF201	GF200	GF200	GF200	GF200	GF201		GF200		GF200	GF200	GF203		GF200	GF201	GF201	GF200	GF201	GF200

1.53158748	-1.6497	-2.6329571	-1.0973784				-1.0298819			-1.2102336			-1.3167138	-1.8620643		-1.1940698		1.30716825				-1.2460475	-1.0625315	1.12891687		1.05875468			1.49046286			-1.1884375	
319.2019	319.0916	319.0307	318.9455				318.7797			318.759			318.5872	318.5749	318.4726	318.4529		318.4505			318.4433	318.39	318.2811	318.1058		317.9606			317.9436	317.7282		317.6093	
RASGRP1		KIAA0853	LAMA4											VCL				RCN1				KIAA0992	XRN2			SFRP4			ACADVL				
RAS guanyl releasing protein 1 (calcium and DAG-regulated)	ESTs	KIAA0853 protein	laminin, alpha 4	Homo sapiens cDNA FLJ10808 fis. clone	NT2RP4000879, weakly	similar to UBIQUITIN-	ACTIVATING ENZYME E1	Homo sapiens mRNA; cDNA	DKFZp762A1712 (from clone	DKFZp762A1712); partial cds	ESTs, Weakly similar to	coding sequence of pol	[R.norvegicus]	vinculin	ESTs	ESTs	reticulocalbin 1, EF-hand	calcium binding domain	ESTs, Weakly similar to	hypothetical protein	[H.sapiens]	KIAA0992 protein	5'-3' exoribonuclease 2	ESTs	secreted frizzled-related	protein 4	acyl-Coenzyme A	dehydrogenase, very long	chain	ESTs	ESTs, Highly similar to	unknown [H.sapiens]	
Hs.182591	Hs.87787	Hs.136102	Hs.78672				Hs.59838			Hs.120844			Hs.269098	Hs.75350	Hs.23751	Hs.38751		Hs.167791			Hs.49753	Hs.258812	Hs.268555	Hs.28313		Hs.105700			Hs.82208	Hs.11090		Hs.18282	
AA394197 Hs.118509	AA251418 Hs.87787	N62788 Hs.85846	R43734 Hs.78672				AA630292 Hs.59838			AA708054 Hs.120844			T70356 Hs.13200	AA486728 Hs.75350	R44564 Hs.23751	H68655 Hs.38751		AA457719 Hs.82826			T47625 Hs.49753	R10545 Hs.84504	AA028164 Hs.5900	R71190 Hs.28313		AA486838 Hs.105700			AA464163 Hs.82208	T62849 Hs.11090		W68127 Hs.18282	
725707	684738	289599	32609				855323			392703			67075	841203	34014	212325		810729			71312	128457	364840	142984		841282			810358	79576		343352	
GF203	GF203	GF203	GF200				GF203			GF203			GF200	GF200	GF201	GF200		GF200			GF201	GF200	GF200	GF200		GF200			GF200	GF201		GF200	

-1.7154495	-1.5697726	1 0400011	100047	-1.5821202	-1.5741395	-1.1678042	-1.7488166	-1.4674766	-2.9024306		-1.2674411						-1.0129679	-1.0861431			-1 025914		-1.7171697		1.30872568		-1.3898209
317.5051	317.0563	317.0484	1800:116	316.9904	316.8596	316.7247	316.7122	316.6755	316.6081		316.5304			316.4668			316.4611	316.3051		316.2799	316 1115		315.9287		315.7976	315./043	315.6991
	IKBKG			MAPK7	LOC51290						PHLDA1						SCYA13			ITGB3BP					PGD		
ESTs inhibitor of kappa light polypeptide gene enhancer in	B-cells, kinase gamma Homo sapiens clone 24628	mRNA sequence	mitogen-activated protein	kinase 7	CDA14	ESTs	ESTs	ESTs	ESTs	pleckstrin homology-like	domain, family A, member 1	ES IS, Weakly Similar to	hypothetical protein, similar to	[H.sapiens]	small inducible cytokine	subfamily A (Cys-Cys),	member 13	ESTs	integrin beta 3 binding protein	(beta3-endonexin)	receptor IH sapiens	ESTS, Moderately similar to ZINC FINGER PROTEIN 75	[H.sapiens]	phosphogluconate	dehydrogenase	ESIS	ESTs
Hs.23589	Hs.43505	Hs.159412	13.244934	Hs.3080	Hs.26813	Hs.117097	Hs.24131	Hs.23603	Hs.14562		Hs.82101			Hs.9414			Hs.11383	Hs.61364		Hs.82084	Hs 129959		Hs.50456		Hs.75888	HS.177155	Hs.121291
Hs.23589	Hs.43505	Hs.13440	US.94200	Hs.3080	Hs.28487	3 Hs.117097	Hs.24131	Hs.23603	AA282206 Hs.14562		AA258396 Hs.82101			Hs.9414			Hs.11383	AA678370 Hs.61364		AA043806 Hs.82084	AA423792 Hs 54849		AA278382 Hs.50456			Hs.44761	AA758152 Hs.121291
R23810	R56102	R39364	W02424	H39192	R64203	AA678006	H98714	R31154	AA282206		AA258396			T52311			T64134	AA678370		AA043806	AA493793		AA278382		AA59875	N72256	AA758152
131668	41072	24632	730041	175123	139593	431790	261609	134235	712884		667883			71977			80146	431863		487338	755494	; }	712499		897673	291342	396829
GF200	GF203	GF201	GFZ00	GF200	GF200	GF203	GF202	GF200	GF203		GF200			GF201			GF200	GF203		GF201	GE203	3	GF203		GF200	GF201	GF203

	-1.5827205	-1.3318703 1.31053112	1.11308121	-1.7298312 1.62892925 -1.0137771	-1.039043	-1.519909	-1.8801574	-1.8011902
315.3149 315.3149 315.2842	315.2326	315.1953 315.1809 315.1785	315.1264 315.0686 315.0403	314.8961 314.8177 314.4729 314.4704	314.4604 314.3654 314.1936 314.0694 313.9964	313.9231	313.5742 313.5545	313.4347
LOC51026	PITX2		DNASE1L3 PIM1	CANPX	RNF13 CALB1 UGDH RPL5	TRIP8 H2AFY	EGR3	BET3 IL1RN
ESTs, Moderately similar to KIAA0745 protein [H.sapiens] CGI-141 protein LESTs, Weakly similar to TYKi protein [M.musculus]	NA	DKFZp586L0120) ESTs ESTs ESTs	ribonuclease I-like 3 oncogene	ESTs calpain-like protease ESTs ESTs	ring finger protein 13 cabindin 1, (28kD) (UDP-glucose dehydrogenase tribosomal protein L5 FESTs thyroid hormone receptor	interactor 8 TRIP8 H2A histone family, member Y H2AFY	early growth response 3 ESTs similar to yeast BET3 (S.	
Hs.39292 Hs.62275 Hs.7155	Hs.92282	Hs.98314 Hs.39912 Hs.172635 Hs.140852	Hs.88646 Hs.81170 Hs.269147	Hs.33347 Hs.169172 Hs.20851 Hs.124918	Hs.6900 Hs.65425 Hs.28309 Hs.180946 Hs.181551	Hs.6685 Hs.75258	Hs.74088 Hs.97989	Hs.24391 Hs.81134
AA002072 Hs.39292 A69622 Hs.62275 H60298 Hs.107757	Hs.92282	Hs.11528 Hs.39912 Hs.24338 Hs.22135		Hs.33347 Hs.8260 Hs.20851 Hs.49066	441965 Hs.13461 188329 Hs.65425 762288 Hs.28309 AA027277 Hs.119735 A625765 Hs.13047	409113 Hs.6685 4A410295 Hs.97911	R39111 Hs.74088 AA405369 Hs.97989	AA429882 Hs.111187 T72877 Hs.81134
AA002072 R69622 H60298	T64905	R63342 H79046 H17960 R41725	T73558 AA071470 W02426	H63223 AA457330 W89074 N64794	R41965 H88329 R62288 AA027277 AA625765	H09113 AA410295	R39111 AA405369	AA429882 T72877
428067 142184 207838	66731	138592 233719 50405 31813	82738 366085 296170	208570 838676 417688 284620	31837 252663 139835 469235 745397	46286	26568 742899	780977
GF201 GF201 GF201	GF200	GF200 GF200 GF201	GF201 GF200 GF200	GF200 GF200 GF201 GF201	GF201 GF201 GF200 GF201 GF203	GF201 GF203	GF201 GF202	GF202 GF200

-1.2948668 -1.393979	-1.1656158 -2.5249882	-1.230867	-1.5771856	1.62531177	-1.358865	-1.1484682	-1.5904743	-1.2034835	1.00658684	1.18780424	-1.2278703
313.0904 312.7437	312.577 312.4619	312.287	312.0681	311.9268 311.7196	311.6697 311.6507	311.338	311.2667	311.2383	311.1948	311.0319 311.0266	310.7571
	PIP5K1C	FGF1	PRKRA	SPK	PDCD9	NR4A2	DYRK2			HARS	APG5L
ESTs, Weakly similar to cDNA EST EMBL.D38107 comes from this gene [C.elegans] ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTS ESTS	prospriate 5-milase, type 1, gamma ESTs	(acidic) protein kinase, interferon-	RNA dependent activator Symplekin: Huntingtin	interacting protein I ESTs	programmed cell death 9 ESTs	group A, member 2 dual-specificity tyrosine-(Y)-	kinase 2 ESTs, Highly similar to HIGH	HMGI-C [H.sapiens]	mRNA sequence ESTs Homo sapiens mRNA; cDNA	DKFZp434K0522) DKFZp434K0522) histidyl-tRNA synthetase	
Hs.184352 Hs.63335	Hs.275182 Hs.191219	Hs.75297	Hs.18571	Hs.107019 Hs.35574	ω.	Hs.82120	Hs.173135	Hs.271888	Hs.188882 Hs.106243	Hs.36727 Hs.77798	Hs.11171
Hs.11820 Hs.63335	Hs.1659 Hs.13868	Hs.75297	Hs.18571	Hs.97851 Hs.35574	Hs.114382 Hs.18501	Hs.82120	Hs.23845	Hs.2726	Hs.3857 Hs.106243	Hs.27818 Hs.2741	Hs.11171
H94469 Hs.11820 AA056697 Hs.63335	AA482251 Hs.1659 R07748 Hs.1386	AA015793 Hs.75297	AA460968 Hs.18571	H79566 N53453	N33236 Hs.11438 AA001611 Hs.18501	AA598611 Hs.82120	R63623	H98218	AA487218 Hs.3857 R69645 Hs.1062	N62965 H61209	N95381
243155 489216	840889 125828	360478	796132	239661 245299	270558 427806	898221	138737	261204	841314 141684	289734 236305	309092
GF200 GF202	GF200 GF200	GF200	GF202	GF201 GF200	GF203 GF201	GF200	GF200	GF200	GF201 GF200	GF201 GF200	GF200

-1.9676658		-1.0205852 -1.6202312	1.34721274			-1.2532337	-1.3647848	-1.2033057				-1.3421022		-1.0055595	1.27966189		1.33228822				-1.5151391			-1.0639917		-1.4390591	1.04264334	-1.5109081		1.20727777 -1.0959949
310.6807		310.6237 310.5782	310.5452		310.5449	310.3943	310.3763	310.3376				310.3312		310.3221	310.2999		310.1976		310.1023	309.9534	309.8205			309.5946		309.5262	309.5178	309.288		309.0383 308.3986
S100A2		RAB6	KIAA0956		ARNT							SFPQ		KNSL5	NID2		NAP1L4		MRJ		KIAA0286			RABGGTB		PSMB10				ARHG ANXA7
S100 calcium-binding protein A2	RAB6, member RAS	oncogene family FSTs	KIAA0956 protein	aryl hydrocarbon receptor	nuclear translocator	ESTs	ESTs	ESTs	splicing factor	proline/glutamine rich	(polypyrimidine tract-binding	protein-associated)	kinesin-like 5 (mitotic kinesin-	like protein 1)	nidogen 2	nucleosome assembly protein	1-like 4	MRJ gene for a member of the	DNAJ protein family	ESTs	KIAA0286 protein	Rab	geranylgeranyttransterase,	beta subunit	proteasome (prosome, macropain) subunit, beta type.	10	ESTs	ESTs	ras homolog gene family,	member G (rho G) annexin A7
Hs.38991		Hs.5636 Hs 4007	Hs.75478		Hs.166172	Hs.112062	Hs.120306	Hs.120090				Hs.180610		Hs.270845	Hs.82733		Hs.78103		Hs.181195	Hs.167661	Hs.14912			Hs.78948		Hs.9661	Hs.94560	Hs.23862		Hs.75082 Hs.78637
AA458884 Hs.38991		4A088745 Hs.5636	Hs.83434		Hs.91090	4A677224 Hs.112062	4A732787 Hs.120306	4A708109 Hs.120090				AA425853 Hs.91379		Hs.109616	4A479199 Hs.82733		Hs.78103		4A431203 Hs.106134	Hs.42754	Hs.14912			AA456028 Hs.78948		Hs.9661	Hs.94560	Hs.23862		Hs.75082 Hs.78637
AA45888		AA088745 N49107	R95887		T67552	AA67722	AA732787	AA708109				AA425850		H84244	AA479199		H92347		AA431200	N67792	T81399			AA456028		T53775	T97257	N67336		R76314 H15504
810813		511816	199286		66965	454232	399336	392544				773254		219709	754093		221808		782176	291523	109221			812155		22689	121420	286450		159118 49352
GF200		GF200	GF200		GF201	GF203	GF203	GF203				GF200		GF203	GF200		GF200		GF201	GF201	GF200			GF200		GF200	GF200	GF202		GF200 GF200

1.08365239	1 00085000	1.0000023	-1.2088155	-1.4018461	1.09211146	-1.5769197	1.05203153	-1.9450758	1.06866628	1.10959656	1.09333739	-1.5377496	-1.5107723	-1.2907882	-1.0232873	4 04050004	-1 405012		1.1416037	1 65800315	1.11872012	
308.3256	900	308.3230	308.2561	308.0144	307.8636	307.4909	307.4064	307.3436	307.2617	307.2383	307.0362	306.781	306.4423	306.4051	306.3927	0110	306.3552		306.3195	90E 1904	305 9115	
U2AF1	74 6	1	KRT10	MAP4K5) CAPZA2		DKFZP586P2219			TBG	LYPLA1	YDD19					2FP 103	j į	RSN	MBB4	KIAA0121	
U2(RNU2) small nuclear RNA auxillary factor 1 (nonstandard symbol)	U2(RNU2) small nuclear RNA auxillary factor 1 (non-	standard symbol) keratin 10 (epidermolytic hyperkeratosis; keratosis	palmaris et plantaris)	mitogen-activated protein Kinase kinase kinase 5 MAP4K5	capping protein (actin filament) muscle Z-line, alpha 2	ESTs	DKFZP586P2219 protein	ESTS Homo sapiens mBNA for	KIAA1223 protein, partial cds	thyroxin-binding globulin	lysophospholipase I	YDD19 protein	ESTs	ESTs	ESTs	zinc finger protein homologous	to Ztp103 in mouse	restin (Reed-Steinberg cell-	filament-associated protein)	membrane protein,	KIAA0121 gene product	
Hs.59271	41.0024	178c:su	Hs.99936	Hs.246970	Hs.75546	Hs.113140	Hs.16951	Hs.170131	Hs.28783	Hs.76838	Hs.12540	Hs.25615	Hs.23545	Hs.88917	Hs.24240		HS.155968	0000	Hs.31638	601	He 155584	10000
W90506 Hs.59271		W80506 HS.116576	AA428454 Hs.99936	AA708269 Hs.120795	AA083228 Hs.75546	4A703233 Hs.113140	391083 Hs.34363	367210 Hs.24689	323302 Hs.23479	T64901 Hs.76838		4A287318 Hs.22486	R32647 Hs.23545	4A281793 Hs.88917	773868 Hs.24240		AA42929/ HS.3/13	0.51.50.51.51.50.0	AA458868 Hs.31638	1000 Hz 4004	4450460 HS.1601	2000 1:511 000000
418126 W		4 8 20 W	772878 A	397635 A	549073 A		_	140830 R	131050 R	66721 Te	150314 H	701103 A	132017 R	712610 A	143208 R		768562 A		810802 A	000000		
GF200	0	GF200	GF200	GF203	GF200	GF203	GF200	GF200	GF200	GF200	GF200	GF203	GF200	GF203	GF200		GF200	20210	GF200	0001	01200	507

	-1.385979	0112#3/11	1.02340103		-1.0174511	-1.1114624	-2.6066014						1.15472716		1.47654808	1.24768758	-1.1348062	-1.6928545			1.16568317	1.34333632			-1.2059004	-1.012807		-1.3394761
100	305.9077	200.0013	305.7079		305.4343	305.3913	305.3571	305.2496					305.2109		305.0758	305.0734	305.0126	304.6045			304.5894	504.3316		304.4836	304.2556	304.1461		303.803
		SAAI						FN1					TNFRSF12		PSIP1	DAZ	NSAP1	FOXJ1						RAC1				
EST, Weakly similar to IIII ALU SUBFAMILY J WARNING ENTRY IIII		amylold A l	ESTs	Homo sapiens mRNA for	KIAA1378 protein, partial cds	ESTs	ESTs	fibronectin 1	tumor necrosis factor receptor	superfamily, member 12	(translocating chain-	association membrane	protein)	PC4 and SFRS1 interacting	protein 1	deleted in azoospermia	_	forkhead box J1	ESTs, Weakly similar to TRANSCRIPTION	INITIATION FACTOR TFIID	135 KD SUBUNIT [H.sapiens]	ESIS	ras-related C3 botulinum toxin	GTP binding protein Rac1)	ESTs	ESTs	ESTs, Weakly similar to	KIAA0775 protein [H.sapiens]
	Hs.117272	HS.181062	Hs.34345		Hs.107279	Hs.18978	Hs.33366	Hs.118162					Hs.180338		Hs.82110	Hs.70936	Hs.155489	Hs.93974			Hs.227699	HS.15550		Hs.173737	Hs.151334	Hs.23450		Hs.172466
	4A682599 Hs.117272	H25546 HS.315/	4A775763 Hs.34345		AA490901 Hs.107279	AA704749 Hs.18978	R83160 Hs.33366	V26285 Hs.108202					W76376 Hs.96093		AA228130 Hs.82110	AA133797 Hs.70936	R21425 Hs.106067	AA458533 Hs.93974			_	189283 HS.15550		AA626787 Hs.109141	_	N57555 Hs.23450		W69775 Hs.3974
;	450819	161456	878212		824525	451161	194395	256820					345586		862299	564962	130120	811600			221761	110436		877782	210523	279974		343932
	GF203	GF200	GF203		GF203	GF203	GF200	GF201					GF200		GF200	GF200	GF200	GF200			GF203	GF200		GF201	GF200	GF203		GF203

-1.9752138	-1.3589318 -1.4718112	-1.2176395		-1.4544964	1.12629728	1.08662547	-1.7436477	1.11755072		-1.5842179	1.23703218	-2.2992998
303.7657	303.6853	303.416	303.1306	303.0685	302.9952	302.8128	302.7942	302.5737 302.5668		302.5384 302.4637	302.438 302.4214 302.3557	302.3298
		XPA LISP15	2		PPP1R1A	PTGER3		ISYNA1 LMNB2			TCL1A	RAB2
ESTs, Weakly similar to acidrich protein [C.elegans] ESTs, Weakly similar to !!!! ALU SUBFAMILY SB2 MARNING FATTEY !!!!	[H.sapiens] H.sapiens polyA site DNA	xeroderma pigmentosum, complementation group A		COLF6543 protein phosphatase 1, regulatory (inhibitor) subunit	1A prostaglandin E recentor 3	(subtype EP3) ESTs, Weakly similar to zeste	[D.melanogaster] myo-inositol 1-phosphate	synthase A1 lamin B2	Homo sapiens cDNA FLJ20727 fis, clone	HEP13238 ESTs	T-cell leukemia/lymphoma 1A TCL1A ESTs ESTs	ESTs RAB2, member RAS oncogene family
Hs.21362	Hs.270202 Hs.4934	Hs.192803 Hs 23168	Hs.49367	Hs.57672	Hs.76780	Hs.170917	Hs.108788	Hs.264414 Hs.76084		Hs.239475 Hs.6363	Hs.2484 Hs.145526 Hs.24258	Hs.271597 Hs.78305
Hs.21362	Hs.107772 Hs.4934	Hs.296 Hs.48546	AA026666 Hs.49367	AA629844 Hs.57672	AA460827 Hs.76780	Hs.495	Hs.108788	Hs.24246 Hs.76084		Hs.23001 Hs.6363	Hs.2484 Hs.37364 Hs.24258	Hs.24576 Hs.78305
R72507	N75729 H48097	AA453300 Hs.296 N79180 Hs.4854	AA02666	AA629844	AA460827	AA406362 Hs.495	W90543	N57858 Hs.24246 AA456868 Hs.76084		R43541 W93510	R97095 H95358 R28267	R32996 T82414
156023	244329	788141	366590	884789	796268	753211	417905	247089 815501		32681 357091	200018 234469 134690	135426
GF200	GF200 GF200	GF200	GF201	GF203	GF200	GF200	GF203	GF201 GF200		GF201 GF200	GF201 GF200 GF201	GF200 GF200

-1.0727542	-1.3988221	-1.3988221	1.11566373	-1.312966	-2.14/3000		-1.1967847	-1.024885		-1.836102					1.00130169		-1.1100367	-1.5367134	-1.116714					-1.0384066		-1.0252955
300.1422 300.1201	300.0938	300.0938	300.0128	299.9489	299.7451		299.6506	299.5179		299.4067					299.3847		299.2552	299.222	299.108		299.0291	298.893		298.7314		298.6732
ID1 LOC51242	RYR2	RYR2	PRKAR2B	CACYBP			INFAIP3	TD02		CAPG							EDR2				GFBP3	KIAA0424		BET1		
inhibitor of DNA binding 1, dominant negative helix-loop- helix protein hypothetical protein	ryanodine receptor 2 (cardiac) R	ryanodine receptor 2 (cardiac) R protein kinase, cAMP- dependent, requlatory, type II,	_	lin binding protein	ESTS	umor necrosis factor, alpha-	_	enase		ilament), gelsolin-like C	Homo sapiens cDNA	FLJ10567 fis, clone	VT2RP2002980, weakly	similar to 30S RIBOSOMAL	PROTEIN S10	a	log of polyhomeotic 2)	ESTs	EST	nsulin-like growth factor			ane		Homo sapiens mRNA; cDNA DKFZb434L0816 (from clone	DKFZp434L0816); partial cds
ii C Hs.75424 Hs.12101	Hs.90821	Hs.90821			Hs.23786 Hs.49275	-	Hs.211600	Hs.183671 t	Ŭ	Hs.82422 f	_	_	_	0,5	Hs.28444 F			Hs.93126 E	Hs.119835 E	-	Hs.77326 t	Hs.54697	•	Hs.23103 t		Hs.10964
Hs.75424 Hs.12101	Hs.90821	Hs.117609	4A181500 Hs.77439	4A629849 Hs.27258	Hs.23786 Hs.49275		Hs.88888	Hs.77568		Hs.82422					Hs.28444		4A598840 Hs.75878	452198 Hs.93126	4A704603 Hs.119835		4A057620 Hs.30807	Hs.54697		Hs.23103		Hs.22707
AA457158 Hs.75424 AA418081 Hs.12101	R15791	R15791	AA181500	AA629849	AA400292 Hs.23/86 N66925 Hs.49275		AA476272 Hs.88888	T72422		AA486942 Hs.82422					R63812		AA598840	H52198	AA704603		AA057620	AA147072 Hs.54697		H54367		W79082
810485 767775	53099	53099	609663	884799	795723		770670	86220		841059					141316		898328	209683	450780		377051	588609		203351		346484
GF200 GF203	GF200	GF200	GF200	GF203	GF202 GF200		GF200	GF200		GF200					GF200		GF200	GF200	GF203		GF201	GF201		GF200		GF200

	-1.3362323 -1.530417	-1.0121269		-1.050664	1.0892033	-1.2720191			-1.7171686	1.0000011	1.00802894	1.33587074	-2.7708631
	298.5995 298.4236	298.271	297.8238	297.7625	297.7017	297.5826			297,5541	0565.782	297.1504	297.1046	296.9747
	IGF1R OIP2	DAG1		SCYE1	e PTPRZ1	CFLAR				4			s SIL C BAZ2A
Appropriate contraction of the c	insulin-like growth factor i receptor Opa-interacting protein 2	associated glycoprotein 1) Homo sapiens cDNA	FLZ0036 its, clone COL00219 small inducible cytokine subfamily E, member 1	(endotnellal monocyte- activating) protein tyrosine phosphatase,	receptor-type, zeta potypeptide 1 CASD8 and EADD-like	apoptosis regulator Human DNA sequence from	clone RP5-1103G7 on chromosome 20p12.2-13. Contains up to five unknown novel genes, the gene for a novel protein kinase domains	containing protein similar to phosphoprotein C8FW an the SOX22 gene for SRY (sex-	determining region Y)- putative chemokine receptor;	ESTS, Moderately similar to	NIMAU412 [n.sapieris] ESTs	ESTS	I ALT (SOL) interrupting locus bromodomain adjacent to zinc finger domain, 2A
	Hs.239176 Hs.274170	Hs.76111	Hs.32922	Hs.146401	Hs.78867	Hs.195175			Hs.28608	HS.13/555	HS.24870	Hs.30151	HS.277401
	300 Hs.2422 379 Hs.7590	AA496691 Hs.76111	45 Hs.93330	29 Hs.101854	AA476460 Hs.78867	AA453850 Hs.10853					92 HS.24870		нээ461 нs.1975 AA699460 Hs.113168
	148379 H13300 282720 N50079	755975 AA49	302997 N91145	182977 H43129	785148 AA47	813714 AA45							154999 H55461 433558 AA6994
	GF200 GF202	GF200	GF201	GF200	GF200	GF200			GF200	002.45	GF200	GF200	GF203

-2.3827878 1.48710766		1.2653446	1.08277403	-1.7411315	1 79/100966	1.70403000	-2.4585984	-1.2149376	1.01849199	-1.1713472	00000	-1.5480382	-1.7921836	-2.63217/1			-1.1868833	1.15117959				
296.4952 296.3423		296.3401	296.0282	295.8626	295.8363	280.7970	295.7048	295.6819	295.5815	295.5351	0	295.2682	295.0498	294.9922			294.9091	294.6599				294.5645
		SPOCK	rss	EIF4B	PAK2		KPNA1	RCD-8										NPP4B	!			
Homo sapiens clone B18 unknown mRNA ESTs	v and	proteoglycan (testican) Sanosterol synthase (2,3- oxidosqualene-lanosterol	ation			ESTs karyopherin alpha 1 (importin		autoantigen	ESTs	ESTs	ESTs, Highly similar to NY-	REN-37 antigen [H.sapiens]	ESTs	ESTs	ESTs, Moderately similar to DIHYDROOROTATE	DEHYDROGENASE	PRECURSOR [H.sapiens]	inositol polyphosphate-4- phosphatase type II 105kD		OVARIAN GRANULOSA	CELL 13.0 KD PROTEIN	HGR74 [H.sapiens]
Hs.91626 u Hs.94542 E	<i>w</i> ×	Hs.93029	Hs.93199	Hs.93379 f		Hs.35372 F	Hs.169149	Hs.75682	0			Hs.173684	Hs.40183	Hs.7968		_	Hs.125846	He 153687				Hs.47209
Hs.91626 Hs.94542		Hs.8122	AA434024 Hs.93199	AA016292 Hs.33779	Hs.107562	Hs.35372	4A180046 Hs.20008	AA481276 Hs.75682	Hs.112250	AA251339 Hs.87856		Hs.35039	Hs.40183	AA399216 Hs.7968			Hs.94925	37075	200			Hs.47209
N62311 N79558		AA436142 Hs.8122	AA434024	AA016292	H22412	R94840	AA180046	AA481276	N49389	AA251339		R93089	N41013	AA399216			W88472	100000	7001			N51315
287791 301678		754358	770355	361250	173561	275634	611956	815235	277621	684564		196849	277226	726421			417385	10000	100001			283089
GF203 GF200		GF200	GF200	GF203	GF201	GF200	GF200	GF200	GE203	GE203		GF200	GF202	GF203			GF200	0001	9225			GF201

1.01672153 -1.1292055 -1.0248076	1.23726059	-1.2032506 -1.5812509 -2.8833282	1.09822725	-1.1542065	-1.4039152 1.09882305 -1.5329392	1.03259929 1.03259929 -1.2309537
294.4331 294.4287 293.952	293.8544 293.7855	293.7354 293.4825 293.4274 293.3302	293.188 293.0608 293.0324 292.7262	292.521 292.5204	292.2977 292.2977 292.2884	292.1227 292.1227 292.1185
		H91620p KIAA1021	CHD2 SRPX	UBE4B	GNAL	TMF1 TMF1 DOCK2
ESTs, Moderately similar to 17- oeta-hydroxysteroid dehydrogenase type 7 M.musculus] ESTs	ESTs, Highly similar to CGI- 110 protein [H.sapiens] ESTs ESTs, Weakly similar to weak	(C.elegans) H91620p protein ESTs KIAA1021 protein	circonnodornain relicase DIVA binding protein 2 ESTs sushi-repeat-containing protein, X chromosome ESTs	ubiquitination factor E4B (homologous to yeast UFD2) ESTs guanine nucleotide binding prorolein (G protein), alpha activiting activity polycoptide.	olfactory type ESTs EATA element modulatory	factor 1 factor 1 factor 1 dedicator of cyto-kinesis 2
Hs.187579 Hs.163118 Hs.70834	Hs.177861 Hs.7133	Hs.23294 Hs.259842 Hs.23754 Hs.29189	Hs.36787 Hs.44382 Hs.15154 Hs.92195	Hs.24594 Hs.114135	Hs.154145 Hs.211516 Hs.29280	Hs.267632 Hs.267632 Hs.17211
Hs.9332 Hs.19963 Hs.17876	Hs.33937 Hs.7133	AA464689 Hs.23294 H64260 Hs.91620 H78863 Hs.23754 N74161 Hs.87401	AA025858 Hs.49338 V48827 Hs.44382 AA448569 Hs.15154 R67983 Hs.92195		AA487247 Hs.39748 W01603 Hs.110524 AA453250 Hs.29280	AA252318 Hs.101580 AA252318 Hs.74985 N70765 Hs.17211
N77671 R07444 T96780	H47450 H16600	AA46468 H64260 H78863 N74161	AA02585 N48827 AA44856 R67983	H56109 AA777855	AA487247 W01603 AA453250	AA25231 AA25231 N70765
247901 125589 121355	193546 49485	810220 210646 233318 298469	365778 279519 785933 138234	203547	841483 294682 795342	684940 684940 298118
GF200 GF200 GF200	GF200 GF203	GF201 GF200 GF200 GF203	GF201 GF201 GF200 GF200	GF200 GF203	GF202 GF200 GF202	GF200 GF200 GF200

ESTs, Weakly similar to	Hasioninator Professor Processor Pro	RAB3GAP 291.9043	RAN binding protein 3 RANBP3 291.7191 -2.9094262	ATPase, H+ transporting,	lysosomal (vacuolar proton	ptide,	56/58kD, isoform 1 ATP6B1 291.5557 -1.1815662	Ras suppressor protein 1 RSU1 291.4694 1.5066705	myosin, light polypeptide	kinase MYLK 291.3739 1.27840623	EST 291.3481 -1.2938385	ESTs, Weakly similar to hTcf-	4 [H.sapiens] 291.2995 -1.8464754	ESTs -1.3514723	ryanodine receptor 3 RYR3 290.8844	exostoses (multiple) 2 EXT2 290.8052 1.01842839	KIAA0480 gene product KIAA0480 290.738 -1.6672158	F-box protein Fbx9 NY-REN-57 290.7223	SCO (cytochrome oxidase	deficient, yeast) homolog 1 SCO1 290.6334 1.06765005	- 290.6065	putative N6-DNA-	transferase N6AMT1 290.4885	ESTs -1.3097358	protein phosphatase 2	(formerly 2A), regulatory	subunit A (PR 65), beta	isoform PPP2R1B 290.1493 1.00411371	basement membrane-induced	gene ICB-1 290.0772 -1.1660182	ESTs 290.024 -1.0001514	cell division cycle 34 CDC34 289.9388 1.17893026	
ŭ	Hs.24529 [H R,	_	Hs.176657 R/	∀ .	š			_	_	Hs.211582 kir	_	Ш	Hs.167507 4		Hs.9349 ry	Hs.75334 ex	Hs.92200 KI	Hs.11050 F-		Hs.14511 de		nd		Hs.221594 E8	Ē.)	ns	Hs.108705 isc	pq	Hs.10649 ge	Hs.219864 E8	Hs.76932 ce	
	Hs.24529	Hs.82510	Hs.106328				Hs.64173	Hs.75551		Hs.77310	Hs.47539		Hs.15483	Hs.12943	Hs.9349	Hs.75334	Hs.92200	Hs.49360		Hs.14511	Hs.7045		Hs.58580	Hs.120774				Hs.37518		Hs.10649	Hs.106010	Hs.76932	
	R76749	AA039231 Hs.82510	R44914				R73402	AA235332 Hs.75551		R06438	N52780		T84996	T66794	N45123	N78831	H91332	AA004484 Hs.49360		AA205413 Hs.14511	W74362		W79499	AA706858 Hs.120774				H57850		W21482	H71752	H20743	
	143919	486113	33881				156211	687397		126341	283401		111884	66316	282907	302292	241113	428476		646657	345090		347020	431425				205490		307255	213754	51328	
	GF200	GF201	GF203				GF200	GF200		GF200	GF202		GF200	GF200	GF201	GF200	GF200	GF201		GF203	GF200		GF202	GF203				GF200		GF200	GF200	GF200	

-1.2776246	1.10706107	-1.1239677	1.20345203	1.05376569	110/04/		1.08870175	-2.223127		-1.7002186	1.00287554		1.28425131					1.10911454	1 2196/50	000000	-2.9364093	-2.331018	-1.164878	-1.0020997		1.10177666
287.6458	287.6417	287.6075	287.5497	287.3677	287.3238		287.2643	287.1768		287.0675	287.0472	286.7949	286.6822		286.6661		286.3316	286.2847	7070 300	2007	286.2123	286.1588	286.1509	286.1316		286.0762
GJA1	KDELR2	MAP4K2	TAX1BP1	BUP	NAA 1203		ADTB2					KIAA0293	GYS2		ZNRD1		DGKZ		LCDCA	5			SEPP1	MMRN		LOC54453
gap junction protein, alpha 1, 43kD (connexin 43)	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	mitogen-activated protein kinase kinase kinase 2 Tax1 (human T-cell leukemia	virus type I) binding protein 1	BUP protein	ESTs	adaptor-related protein	complex 2, beta 1 subunit	ESTs	ESTs, Weakly similar to coded for by C. elegans cDNA	yk86e5.5 [C.elegans]	ESTs	KIAA0293 protein	glycogen synthase 2 (liver)	zinc ribbon domain containing,	-	diacylglycerol kinase, zeta	(104kD)	Homo sapiens CTL2 gene	ileat shock sond protein 1,	Epris 1	ESIS	ESTs	selenoprotein P, plasma, 1	multimerin	ras association (RaIGDS/AF-6) domain containing protein	JC265
Hs.74471	Hs.118778	Hs.82979	Hs.5437	Hs.35660	Hs.47099		Hs.74626	Hs.222830		Hs.146245	Hs.203933	Hs.12784	Hs.82614		Hs.57813		Hs.89981	Hs.105509	Us 100E22	11.00000	HS.381/0	Hs.35052	Hs.3314	Hs.268107		Hs.62349
AA487623 Hs.74471	T98559 Hs.3485	R35283 Hs.82979	ထ္ထ	R16964 Hs.106018	9/		V72918 Hs.74626	AA702720 Hs.114922		4A085713 Hs.103660	396206 Hs.44879	343605 Hs.12784	V72934 Hs.82614		AA464582 Hs.57813		4A458969 Hs.4882	R39578 Hs.105509	ACOUNT III DE SECES			392962 Hs.35052	4A070226 Hs.3314	4A423867 Hs.32934		R83224 Hs.62349
839101	123117	37234	898109	129748	502625		245853	383933		511218	197843	32697	245920		810575		810868	137581	00000	20007	208/80	196222	530814	759865		187147
GF200	GF200	GF200	GF200	GF200	GF201		GF200	GF203		GF202	GF200	GF201	GF200		GF201		GF201	GF200	0000	200	GFZ00	GF200	GF200	GF200		GF200

1.1422762 -1.7063513 1.26783876 -1.8702191 -1.1630079	-2.1239688 1.03365758 -1.4741642 -2.2224887	-1.2308562 -1.7870232 -2.4583701	-1,9279747 -1,9279747 -1,18750597 -1,126627 -1,7237974	-1.0780309	-2.3163014 -1.3237435 -1.2240879
285.9468 285.8943 285.8281 285.6716 285.4962 285.2665	285.1709 285.1684 285.0737 285.0428	285.0331 284.8968 284.8578	284.827 284.837 284.773 284.6664 284.5735	284.3329 284.263 284.2304 284.2304	283.8119 283.8003
MYD88	MCM6 DKFZP727A071 NOS2A	_	GUKI TOP1 MRC1 KIAA0251 DKFZP58611023	CDC25B	KRT13 KIA41067 RAB2
ESTS ESTS ESTS myeloid differentiation primary response gene (88) ESTS ESTS placental protein 11 (serine Proteinase) ESTS	minichromosome maintenance dericient (misS, S, pombe) 6 DKFZP727A071 protein nitric oxide synthase 2A (Inducible, hepatocytes)	high density lipoprotein binding protein (vigilin) ESTs ESTs	adunylate krinase 1 topoisomerase (DNA) 1 mannose receptor, C type 1 KIAA0251 protein DKFZP5861 (023 protein gannylate cyclase 1, soluble,	apria 3 cell division cycle 25B NAD(P) dependent steroid dehydrogenase-like; H105e3 ESTs	E. 23 KIA41067 protein RAB2, member RAS oncogene family
Hs.44373 Hs.56276 Hs.82116 Hs.58485 Hs.997 Hs.103395	Hs.155462 Hs.13036 Hs.193788 Hs.50492	Hs.277516 Hs.220821 Hs.24943	Hs.3764 Hs.317 Hs.75182 Hs.170218 Hs.111515	Hs.23480 Hs.153752 Hs.57698 Hs.100343	Hs.78305
N73563 Hs.44373 AA213669 Hs.56276 H38383 Hs.82116 W80709 Hs.58485 H04028 Hs.997 R25166 Hs.103395	N57722 Hs.114451 T67095 Hs.13036 AA877840 Hs.946 M00834 Hs.51490	AA457697 Hs.57090 AA703526 Hs.121046 R69244 Hs.24943	Hs.3764 Hs.317 Hs.75182 Hs.6558 Hs.14474	135579 Hs.23480 114343 Hs.106430 AA436425 Hs.57698 198083 Hs.93080	Hs.5000 Hs.5000 Hs.118759
N73563 AA213669 H38383 W80709 H04028 R25166	N5722 Hs.1144 T67095 Hs.1305 AA877840 Hs.946	AA457697 AA703526 R69244	AA490902 Hs.3764 AA223856 Hs.317 H16389 Hs.7518 T70487 Hs.6558 H15116 Hs.1447	N35579 N35579 H14343 AA436425	W23757 H30094 T82415
295997 683278 190887 415565 151662 131887	246659 66584 1160732	810703 450198 142090	824527 666425 4886 82976 49569	272238 272238 48398 756509	49919 327676 159166 79520
GF200 GF203 GF200 GF200 GF200 GF200	GF203 GF200 GF203	GF200 GF200 GF200	GF200 GF200 GF200 GF200	GF200 GF200 GF200 GF201	GF200 GF200 GF200

Westbrook et al.	k et al.				APPENDIXA		Atty	Atty Docket No. 21
GF201 GF203	795803 412927	AA45986! AA707728	AA459865 Hs.9501 AA707728 Hs.120851	Hs.109706 Hs.120851	ESTs, Moderately similar to HN1 [M.musculus] ESTs		283.7866 283.7037	-1.1881874
GF200	46916	H09997	Hs.90800	Hs.90800	(membrane-inserted)	MMP16	283.6039	-1.4171376
GF200	46916	H09997	Hs.113763	Hs.90800	(membrane-inserted)	MMP16	283.6039	-1.4171376
GF201 GF200	417251 212620	W87752 H70554	Hs.100594 Hs.82860	Hs.247433 Hs.219683	activating transcription factor 6 ATF6 ESTs Homo sapiens mRNA; cDNA	ATF6	283.5895 283.3549	-1.1265969
GF200 GF200	138929 110467	R62566 T89391	Hs.9396 Hs.117922	Hs.239870 Hs.139851	DKFZp564H0764 (from clone DKFZp564H0764) caveolin 2	CAV2	283.3412 283.2386	1.04567723 -1.4350848
GF200	80109	T63324	Hs.53875	Hs.198253	major histocompatibility complex, class II, DQ alpha 1 HLA-DQA1	HLA-DQA1	283.1982	2.37255261
GF200 GF200 GF201	80109 234664 143062	T63324 H77737 R71335	Hs.83231 Hs.39803 Hs 106172	Hs.198253 Hs.39803 Hs.122505	major histocompatibility complex, class II, DQ alpha 1 ESTs	HLA-DQA1	283.1982 283.0504 283.0281	2.37255261
GF200 GF203	503097	AA151486 R42569	AA151486 Hs.2910 R42569 Hs.22444	Hs.22444	phosphoribosyl pyrophosphate synthetase 2 ESTS ESTS HOME	PRPS2	283.005 282.88	-1.2324385 -1.848435
GF201	181541	H28681	Hs.21041	Hs.234074	Homo sapiens minus, cuns DKFZp761G02121 (from clone DKFZp761G02121); partial cds mannosidase alnha class 1A		282.8061	
GF200 GF201	112629 343380	T85698 W68845	Hs.2750 Hs.24095	Hs.2750 Hs.24095	member 1 ESTs	MAN1A1	282.7254 282.6463	-1.8281308
GF201 GF203	504689 454326	AA14917; AA67724(AA149172 Hs.55781 AA677240 Hs.100768	Hs.55781 Hs.100768	Homo sapiens cDNA FL/20604 fis, clone KAT06449 ESTs		282.3242 282.2704	-2.1851691

	-2.2494422	1.09052437	-1.0009613		-1.0009613	1 688428E	0074000	1.13593204				-1.3101649			.29364094	-2.7029915	1.2877092	1.8225918	1.9099777		-1.623524			1.0306579	1.05545586
	282.2231	282.0126 1.	281.9675 -1		281.9675 -1	981 7993			281.5903			281.5852 -1			281.3975 1.	281.1886 -2	280.7218 -1	280.5859 -1	280.521 -1		280.4256 -1	280.4142	280.3326	280.0902	279.8832 1.
																		D1335							
		CCR2	coL3A1	Φ.	COL3A1	_		ACADL				TCEB1			SNCA		KIAA0134	DKFZP434D1335						PLG	, GTF2A1
ESTs, Weakly similar to weak	[C.elegans]	receptor 2 collagen, type III, alpha 1	(Ehlers-Danlos syndrome type IV, autosomal dominant)	collagen, type III, alpha 1 (Ehlers-Danlos syndrome type	IV, autosomal dominant)	ESTs, Highly similar to VILLIN	acyl-Coenzyme A	dehydrogenase, long chain	ESTs	transcription elongation factor	B (SIII), polypeptide 1 (15kD,	elongin C)	synuclein, alpha (non A4	component of amyloid	precursor)	ESTs	KIAA0134 gene product	DKFZP434D1335 protein	ESTs	Homo sapiens cDNA FI.120080 fis. clone	COL03184	ESTs	ESTs	plasminogen	general transcription factor IIA, 1 (37kD and 19kD subunits)
	Hs.23294	Hs.395	Hs.119571		Hs.119571	Hs 239790		Hs.1209	Hs.31246			Hs.184693			Hs.76930	Hs.64313	Hs.151706	Hs.8258	Hs.22412		Hs.7942	Hs.183617	Hs.187554	Hs.75576	Hs.76362
	Hs.23909	Hs.395	Hs.67102		Hs.119571	He 3046		Hs.1209	Hs.31246			Hs.77939			4A455067 Hs.76930	Hs.12951	4A478078 Hs.64994	Hs.8258	4A399248 Hs.22412		Hs.7942	Hs.106158	Hs.15968	Hs.75576	Hs.2354
	R68473	H58254	T98612		T98612	AA876039 Hs 3046		R66006	N30327			W81684			AA455067	T66828	AA478078	N54049 Hs.8258	AA399248		AA402965 Hs.7942	N92699	W85812	T73187	T55801
	139217	204539	122159		122159	1161775		140131	258061			347373			812276	66333	739990	247240	726445		741790	306420	415961	82979	73381
	GF200	GF200	GF200		GF200	GF203		GF200	GF201			GF200			GF200	GF200	GF200	GF203	GF203		GF203	GF201	GF201	GF200	GF200

1.03621356 -1.2074214

1.03171197

-1.1048946 -2.3759634 -1.0828604

-1.0355829 -1.9204141

CCGGGG	GAMT 279.8775 279.446	inc ens] 279.3436 NA A	279.0663 279.0639 TLK2 279.0288	APP20 278.9008 278.8809	one 278.8489	MFAP1 278.7929 278.4865 278.3162	USP14 278.1421 DPYS 278.038	3 277.9444 1.3 1.0Gi	277.8127 277.6453 LMO7 277.5981
TOZOKO" BEKKEBED APPENDIXA	guanidinoacetate N- methyltransferase ESTs	ESTs, Weakly similar to zinc finger protein ZFY [H.sapiens] Homo sapiens mRNA; cDNA DKEZMAAO1 4729 ffrom close	DNT 2pt-040 1572 (1701) C DKFZp43401572) ESTs tousled-like kinase 2	precursor, S. cerevisiae) homolog ESTs Homo sapiens mRNA; cDNA	DKFZp564C1Z16 (Ifom c DKFZp564C1216) microfibrillar-associated	protein 1 ESTs ESTs ubiquitin specific protease 14	transglycosylase) dihydropyrimidinase ESTs. Weakly similar to	ankyrin [H.sapiens] Homo sapiens BAC 137K3 chromosome 8 map 8q24.3 containing part of gene for CGI 72 protein and part of	LiftOglobdini gene, comp sequence ESTs LIM domain only 7
	Hs.81131 Hs.114055	Hs.22879	Hs.194478 Hs.117102 Hs.57553	Hs.18747 Hs.183733	Hs.7822	Hs.61418 Hs.186823 Hs.25933	Hs.75981 Hs.10755	Hs.135560	Hs.18341 Hs.177726 Hs.5978
	AA521337 Hs.81131 AA701352 Hs.114055	R44816 Hs.22879	AA505067 Hs.22454 AA678088 Hs.117102 AA599008 Hs.57553	H71217 Hs.18747 AA206225 Hs.86251	AA281798 Hs.7822	R01323 Hs.61418 AA707686 Hs.119826 R11605 Hs.20854	T66018 Hs.75981 N73761 Hs.33836	AA148735 Hs.27284	AA481552 Hs.104405 AA489092 Hs.96553 AA005112 Hs.101311
k et al.	826138 435490	33839	825649 430722 897751	214577 645662	712624	123802 451751 130004	81599 297061	504761	815281 824994 429186
Westbrook et al.	GF200 GF203	GF203	GF203 GF203 GF200	GF200 GF203	GF203	GF200 GF203 GF200	GF200 GF200	GF201	GF203 GF203 GF201

1.68179621

1.2464611 -2.0510386 -1.7956704

-1.5596712

1.2599304

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	-2.949409		1.01877183			-1.0543317	-2.6905151		-1.4013597	1.45681208	-2.5876141	4 4 4 9 9 9 4 6	-1.1433340	-1.3198749	-1.3198749			-2.7532579	-1.0724113	-1.2032466	-1.5926892		1.16970088	-1.3782525
	277.5723	277.5602	277.454		277.2632	277.152	276.956	276.9461	276.7646	276.6634	276.6376	1077	2/6.4/61	276.3691	276.3691			276.1693	276.1662	275.9872	275.9037		275.7509	275.5625
	_OC51593	HSPF1	SPC18		TAF2E			RBP3		RBM6				IYR2	RYR2	000			RFC3				ARPC5	CDH13
arcanata rasistanca nrotain		heat shock 40kD protein 1 H signal peotidase complex		TATA box binding protein (TBP)-associated factor, RNA	polymerase II, E, 70/85kD T ESTs, Weakly similar to trg	R.norvegicus]	ESTs rotinol-binding protein 3			RNA binding motif protein 6 F		Chromosome 1 specific	transcript KIAA0491	ryanodine receptor 2 (cardiac) RYR2	ryanodine receptor 2 (cardiac) F	≣ Ω	WARNING ENTRY !!!!	H.sapiens]	acion o (acinario				complex, subunit 5 (16 kD) /	
greene		heat sl signal	(18kD)	TATA (TBP)	polyme ESTs,	[R.nor	ESTs	interstitial	7 ESTs		ESTs			ryanoc			WAR				_	actin r		
	Hs.111801	Hs.82646	Hs.9534		Hs.78865	Hs.93560	Hs.38123	Hs.857	Hs.269807	Hs.173993	Hs.50425		Hs.136309	Hs.90821	Hs.90821	US. 109320		Hs.15036	Hs.115474	Hs.226410	Hs.221894		Hs.82425	Hs.63984
	AA021127 Hs.102251	4A435948 Hs.100801	Hs.9534		Hs.106790	Hs.93560	Hs.38123	Hs.857	Hs.131844	Hs.9423	Hs.50425		Hs.35191	Hs.90821	Hs.117609	AA11553/ HS.51749		Hs.15036	Hs.115474	Hs.15848	Hs.38021		Hs.82425	Hs.63984
	AA021127	AA435948	AA465156 Hs.9534		R44112	N59738	H62842	AA011014 Hs.857	H82828	H50677	N74055		R93782	R15791	R15791	AA 1553/		N77368	N39611	T97616	H62166		W55964	R17717
	364077	730555	815040		33438	246749	208383	360854	199061	194364	296741		197791	53099	53099	491418		245885	277112	121661	208434		340558	31093
	GF203	GF201	GF203		GF201	GF200	GF200	GF201	GF203	GF200	GF200		GF200	GF200	GF200	GF201		GF200	GF203	GF200	GF200		GF200	GF200

Homo sapiens cDNA FLJ10975 fis, clone

	-2 0093781	100007	-1.1010255		-1.0273548	1.16058093	1.21273347	-1.4305356		-1.908449						-1.1338383	4 2500000	-1.5305395		-2.216724		-1.3324336		1.06016694	1.11764731		-1.0637568			-1.2042565		
	979 516	27.0.010	273.481		273.3615	273.2423	273.1687	273.15		272.9807			272.8994			272.5662	070 0444	1417.77	272.1545	271.9443	271.9253	271.7152	271.6828	271.3915	271.0302		270.2537			270.2239		270.1978
			RPS8		OPCML			p100		ITPR3							707127				YDD19						EEF1A1					
PLACE1001383, weakly	similar to ZINC-FINGER	PROTEIN OBI-D4	ribosomal protein S8	opioid-binding protein/cell	adhesion molecule-like	ESTs	ESTs	EBNA-2 co-activator (100kD)	inositol 1,4,5-triphosphate	receptor, type 3	Homo sapiens cDNA	FLJ20276 fis, clone	HEP02437	ESTs, Weakly similar to	predicted using Genefinder	[C.elegans]		myotubularin related protein i Milmin	ESTs	ESTs	YDD19 protein	ESTs	ESTs	ESTs	ESTs	eukaryotic translation	elongation factor 1 alpha 1	Homo sapiens cDNA	FLJ10105 fis, clone	HEMBA1002542	ESTs, Weakly similar to ORF	YGR101w [S.cerevisiae]
	115.074004	HS.Z/4Z04	Hs.151604		Hs.99902	Hs.220993	Hs.7740	Hs.79093		Hs.77515			Hs.270502			Hs.23047		HS.23200	Hs.26744	Hs.100343	Hs.25615	Hs.146310	Hs.8958	Hs.244461	Hs.88445		Hs.181165			Hs.93872		Hs.13094
		H65/59 HS.9Z158	AA490922 Hs.28968		R38201 Hs.99902	N59134 Hs.107153		젎		AA281753 Hs.7068			AA481757 Hs.49499			AA630221 Hs.23047		AA490610 Hs.23200	H16989 Hs.26744			AA159994 Hs.55825	T49236 Hs.8958		AA281719 Hs.88445		AA490609 Hs.3717			AA775273 Hs.93872		AA131464 Hs.108282
	007077	140422	824553		23878	287633	247655	361048		712466			810785			855143		824124	50130	231944	264162	592771	67330	221561	712388		824122			878615		503737
	0	GF200	GF203		GF200	GF203	GF200	GF200		GF203			GF201			GF203		GF203	GF201	GF203	GF201	GF202	GF201	GF203	GF203		GF203			GF203		GF201

-1.2692621	-1.9871004 1.13054951 -1.4619425	-1,2609921 -2.1960897	-1.5340525 -1.6081978		-1.4613433	-1.1835622 -1.4653457	-1.0785881	-2.5056995 -2.0358076 -1.6762902 -1.8252106	1.0505
270.0059	269.6397 269.6308 1 269.2178	269.0501 269.009 268.9811 268.6164	267.8602 267.5419 267.2745	267.1142	266.4323 265.8689 265.7486			264.2929 263.3239 263.2801	
	VAMP5		FOSL1	RBBP1	HSU79275		EIF4B	YDD19 NTPBP	
ESTs	Φ.	ESI Is, Weakly similar to Prit homolog [H.saplens] ESTs, ESTs, Weakly similar to ORF ESTs, Corevisiae] ESTs	Homo sapiens cDNA FLJ11346 fis, clone PLACE1010900 ESTs FOS-like antigen-1	ESTs, Highly similar to 45kDa splicing factor [H.sapiens] retinoblastoma-binding protein	ESTs hypothetical protein ESTs	ESTs ESTs eukaryotic translation initiation	factor 4B ESTs ESTs	YDD19 protein putative ATP(GTP)-binding protein ESTS	ESIS
Hs.171637	Hs.74669 Hs.21887 Hs.41167	Hs.111650 Hs.21236 Hs.21943 Hs.186572	Hs.274434 Hs.119878 Hs.4245	Hs.107001 Hs.91797	Hs.269246 Hs.27414 Hs.21627	Hs.131860 Hs.26418	Hs.93379 Hs.23987 Hs.29397	Hs.25615 Hs.18259 Hs.96607	Hs.22144/
N21514 Hs.22455	AA521036 Hs.74669 AA504513 Hs.21887 AA405245 Hs.41167	AA046328 Hs.24213 R44930 Hs.21236 AA205969 Hs.21943 N51296 Hs.47222	2 4	AA446021 Hs.111855 AA128328 Hs.91797	AA057433 Hs.117933 N39071 Hs.27414 H06154 Hs.21627		AA454988 Hs.57621 AA454675 Hs.23987 N51367 Hs.29397	ഹ ത	H85855 Hs.33592
266019	826355 825363 712361	376767 34096 645368	502689 451804 251591	781026	381064 276469 44154	302873	811916 809652 283208	624785 712360	222559
GF203	GF203 GF203 GF203	GF201 GF201 GF203 GF203	GF203 GF203 GF201	GF201	GF203 GF201 GF201	GF203 GF203	GF203 GF201 GF203	GF203 GF203 GF203	GF203

1.21400969 2.1233143 1.03828878 -1.8647426 -1.8513282 -1.8278577 1.06078697 -1.0920428 -1.1203865 -1.0196268 -1.7525232 -1.7488003 1,7065978 -2.2360891 -1.2628571 1.4787623 1.1651354 1.358761 258.8718 258.5162 258.0104 257,8665 257.8519 257.6242 257,4245 260.3912 259.9379 259,7358 259.2596 258.3831 262,9343 260.9803 260.7194 260.4045 259.9577 258.513 263.0106 261,6961 261.0431 260.4764 DOMONION GANNON KIAA0766 FGF12B 3M-005 ACOX2 CPNE6 YDD19 synovial sarcoma, translocated acyl-Coenzyme A oxidase 2, ibroblast growth factor 12B ESTs, Weakly similar to Chromosome 1 specific <IAA0766 gene product</p> APPENDIX A (IAA0423 [H.sapiens] copine VI (neuronal) transcript KIAA0491 nypothetical protein o X chromosome oranched chain YDD19 protein ESTS STS ESTS ESTs ESTs ESTS ESTS ESTS ESTS STS ESTS **ESTs** ESTS STS 4s.191959 4s.136309 4s.173001 4s.114432 Hs.193689 Hs.104572 4s.173095 4s.119508 4s.125058 4s.183001 Hs.278437 Hs.28020 4s.88349 4s.153221 4s.20800 4s.20707 4s.18631 4s.25615 4s.88602 4s.6132 4s.7967 4s.9795 Hs.6647 AA001861 Hs.125058 AA678183 Hs.125776 Hs.114432 4A491212 Hs.104441 AA504346 Hs.104572 AA017706 Hs.118451 AA485732 Hs.119508 AA045342 Hs.20800 AA005350 Hs.20707 AA465374 Hs.24481 AA465238 Hs.28020 AA259131 Hs.88349 AA252470 Hs.50418 AA465239 Hs.88602 AA292065 Hs.88057 Hs.27430 AA465147 Hs,10257 Hs.52871 AA676931 Hs.18631 Hs.6132 Hs.9795 AA477250 Hs.6647 AA777493 Hs.7967 N52946 H11051 144861 159206 71782 487152 824062 069989 825464 739457 176904 430844 815034 428377 283695 460163 685019 814227 725394 428131 314114 88695 449126 361363 311146 314225 5450 Westbrook et al. GF203 GF201 3F201 3F201

APPENDIX A

-1.0815013 -2.0455282 -1.1652611 -1.7941792 -1.8633787 -1.0740958 256.4848 254.1273 253.7948 253.3104 253.2613 256.8247 255.0542 254.9199 254.2972 253,3908 KIAA1033 KIAA0256 HMGCS2 TMEFF1 HSGT1 MAF EGF-like and two follistatin-like clone 889N15 on chromosome chromosome 22q13.32-13.33. Kq22.1-22.3. Contains part of novel genes or pseudogenes, he gene for a novel forkhead Human DNA sequence from Thymocyte Marker CTX, the Human DNA sequence from oossibly alternatively spliced (forkhead box D4, FREAC5) ransmembrane protein with he gene for a novel protein subunit p28 (Ankyrin repeat similar to X. Iaevis Cortical 3-hydroxy-3-methylglutaryl-Contains (part of) up to six suppressor of S. cerevisiae y-maf musculoaponeurotic gene for 26S Proteasome phosphoglucomutase like Soenzyme A synthase 2 protein similar to FOXD4 KIAA0256 gene product slone RP11-395L14 on ibrosarcoma (avian) the gene for a novel polomor homolog KIAA1033 protein (mitochondrial) domains 1 ESTS protei 4s.118978 Hs.193514 Hs.59889 Hs.19673 Hs.8763 Hs.12144 Hs.78531 Hs.30250 Hs.71440 Hs.7535 AA707696 Hs.106190 AA633872 Hs.118978 AA520982 Hs.104414 Hs.113927 Hs.30250 AA131471 Hs.71440 AA701351 Hs.19673 AA496149 Hs.59889 Hs.8763 AA262727 Hs.9591 N34436 70892 N40940 686100 858181 757222 826266 503760 277165 277414 412881 435488 83999 GF203 GF203 GF203 GF203 3F201 3F201 GF201 GF203 GF203 GF201

APPENDIX A

-1,7108862 -1,4743619 -1,0985749	1.08524063		-2.401652 -1.5480121	-1.5291404	-1.0280079 -2.4847094 -1.6419925	10000
252.8022 252.1992 251.8267 251.6617	251.4572 250.8966	249.9407	249.7889 249.55 249.2663 248.7266 247.8851	247.2854 246.606 246.0548	245.3862 243.7417 243.3876 242.5881	241.0114
MRS1		UTRN	KIAA0737	RCN1		<i>ي</i>
ESTs MRS1 protein ESTs ESTs Homo sapiens mRNA; cDNA	DKF2p58611518 (from clone DKF2p58611518) ESTs ESTs, Highly similar to very long-chain acyl-CoA	[H.sapiens] utrophin (homologous to dystrophin) Homo sapiens clone 25020	mFNA sequence ESTs ESTs KIAA0737 gene product	reticulocalbin 1, EF-hand calcium binding domain ESTs Homo sapiens HDCKB03P mRNA, partial cds	Homo sapiens cDNA FLJ10348 lts, clone NT2RM2001065 ESTs ESTs	ESTs Human phosphatidylinositol (4,5) bisphosphate 5- phosphatase homolog mRNA, partial cds
Hs.28890 Hs.30985 Hs.186837 Hs.11006	Hs.21739 Hs.13500	Hs.49765 Hs.17401	Hs.62119 Hs.42679 Hs.17667 Hs.194035 Hs.18343	Hs.167791 Hs.43691 Hs.7953	Hs.6671 Hs.54547 Hs.27039 Hs.191389	Hs.25156
AA430410 Hs.28890 AA428957 Hs.115479 AA758470 Hs.121085 T62068 Hs.11006	AA287917 Hs.21739 AA131934 Hs.13500	AA412064 Hs.49765 W84486 Hs.107574	H16514 Hs.62119 N81017 Hs.42679 AA156032 Hs.17667 W86221 Hs.20837 AA034014 Hs.18343	AA453460 Hs.110822 N62171 Hs.106235 AA101072 Hs.7953	AA491222 Hs.6671 AA207165 Hs.54547 W93682 Hs.27039 AA676227 Hs.118350	N22766 Hs.42419 R36587 Hs.92997
769947 769754 431029 85660	701371	731426 35 6 732	49481 301043 590145 416419 430004	795159 287665 549911	824061 682713 357285 431511	266631
GF203 GF203 GF203 GF201	GF203 GF201	GF201 GF201	GF203 GF201 GF203 GF201	GF201 GF203	GF203 GF203 GF201 GF201 GF203	GF203

Atty Docket No. 2172		-2.270666	-1.5775813	-1.6452373	-1.4292745	-2.1131155	1.11747199	-1.3929123	-1.8308693
Atty	240.2281	239.4595	238.7909	238.1747	235.9678	235.6555	235.6145	235.0859	234.6351
0000	KIAA0937						NET-6		
TOZOZO'86ZZ6860 APPENDIXA	KIAA0937 protein ESTs. Weakly similar to DEC1	[H.sapiens] Homo sapiens cDNA FI. 11029 fis. clone	HEMBB1000136	ESIS	ESTs	EST	tetraspan NET-6 protein	ESTs	Human DNA sequence from done RP1-200k2 on chorn RP1-200k2 on chromosome 6d24. Contains the gene for a novel protein smillar to yeast and bacterial cytosine dearminase, a possible pseudogene similar to per or Tubulin beta chain, the PEX3 gene for peroxisomal biogenesis facto
	Hs.62264	Hs.33829	Hs.274415	Hs.264347	Hs.132659	Hs.119778	Hs.102737	Hs.33024	Hs.119976
	AA043790 Hs.18336	AA279980 Hs.33829	AA490828 Hs.12659	N59251 Hs.109378	AA707066 Hs.119989	AA703625 Hs.119778	W86202 Hs.11663	H40886 Hs.33024	32
k et al.	487151	712544	824312	289534	451570	450338	416374	175968	451654
Westbrook et al.	GF201	GF203	GF203	GF203	GF203	GF203	GF203	GF203	GF203

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